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<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
INVOLVED IN HOMEOSTASIS AND ADAPTATION

<130> BGI-132CP

<140> 09/603124

<141> 2000-06-23

<150> US 60/141031

<151> 1999-06-25

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<223> RXA02702

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Val Thr Thr Pro His
1 5
ttg gat tct gca caa gat att gat ctg tcc cgc gtc cac ctc atc ggt 163
Leu Asp Ser Ala Gln Asp Ile Asp Leu Ser Arg Val His Leu Ile Gly
10 15 20
att ggc gga gcc gga atg tct ggc gtt gcc cga atc ctg ctt gcc cgc 211
Ile Gly Gly Ala Gly Met Ser Gly Val Ala Arg Ile Leu Leu Ala Arg
25 30 35
ggg aag aca gtc act ggt tcc gat gcc aaa gat tcc cgc acc ttg ctt 259
Gly Lys Thr Val Thr Gly Ser Asp Ala Lys Asp Ser Arg Thr Leu Leu
40 45 50
cca ctc cgc gcc gtg gga gcc acc atc gca gtg gga cac gct gcg gaa 307
Pro Leu Arg Ala Val Gly Ala Thr Ile Ala Val Gly His Ala Ala Glu
55 60 65
aac ctt gag ctt tcc ggc gaa ctt ccc acc gtc gtg gtg acc tct ttt 355
Asn Leu Glu Leu Ser Gly Glu Leu Pro Thr Val Val Val Thr Ser Phe
70 75 80 85
gcc gcc att ccg caa gac aac ccg gaa ctt gtt cgt gca cgt gaa gaa 403
Ala Ala Ile Pro Gln Asp Asn Pro Glu Leu Val Arg Ala Arg Glu Glu
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Gly Ile Pro Val Ile Arg Arg Ser Asp Leu Leu Gly Glu Leu Leu Glu	
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ggc tcc acc cag gtc ttg atc gcg ggt acc cac ggt aag acc tcc acc	499
Gly Ser Thr Gln Val Leu Ile Ala Gly Thr His Gly Lys Thr Ser Thr	
120 125 130	
acc tct atg tct gtg gta gct atg cag gca gcg ggc atg gat cca agc	547
Thr Ser Met Ser Val Val Ala Met Gln Ala Ala Gly Met Asp Pro Ser	
135 140 145	
ttt gct atc ggc gga cag ctc aac aag gct ggc acc aat gcg cac cat	595
Phe Ala Ile Gly Gly Gln Leu Asn Lys Ala Gly Thr Asn Ala His His	
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Gly Thr Gly Glu Val Phe Ile Ala Glu Ala Asp Glu Ser Asp Ala Ser	
170 175 180	
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Leu Leu Arg Tyr Lys Pro Asn Val Ala Val Val Thr Asn Val Glu Pro	
185 190 195	
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Asp His Leu Asp Phe Phe Lys Thr Pro Glu Ala Tyr Phe Gln Val Phe	
200 205 210	
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Asp Asp Phe Ala Gly Arg Ile Thr Pro Asn Gly Lys Leu Val Val Cys	
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Leu Asn Asp Pro His Ala Ala Glu Leu Gly Glu Arg Ser Val Arg Lys	
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Gly Ile Lys Thr Val Gly Tyr Gly Thr Ala Asp Ala Val Gln Ala His	
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Pro Glu Val Pro Ala Met Ala Thr Ile Val Asp Ser Gln Val Val Ala	
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Glu Gly Thr Arg Ala Thr Ile Asn Ile Asp Gly Gln Glu Val Ser Val	
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Ile Leu Gln Ile Pro Gly Asp His Met Val Leu Asn Gly Ala Ala Ala	
295 300 305	
ctg ctg gcc gga tac ctg gtg ggt ggg gac gtc gac aag ctt gtt gaa	1075
Leu Leu Ala Gly Tyr Leu Val Gly Gly Asp Val Asp Lys Leu Val Glu	
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Gly Leu Ser Asp Phe Ser Gly Val Arg Arg Arg Phe Glu Phe His Gly	
330 335 340	
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Ala Ile Glu Gly Gly Lys Phe Asn Gly Ala Ala Ile Tyr Asp Asp Tyr
 345 350 355

gca cac cac cca acg gaa gta act gca gtg ctc agc gct gcg cgc acc 1219
 Ala His His Pro Thr Glu Val Thr Ala Val Leu Ser Ala Ala Arg Thr
 360 365 370

cgg gtg aag gcc gct gga aag ggc cgt gtc atc gtc gcg ttc caa cca 1267
 Arg Val Lys Ala Ala Gly Lys Gly Arg Val Ile Val Ala Phe Gln Pro
 375 380 385

cat tta tac tca cgc acc ata gaa ttc caa aag gag ttc gcg ggg gca 1315
 His Leu Tyr Ser Arg Thr Ile Glu Phe Gln Lys Glu Phe Ala Gly Ala
 390 395 400 405

ctg tca ctg gca gac gct gcc gtg gtg ctt gag att tac gga gcg cgc 1363
 Leu Ser Leu Ala Asp Ala Ala Val Val Leu Glu Ile Tyr Gly Ala Arg
 410 415 420

gaa caa ccg gtg gat ggc gtg tcc tcg gaa atc atc acc gat gcg atg 1411
 Glu Gln Pro Val Asp Gly Val Ser Ser Glu Ile Ile Thr Asp Ala Met
 425 430 435

acc att cca gtg gtg tac gaa cct aat ttc tct gca gtc cca gaa cgc 1459
 Thr Ile Pro Val Val Tyr Glu Pro Asn Phe Ser Ala Val Pro Glu Arg
 440 445 450

att gca gaa atc gca gga cct aat gac atc gtg ctc acc atg ggt gca 1507
 Ile Ala Glu Ile Ala Gly Pro Asn Asp Ile Val Leu Thr Met Gly Ala
 455 460 465

ggg tcc gtg acc atg ctt gct cca gaa atc ctg gat cag ctg caa aac 1555
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<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45

Ser Arg Thr Leu Leu Pro Leu Arg Ala Val Gly Ala Thr Ile Ala Val
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Gly His Ala Ala Glu Asn Leu Glu Leu Ser Gly Glu Leu Pro Thr Val
 65 70 75 80

Val Val Thr Ser Phe Ala Ala Ile Pro Gln Asp Asn Pro Glu Leu Val
 85 90 95
 Arg Ala Arg Glu Glu Gly Ile Pro Val Ile Arg Arg Ser Asp Leu Leu
 100 105 110
 Gly Glu Leu Leu Glu Gly Ser Thr Gln Val Leu Ile Ala Gly Thr His
 115 120 125
 Gly Lys Thr Ser Thr Thr Ser Met Ser Val Val Ala Met Gln Ala Ala
 130 135 140
 Gly Met Asp Pro Ser Phe Ala Ile Gly Gly Gln Leu Asn Lys Ala Gly
 145 150 155 160
 Thr Asn Ala His His Gly Thr Gly Glu Val Phe Ile Ala Glu Ala Asp
 165 170 175
 Glu Ser Asp Ala Ser Leu Leu Arg Tyr Lys Pro Asn Val Ala Val Val
 180 185 190
 Thr Asn Val Glu Pro Asp His Leu Asp Phe Phe Lys Thr Pro Glu Ala
 195 200 205
 Tyr Phe Gln Val Phe Asp Asp Phe Ala Gly Arg Ile Thr Pro Asn Gly
 210 215 220
 Lys Leu Val Val Cys Leu Asn Asp Pro His Ala Ala Glu Leu Gly Glu
 225 230 235 240
 Arg Ser Val Arg Lys Gly Ile Lys Thr Val Gly Tyr Gly Thr Ala Asp
 245 250 255
 Ala Val Gln Ala His Pro Glu Val Pro Ala Met Ala Thr Ile Val Asp
 260 265 270
 Ser Gln Val Val Ala Glu Gly Thr Arg Ala Thr Ile Asn Ile Asp Gly
 275 280 285
 Gln Glu Val Ser Val Ile Leu Gln Ile Pro Gly Asp His Met Val Leu
 290 295 300
 Asn Gly Ala Ala Ala Leu Leu Ala Gly Tyr Leu Val Gly Gly Asp Val
 305 310 315 320
 Asp Lys Leu Val Glu Gly Leu Ser Asp Phe Ser Gly Val Arg Arg Arg
 325 330 335
 Phe Glu Phe His Gly Ala Ile Glu Gly Gly Lys Phe Asn Gly Ala Ala
 340 345 350
 Ile Tyr Asp Asp Tyr Ala His His Pro Thr Glu Val Thr Ala Val Leu
 355 360 365
 Ser Ala Ala Arg Thr Arg Val Lys Ala Ala Gly Lys Gly Arg Val Ile
 370 375 380
 Val Ala Phe Gln Pro His Leu Tyr Ser Arg Thr Ile Glu Phe Gln Lys
 385 390 395 400
 Glu Phe Ala Gly Ala Leu Ser Leu Ala Asp Ala Ala Val Val Leu Glu

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Ile Tyr Gly Ala Arg Glu Gln Pro Val Asp Gly Val Ser Ser Glu Ile	420	425	430
Ile Thr Asp Ala Met Thr Ile Pro Val Val Tyr Glu Pro Asn Phe Ser	435	440	445
Ala Val Pro Glu Arg Ile Ala Glu Ile Ala Gly Pro Asn Asp Ile Val	450	455	460
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Asp Gln Leu Gln Asn Asn	485		

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 <223> RXA02705

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 Met Gly Ser Leu Ser
 1 5
 cat tta cct cag gcg ctg cag ggc cgt att ctt gtg gcc ggc gct ggt 163
 His Leu Pro Gln Ala Leu Gln Gly Arg Ile Leu Val Ala Gly Ala Gly
 10 15 20
 gtt tcc ggc ctg tcc att gca aag atg ctc agt gag ttg cat tgc gat 211
 Val Ser Gly Leu Ser Ile Ala Lys Met Leu Ser Glu Leu His Cys Asp
 25 30 35
 gtt gtg gtc gcc gac gat aac gaa act gca cgt cac atg ctc att gaa 259
 Val Val Val Ala Asp Asp Asn Glu Thr Ala Arg His Met Leu Ile Glu
 40 45 50
 gta gta gac gtt gca gat atc agc acc gcg cag gct cag gaa cag ctg 307
 Val Val Asp Val Ala Asp Ile Ser Thr Ala Gln Ala Gln Glu Gln Leu
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 Asp Ser Phe Ser Ile Val Val Thr Ser Pro Gly Trp Arg Pro Thr Ser
 70 75 80 85
 act ttg ctt gtc gac gcc cac cgc cag ggc ctt gag gtt atc ggt gac 403
 Thr Leu Leu Val Asp Ala His Arg Gln Gly Leu Glu Val Ile Gly Asp
 90 95 100
 gtc gag ctt gct tgg cgc ctg gac cag gca ggt gtt ttc ggc gag cca 451
 Val Glu Leu Ala Trp Arg Leu Asp Gln Ala Gly Val Phe Gly Glu Pro

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His	Thr	Trp	Leu	Ala	Val	Thr	Gly	Thr	Asn	Gly	Lys	Thr	Thr	Thr	Thr	
		120					125					130				
tca	atg	ctc	gcc	gcg	atg	atg	aat	gag	ggc	ggt	ttt	act	gcc	aag	gca	547
Ser	Met	Leu	Ala	Ala	Met	Met	Asn	Glu	Gly	Gly	Phe	Thr	Ala	Lys	Ala	
		135				140					145					
gtg	ggc	aat	atc	ggc	atc	ccg	gtg	tct	gag	gct	ttg	gta	gcg	aaa	aac	595
Val	Gly	Asn	Ile	Gly	Ile	Pro	Val	Ser	Glu	Ala	Leu	Val	Ala	Lys	Asn	
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cgc	att	gat	gtg	tta	gtt	gca	gag	ctg	tct	agt	ttc	caa	ttg	cac	tgg	643
Arg	Ile	Asp	Val	Leu	Val	Ala	Glu	Leu	Ser	Ser	Phe	Gln	Leu	His	Trp	
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Ser	Pro	Thr	Phe	Thr	Pro	Asp	Ala	Gly	Val	Val	Leu	Asn		Ala	Glu	
			185					190					195			
gat	cac	atc	gat	tgg	cac	ggt	tcc	atg	cgt	gat	tat	gcg	ttg	gcc	aag	739
Asp	His	Ile	Asp	Trp	His	Gly	Ser	Met	Arg	Asp	Tyr	Ala	Leu	Ala	Lys	
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Met	Glu	Val	Leu	Lys	Gly	Lys	Val	Ala	Ile	Ile	Gly	Ala	Asp	Asp	Pro	
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tat	ttg	gtg	cag	ctg	act	tct	gaa	gca	gac	ttg	agt	ggt	ctc	att	gga	835
Tyr	Leu	Val	Gln	Leu	Thr	Ser	Glu	Ala	Asp	Leu	Ser	Gly	Leu	Ile	Gly	
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Phe	Thr	Val	Asn	Glu	Pro	Ala	Thr	Gly	Gln	Leu	Gly	Val	Lys	Ala	Gly	
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Glu	Leu	Val	Asp	Asn	Ala	Tyr	Gly	Asn	Asn	Val	Val	Leu	Ala	Ser	Ala	
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Arg	Ala	Leu	Asp	Ser	Phe	Glu	Val	Ala	Gly	His	Arg	Gly	Gln	Val	Val	
		310			315				320						325	
gcc	gag	cat	gac	ggt	gtt	cat	ttc	att	gac	aac	tcc	aag	gcg	acc	aac	1123
Ala	Glu	His	Asp	Gly	Val	His	Phe	Ile	Asp	Asn	Ser	Lys	Ala	Thr	Asn	
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ccc	cac	gct	gct	gat	tct	gcg	cta	gct	ggg	cat	gat	tca	gtc	att	tgg	1171
Pro	His	Ala	Ala	Asp	Ser	Ala	Leu	Ala	Gly	His	Asp	Ser	Val	Ile	Trp	
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 Val Val Gly Gly Gln Leu Lys Gly Ala Asp Ile Ala Pro Leu Val Lys
 360 365 370

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 Lys His Glu Gln Arg Ile Lys Ala Ala Leu Val Leu Gly Ala Asp Arg
 375 380 385

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 Ala Glu Ile Val Ala Leu Lys Glu His Ala Ser Gln Ala Ser Val
 390 395 400 405

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 Phe Val Thr Asp Lys Thr Glu Pro Phe Glu Ala Met Glu Glu Ile Val
 410 415 420

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 Thr Glu Ala Phe Ser Ile Ser Glu Pro Gly Asp Thr Val Leu Leu Ala
 425 430 435

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 Pro Ala Ala Ala Ser Leu Asp Met Phe Lys Gly Met Gly Gln Arg Gly
 440 445 450

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<213> Corynebacterium glutamicum

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 35 40 45

His Met Leu Ile Glu Val Val Asp Val Ala Asp Ile Ser Thr Ala Gln
 50 55 60

Ala Gln Glu Gln Leu Asp Ser Phe Ser Ile Val Val Thr Ser Pro Gly
 65 70 75 80

Trp Arg Pro Thr Ser Thr Leu Leu Val Asp Ala His Arg Gln Gly Leu
 85 90 95

Glu Val Ile Gly Asp Val Glu Leu Ala Trp Arg Leu Asp Gln Ala Gly
 100 105 110

Val Phe Gly Glu Pro His Thr Trp Leu Ala Val Thr Gly Thr Asn Gly
 115 120 125
 Lys Thr Thr Thr Thr Ser Met Leu Ala Ala Met Met Asn Glu Gly Gly
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 Phe Thr Ala Lys Ala Val Gly Asn Ile Gly Ile Pro Val Ser Glu Ala
 145 150 155 160
 Leu Val Ala Lys Asn Arg Ile Asp Val Leu Val Ala Glu Leu Ser Ser
 165 170 175
 Phe Gln Leu His Trp Ser Pro Thr Phe Thr Pro Asp Ala Gly Val Val
 180 185 190
 Leu Asn Leu Ala Glu Asp His Ile Asp Trp His Gly Ser Met Arg Asp
 195 200 205
 Tyr Ala Leu Ala Lys Met Glu Val Leu Lys Gly Lys Val Ala Ile Ile
 210 215 220
 Gly Ala Asp Asp Pro Tyr Leu Val Gln Leu Thr Ser Glu Ala Asp Leu
 225 230 235 240
 Ser Gly Leu Ile Gly Phe Thr Val Asn Glu Pro Ala Thr Gly Gln Leu
 245 250 255
 Gly Val Lys Ala Gly Glu Leu Val Asp Asn Ala Tyr Gly Asn Asn Val
 260 265 270
 Val Leu Ala Ser Ala Asp Gly Ile Asn Pro Ala Gly Pro Ala Gly Val
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 290 295 300
 Pro Glu Ala Ile Ala Arg Ala Leu Asp Ser Phe Glu Val Ala Gly His
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 Arg Gly Gln Val Val Ala Glu His Asp Gly Val His Phe Ile Asp Asn
 325 330 335
 Ser Lys Ala Thr Asn Pro His Ala Ala Asp Ser Ala Leu Ala Gly His
 340 345 350
 Asp Ser Val Ile Trp Val Val Gly Gly Gln Leu Lys Gly Ala Asp Ile
 355 360 365
 Ala Pro Leu Val Lys Lys His Glu Gln Arg Ile Lys Ala Ala Leu Val
 370 375 380
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 385 390 395 400
 Ser Gln Ala Ser Val Phe Val Thr Asp Lys Thr Glu Pro Phe Glu Ala
 405 410 415
 Met Glu Glu Ile Val Thr Glu Ala Phe Ser Ile Ser Glu Pro Gly Asp
 420 425 430
 Thr Val Leu Leu Ala Pro Ala Ala Ala Ser Leu Asp Met Phe Lys Gly

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<223> RXA01254

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                        Met Lys Leu Ser Leu
                        1              5

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Pro Ala Pro Leu Arg Arg Leu Arg Ser Ala Ala Ala Ile Ile Ser Ala
              10              15              20

aaa gtt gcg aca tcc gcg tcc aaa gcc aca ggt cgc gga tcc ggt ggc 211
Lys Val Ala Thr Ser Ala Ser Lys Ala Thr Gly Arg Gly Ser Gly Gly
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atg atc ggc gga ctg gtg gcc agc aag gta gac ccg gac atc atg tcc 259
Met Ile Gly Gly Leu Val Ala Ser Lys Val Asp Pro Asp Ile Met Ser
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Asn Leu Ile Asn Asn Arg Pro Thr Val Leu Val Thr Gly Thr Asn Gly
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Lys Ser Thr Thr Thr Arg Met Leu Ala Ala Ala Met Arg Ser Thr Tyr
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Thr Val Ala Thr Asn Glu Gly Gly Asp Asn Met Asp Ala Gly Ile Ile
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Ser Ala Leu Leu Ala Gly Arg Asn Ala Ser His Val Val Leu Glu Val
              105              110              115

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Asp Glu Leu His Val Pro Ala Ala Ile Glu Arg Leu Lys Pro Asp Ala
              120              125              130

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Glu Met Thr Val Ile Ala Asn Cys Asp Asp Val Leu Val Thr Ser Val	
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Ala Phe Asp Ala Glu Asn Val Ile Trp Val Gly Ala Gly Thr Gly Trp	
185 190 195	
caa ggt gaa tcc gcc acc tgc cca cgc acc gaa tcc cgc atc ctc cac	739
Gln Gly Glu Ser Ala Thr Cys Pro Arg Thr Glu Ser Arg Ile Leu His	
200 205 210	
gac gga cgc cac tgg agc gcc gaa aag acg ctt ctc gac ggc cgc acc	787
Asp Gly Arg His Trp Ser Ala Glu Lys Thr Leu Leu Asp Gly Arg Thr	
215 220 225	
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Phe Ala Arg Pro Thr Pro Ser Trp Glu Val Asp Gly Asp Thr Ile His	
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Ser Pro Ser Gly Asp Leu Thr Leu Asp Leu Asn Leu Pro Gly Gln Ala	
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Asn Arg Gly Asn Ala Ala Gln Ala Ile Ala Ala Ser Thr Val Phe Asn	
265 270 275	
gtg ccc gtt tcc tcc gca ctg ccc gca gtc aac tcc gtc aac aac gtt	979
Val Pro Val Ser Ser Ala Leu Pro Ala Val Asn Ser Val Asn Asn Val	
280 285 290	
gct gga cgc tat tcc acc atc act gtc ggt gaa cac aag gtc cac ctc	1027
Ala Gly Arg Tyr Ser Thr Ile Thr Val Gly Glu His Lys Val His Leu	
295 300 305	
ctg ctc gcc aaa aac cca gca ggc tgg caa gaa gcc ctc tcc atg gtt	1075
Leu Leu Ala Lys Asn Pro Ala Gly Trp Gln Glu Ala Leu Ser Met Val	
310 315 320 325	
gat cgc aca gct gat ggc tta gtc atc gtc gtc aat ggc cag gtt gcc	1123
Asp Arg Thr Ala Asp Gly Leu Val Ile Val Val Asn Gly Gln Val Ala	
330 335 340	
gac ggc gaa gac ctc tcc tgg ctt tgg gac gtc cgc ttc gaa gac ttc	1171
Asp Gly Glu Asp Leu Ser Trp Leu Trp Asp Val Arg Phe Glu Asp Phe	
345 350 355	
gaa aac ctc tcc gtc aaa gcc tcc ggc gag cgc ggc acc gac ctg gca	1219
Glu Asn Leu Ser Val Lys Ala Ser Gly Glu Arg Gly Thr Asp Leu Ala	
360 365 370	
gtc cgc ctc acc tac gcc gaa atc gac cac gaa ctc atc tcc aac ccc	1267
Val Arg Leu Thr Tyr Ala Glu Ile Asp His Glu Leu Ile Ser Asn Pro	
375 380 385	

gtc gac gcc atc gca gcc tgc cct cct ggc cgc atc gaa gtc ctc gcc 1315
 Val Asp Ala Ile Ala Ala Cys Pro Pro Gly Arg Ile Glu Val Leu Ala
 390 395 400 405

aac tac acc gca ttc cga gac ctc aaa aag gct ctg gag aaa ggg acc 1363
 Asn Tyr Thr Ala Phe Arg Asp Leu Lys Lys Ala Leu Glu Lys Gly Thr
 410 415 420

gaa caa taatgaccac cctcaacatc ggc 1392
 Glu Gln

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 <213> Corynebacterium glutamicum

<400> 6
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Arg Gly Ser Gly Gly Met Ile Gly Gly Leu Val Ala Ser Lys Val Asp
 35 40 45

Pro Asp Ile Met Ser Asn Leu Ile Asn Asn Arg Pro Thr Val Leu Val
 50 55 60

Thr Gly Thr Asn Gly Lys Ser Thr Thr Thr Arg Met Leu Ala Ala Ala
 65 70 75 80

Met Arg Ser Thr Tyr Thr Val Ala Thr Asn Glu Gly Gly Asp Asn Met
 85 90 95

Asp Ala Gly Ile Ile Ser Ala Leu Leu Ala Gly Arg Asn Ala Ser His
 100 105 110

Val Val Leu Glu Val Asp Glu Leu His Val Pro Ala Ala Ile Glu Arg
 115 120 125

Leu Lys Pro Asp Ala Leu Val Leu Leu Asn Leu Ser Arg Asp Gln Leu
 130 135 140

Asp Arg Val Gly Glu Ile Asn Lys Ile Glu Arg Val Leu Arg Asp Ala
 145 150 155 160

Val Arg Ser Arg Pro Glu Met Thr Val Ile Ala Asn Cys Asp Asp Val
 165 170 175

Leu Val Thr Ser Val Ala Phe Asp Ala Glu Asn Val Ile Trp Val Gly
 180 185 190

Ala Gly Thr Gly Trp Gln Gly Glu Ser Ala Thr Cys Pro Arg Thr Glu
 195 200 205

Ser Arg Ile Leu His Asp Gly Arg His Trp Ser Ala Glu Lys Thr Leu
 210 215 220

Leu Asp Gly Arg Thr Phe Ala Arg Pro Thr Pro Ser Trp Glu Val Asp
 225 230 235 240
 Gly Asp Thr Ile His Ser Pro Ser Gly Asp Leu Thr Leu Asp Leu Asn
 245 250 255
 Leu Pro Gly Gln Ala Asn Arg Gly Asn Ala Ala Gln Ala Ile Ala Ala
 260 265 270
 Ser Thr Val Phe Asn Val Pro Val Ser Ser Ala Leu Pro Ala Val Asn
 275 280 285
 Ser Val Asn Asn Val Ala Gly Arg Tyr Ser Thr Ile Thr Val Gly Glu
 290 295 300
 His Lys Val His Leu Leu Leu Ala Lys Asn Pro Ala Gly Trp Gln Glu
 305 310 315 320
 Ala Leu Ser Met Val Asp Arg Thr Ala Asp Gly Leu Val Ile Val Val
 325 330 335
 Asn Gly Gln Val Ala Asp Gly Glu Asp Leu Ser Trp Leu Trp Asp Val
 340 345 350
 Arg Phe Glu Asp Phe Glu Asn Leu Ser Val Lys Ala Ser Gly Glu Arg
 355 360 365
 Gly Thr Asp Leu Ala Val Arg Leu Thr Tyr Ala Glu Ile Asp His Glu
 370 375 380
 Leu Ile Ser Asn Pro Val Asp Ala Ile Ala Ala Cys Pro Pro Gly Arg
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 Leu Glu Lys Gly Thr Glu Gln
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 <213> Corynebacterium glutamicum

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 <223> RXN02707

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 Met Thr Leu Gly Glu
 1 5
 atc gct gac atc gtt gga ggc agg ctt act ggc ggt gct caa gaa gat 163
 Ile Ala Asp Ile Val Gly Gly Arg Leu Thr Gly Gly Ala Gln Glu Asp
 10 15 20

acg ctt gtg agc tcc agc gtg gag ttt gat tct cga tcc ctc aca ccg	211
Thr Leu Val Ser Ser Val Glu Phe Asp Ser Arg Ser Leu Thr Pro	
25 30 35	
ggg ggc ttg ttt tta gca ctt ccg ggt gct cgt gta gac ggc cat gat	259
Gly Gly Leu Phe Leu Ala Leu Pro Gly Ala Arg Val Asp Gly His Asp	
40 45 50	
ttt gct gca act gca att gag aaa ggt gcg gtt gca gta ttg gca gcc	307
Phe Ala Ala Thr Ala Ile Glu Lys Gly Ala Val Ala Val Leu Ala Ala	
55 60 65	
cgt gag gtt gac gta cct gcg atc gtc gtg cct cca gta aaa atc cag	355
Arg Glu Val Asp Val Pro Ala Ile Val Val Pro Pro Val Lys Ile Gln	
70 75 80 85	
gaa tcc aat gct gac att tat gct cat gat cca gat ggg cat ggc gcg	403
Glu Ser Asn Ala Asp Ile Tyr Ala His Asp Pro Asp Gly His Gly Ala	
90 95 100	
gcg gta gtg gag gcg ttg tct cgg ttg gct cgc cac gtg gtg gat atc	451
Ala Val Val Glu Ala Leu Ser Arg Leu Ala Arg His Val Val Asp Ile	
105 110 115	
tgc gtg gct ggc cat caa ttg aac gtt gtg gct att act ggt tct gcg	499
Cys Val Ala Gly His Gln Leu Asn Val Val Ala Ile Thr Gly Ser Ala	
120 125 130	
gga aag act tct acg aag gat ttc atc gcg acg gtt ctt gac caa gat	547
Gly Lys Thr Ser Thr Lys Asp Phe Ile Ala Thr Val Leu Asp Gln Asp	
135 140 145	
ggg cca act gtg gct cct ccg ggc tcg ttt aac aat gag ctt ggt ttg	595
Gly Pro Thr Val Ala Pro Pro Gly Ser Phe Asn Asn Glu Leu Gly Leu	
150 155 160 165	
cca cac acc gcg ctc cgc tgc aca acc gat act aag tat ttg gtg gct	643
Pro His Thr Ala Leu Arg Cys Thr Thr Asp Thr Lys Tyr Leu Val Ala	
170 175 180	
gag atg tcc gcg cgt ggc att gga cat att aag cac ctg aca gag att	691
Glu Met Ser Ala Arg Gly Ile Gly His Ile Lys His Leu Thr Glu Ile	
185 190 195	
gct ccg cca cgg att gca gct gtg ctc aac gtc ggc cat gcg cac ctg	739
Ala Pro Pro Arg Ile Ala Ala Val Leu Asn Val Gly His Ala His Leu	
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Gly Glu Phe Gly Ser Arg Glu Asn Ile Ala Gln Ala Lys Gly Glu Ile	
215 220 225	
att gaa gcg ctg ccc tcg aag aaa acg agc tcg gta cca gtc ctg aat	835
Ile Glu Ala Leu Pro Ser Lys Lys Thr Ser Ser Val Pro Val Leu Asn	
230 235 240 245	
act gat cct ttt gtc gcc cgg atg gct cca cgc act aag gcg cgc gtg	883
Thr Asp Pro Phe Val Ala Arg Met Ala Pro Arg Thr Lys Ala Arg Val	
250 255 260	
gtg tgg ttt acc acc gat gca ggc caa gca aaa aag tct gat tat tgg	931

Val	Trp	Phe	Thr	Thr	Asp	Ala	Gly	Gln	Ala	Lys	Lys	Ser	Asp	Tyr	Trp	
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gca	acg	agt	att	tca	ctg	gac	gct	gtt	gcg	cgg	gca	agc	ttt	acg	ctg	979
Ala	Thr	Ser	Ile	Ser	Leu	Asp	Ala	Val	Ala	Arg	Ala	Ser	Phe	Thr	Leu	
		280					285					290				
aac	acg	aag	gac	ggc	tct	tgg	ccg	gtc	acc	ctg	cag	gtt	ttt	ggc	gag	1027
Asn	Thr	Lys	Asp	Gly	Ser	Trp	Pro	Val	Thr	Leu	Gln	Val	Phe	Gly	Glu	
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cac	cag	gtt	gct	aat	gca	ctt	gct	gct	gct	gcc	att	gcc	atg	gaa	gct	1075
His	Gln	Val	Ala	Asn	Ala	Leu	Ala	Ala	Ala	Ala	Ile	Ala	Met	Glu	Ala	
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Gly	Val	Ala	Pro	Glu	Leu	Val	Val	Ala	Gly	Leu	Glu	Ala	His	Ser	Ala	
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gct	tcc	gcg	cac	cgc	atg	gat	gta	aag	acc	cgt	gcc	gac	ggc	gtg	acc	1171
Ala	Ser	Ala	His	Arg	Met	Asp	Val	Lys	Thr	Arg	Ala	Asp	Gly	Val	Thr	
			345					350					355			
atc	atc	aac	gat	tct	tac	aac	gcg	aat	cct	gat	tct	atg	cgt	gca	ggc	1219
Ile	Ile	Asn	Asp	Ser	Tyr	Asn	Ala	Asn	Pro	Asp	Ser	Met	Arg	Ala	Gly	
		360					365					370				
atc	gcg	gct	ctt	gcg	tac	aca	gct	agt	ggc	cgt	tct	gaa	gca	aca	agc	1267
Ile	Ala	Ala	Leu	Ala	Tyr	Thr	Ala	Ser	Gly	Arg	Ser	Glu	Ala	Thr	Ser	
		375				380					385					
tgg	gca	gtg	ctt	ggc	caa	atg	ggc	gag	ctt	ggc	gat	gac	gcc	tcg	gaa	1315
Trp	Ala	Val	Leu	Gly	Gln	Met	Gly	Glu	Leu	Gly	Asp	Asp	Ala	Ser	Glu	
390					395					400					405	
gcc	cat	gcc	gaa	ctt	ggc	gct	gag	ctg	gct	aaa	tac	aat	gtt	caa	gaa	1363
Ala	His	Ala	Glu	Leu	Gly	Ala	Glu	Leu	Ala	Lys	Tyr	Asn	Val	Gln	Glu	
				410					415					420		
ctt	gtc	gca	gtg	ggg	gag	aac	cct	aac	tgt	gca	gca	ctt	gca	gag	tcc	1411
Leu	Val	Ala	Val	Gly	Glu	Asn	Pro	Asn	Cys	Ala	Ala	Leu	Ala	Glu	Ser	
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gca	gcg	agc	ctg	ggc	gtg	agt	act	cac	gta	gtt	tca	gac	gtt	gat	gca	1459
Ala	Ala	Ser	Leu	Gly	Val	Ser	Thr	His	Val	Val	Ser	Asp	Val	Asp	Ala	
		440					445					450				
gcg	ctc	gag	ttg	ctc	gca	ggc	cat	att	aag	cgg	gat	gat	gta	gtg	ctg	1507
Ala	Leu	Glu	Leu	Leu	Ala	Gly	His	Ile	Lys	Arg	Asp	Asp	Val	Val	Leu	
		455				460					465					
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Val																

505

510

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<211> 510

<212> PRT

<213> *Corynebacterium glutamicum*

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 20 25 30

Arg Ser Leu Thr Pro Gly Gly Leu Phe Leu Ala Leu Pro Gly Ala Arg
 35 40 45

Val Asp Gly His Asp Phe Ala Ala Thr Ala Ile Glu Lys Gly Ala Val
 50 55 60

Ala Val Leu Ala Ala Arg Glu Val Asp Val Pro Ala Ile Val Val Pro
 65 70 75 80

Pro Val Lys Ile Gln Glu Ser Asn Ala Asp Ile Tyr Ala His Asp Pro
 85 90 95

Asp Gly His Gly Ala Ala Val Val Glu Ala Leu Ser Arg Leu Ala Arg
 100 105 110

His Val Val Asp Ile Cys Val Ala Gly His Gln Leu Asn Val Val Ala
 115 120 125

Ile Thr Gly Ser Ala Gly Lys Thr Ser Thr Lys Asp Phe Ile Ala Thr
 130 135 140

Val Leu Asp Gln Asp Gly Pro Thr Val Ala Pro Pro Gly Ser Phe Asn
 145 150 155 160

Asn Glu Leu Gly Leu Pro His Thr Ala Leu Arg Cys Thr Thr Asp Thr
 165 170 175

Lys Tyr Leu Val Ala Glu Met Ser Ala Arg Gly Ile Gly His Ile Lys
 180 185 190

His Leu Thr Glu Ile Ala Pro Pro Arg Ile Ala Ala Val Leu Asn Val
 195 200 205

Gly His Ala His Leu Gly Glu Phe Gly Ser Arg Glu Asn Ile Ala Gln
 210 215 220

Ala Lys Gly Glu Ile Ile Glu Ala Leu Pro Ser Lys Lys Thr Ser Ser
 225 230 235 240

Val Pro Val Leu Asn Thr Asp Pro Phe Val Ala Arg Met Ala Pro Arg
 245 250 255

Thr Lys Ala Arg Val Val Trp Phe Thr Thr Asp Ala Gly Gln Ala Lys
 260 265 270

Lys Ser Asp Tyr Trp Ala Thr Ser Ile Ser Leu Asp Ala Val Ala Arg

275					280					285					
Ala	Ser	Phe	Thr	Leu	Asn	Thr	Lys	Asp	Gly	Ser	Trp	Pro	Val	Thr	Leu
290					295					300					
Gln	Val	Phe	Gly	Glu	His	Gln	Val	Ala	Asn	Ala	Leu	Ala	Ala	Ala	Ala
305					310					315					320
Ile	Ala	Met	Glu	Ala	Gly	Val	Ala	Pro	Glu	Leu	Val	Val	Ala	Gly	Leu
				325					330					335	
Glu	Ala	His	Ser	Ala	Ala	Ser	Ala	His	Arg	Met	Asp	Val	Lys	Thr	Arg
			340					345					350		
Ala	Asp	Gly	Val	Thr	Ile	Ile	Asn	Asp	Ser	Tyr	Asn	Ala	Asn	Pro	Asp
		355					360					365			
Ser	Met	Arg	Ala	Gly	Ile	Ala	Ala	Leu	Ala	Tyr	Thr	Ala	Ser	Gly	Arg
	370						375				380				
Ser	Glu	Ala	Thr	Ser	Trp	Ala	Val	Leu	Gly	Gln	Met	Gly	Glu	Leu	Gly
385							390				395				400
Asp	Asp	Ala	Ser	Glu	Ala	His	Ala	Glu	Leu	Gly	Ala	Glu	Leu	Ala	Lys
				405					410					415	
Tyr	Asn	Val	Gln	Glu	Leu	Val	Ala	Val	Gly	Glu	Asn	Pro	Asn	Cys	Ala
			420					425					430		
Ala	Leu	Ala	Glu	Ser	Ala	Ala	Ser	Leu	Gly	Val	Ser	Thr	His	Val	Val
	435						440					445			
Ser	Asp	Val	Asp	Ala	Ala	Leu	Glu	Leu	Leu	Ala	Gly	His	Ile	Lys	Arg
	450					455					460				
Asp	Asp	Val	Val	Leu	Val	Lys	Ala	Ser	Asn	Ala	Asp	Arg	Leu	Trp	Arg
465						470					475				480
Val	Ala	Glu	Ala	Leu	His	Gly	Met	Val	Pro	Gly	Leu	Lys	Asn	Thr	Gly
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Gly	Ser	Val	Asn	Asp	Asp	Ser	Arg	Arg	Asn	Val	Glu	Gly	Gln		
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(445)
 <223> FRXA02707

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 Met Gly Glu Leu Gly
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gat gac gcc tcg gaa gcc cat gcc gaa ctt ggt gct gag ctg gct aaa 163
Asp Asp Ala Ser Glu Ala His Ala Glu Leu Gly Ala Glu Leu Ala Lys
      10              15              20

tac aat gtt caa gaa ctt gtc gca gtg ggg gag aac cct aac tgt gca 211
Tyr Asn Val Gln Glu Leu Val Ala Val Gly Glu Asn Pro Asn Cys Ala
      25              30              35

gca ctt gca gag tcc gca gcg agc ctg ggt gtg agt act cac gta gtt 259
Ala Leu Ala Glu Ser Ala Ala Ser Leu Gly Val Ser Thr His Val Val
      40              45              50

tca gac gtt gat gca gcg ctc gag ttg ctc gca ggc cat att aag cgg 307
Ser Asp Val Asp Ala Ala Leu Glu Leu Leu Ala Gly His Ile Lys Arg
      55              60              65

gat gat gta gtg ctg gtt aag gct tca aat gct gat cgc ctg tgg agg 355
Asp Asp Val Val Leu Val Lys Ala Ser Asn Ala Asp Arg Leu Trp Arg
      70              75              80              85

gtc gca gaa gca cta cat ggc atg gtg ccg ggc ctc aaa aac aca ggt 403
Val Ala Glu Ala Leu His Gly Met Val Pro Gly Leu Lys Asn Thr Gly
      90              95              100

ggc tcg gtc aac gac gat tct cgt cgg aac gtg gaa gga cag 445
Gly Ser Val Asn Asp Asp Ser Arg Arg Asn Val Glu Gly Gln
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<210> 10
<211> 115
<212> PRT
<213> Corynebacterium glutamicum

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  20          25          30

Asn Pro Asn Cys Ala Ala Leu Ala Glu Ser Ala Ala Ser Leu Gly Val
  35          40          45

Ser Thr His Val Val Ser Asp Val Asp Ala Ala Leu Glu Leu Leu Ala
  50          55          60

Gly His Ile Lys Arg Asp Asp Val Val Leu Val Lys Ala Ser Asn Ala
  65          70          75          80

Asp Arg Leu Trp Arg Val Ala Glu Ala Leu His Gly Met Val Pro Gly
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Leu Lys Asn Thr Gly Gly Ser Val Asn Asp Asp Ser Arg Arg Asn Val
  100         105         110

Glu Gly Gln
  115

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<210>	12
<211>	145
<212>	PRT

<213> Corynebacterium glutamicum

<400> 12

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Gly Gln Ala Lys Lys Ser Asp Tyr Trp Ala Thr Ser Ile Ser Leu Asp
          20             25             30

Ala Val Ala Arg Ala Ser Phe Thr Leu Asn Thr Lys Asp Gly Ser Trp
          35             40             45

Pro Val Thr Leu Gln Val Phe Gly Glu His Gln Val Ala Asn Ala Leu
 50             55             60

Ala Ala Ala Ala Ile Ala Met Glu Ala Gly Val Ala Pro Glu Leu Val
 65             70             75             80

Val Ala Gly Leu Glu Ala His Ser Ala Ala Ser Ala His Arg Met Asp
          85             90             95

Val Lys Thr Arg Ala Asp Gly Val Thr Ile Ile Asn Asp Ser Tyr Asn
          100            105            110

Ala Asn Pro Asp Ser Met Arg Ala Gly Ile Ala Ala Leu Ala Tyr Thr
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Ala Ser Gly Arg Ser Glu Ala Thr Lys Leu Gly Ser Ala Trp Pro Asn
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Gly
145

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<210> 13

<211> 852

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<223> FRXA02709

<400> 13

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ccttactacg gaagaaggat aggccacagt catgatcaca atg acc ctt ggg gaa 115
                               Met Thr Leu Gly Glu
                               1             5

atc gct gac atc gtt gga ggc agg ctt act ggc ggt gct caa gaa gat 163
Ile Ala Asp Ile Val Gly Gly Arg Leu Thr Gly Gly Ala Gln Glu Asp
          10             15             20

acg ctt gtg agc tcc agc gtg gag ttt gat tct cga tcc ctc aca ccg 211
Thr Leu Val Ser Ser Ser Val Glu Phe Asp Ser Arg Ser Leu Thr Pro
          25             30             35

ggg ggc ttg ttt tta gca ctt ccg ggt gct cgt gta gac ggc cat gat 259
Gly Gly Leu Phe Leu Ala Leu Pro Gly Ala Arg Val Asp Gly His Asp

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40	45	50	
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Phe Ala Ala Thr Ala Ile Glu Lys Gly Ala Val Ala Val Leu Ala Ala			
55	60	65	
cgt gag gtt gac gta cct gcg atc gtc gtg cct cca gta aaa atc cag			355
Arg Glu Val Asp Val Pro Ala Ile Val Val Pro Pro Val Lys Ile Gln			
70	75	80	85
gaa tcc aat gct gac att tat gct cat gat cca gat ggg cat ggc gcg			403
Glu Ser Asn Ala Asp Ile Tyr Ala His Asp Pro Asp Gly His Gly Ala			
90	95	100	
gcg gta gtg gag gcg ttg tct cgg ttg gct cgc cac gtg gtg gat atc			451
Ala Val Val Glu Ala Leu Ser Arg Leu Ala Arg His Val Val Asp Ile			
105	110	115	
tgc gtg gct ggc cat caa ttg aac gtt gtg gct att act ggt tct gcg			499
Cys Val Ala Gly His Gln Leu Asn Val Val Ala Ile Thr Gly Ser Ala			
120	125	130	
gga aag act tct acg aag gat ttc atc gcg acg gtt ctt gac caa gat			547
Gly Lys Thr Ser Thr Lys Asp Phe Ile Ala Thr Val Leu Asp Gln Asp			
135	140	145	
ggg cca act gtg gct cct ccg ggc tcg ttt aac aat gag ctt ggt ttg			595
Gly Pro Thr Val Ala Pro Pro Gly Ser Phe Asn Asn Glu Leu Gly Leu			
150	155	160	165
cca cac acc gcg ctc cgc tgc aca acc gat act aag tat ttg gtg gct			643
Pro His Thr Ala Leu Arg Cys Thr Thr Asp Thr Lys Tyr Leu Val Ala			
170	175	180	
gag atg tcc gcg cgt ggc att gga cat att aag cac ctg aca gag att			691
Glu Met Ser Ala Arg Gly Ile Gly His Ile Lys His Leu Thr Glu Ile			
185	190	195	
gct ccg cca cgg att gca gct gtg ctc aac gtc ggc cat gcg cac ctg			739
Ala Pro Pro Arg Ile Ala Ala Val Leu Asn Val Gly His Ala His Leu			
200	205	210	
ggt gaa ttt gga tcc cgc gag aat atc gcg cag gca aaa ggc gag atc			787
Gly Glu Phe Gly Ser Arg Glu Asn Ile Ala Gln Ala Lys Gly Glu Ile			
215	220	225	
att gaa gcg ctg ccc tcg aag aaa acg gct cgg tac cag tcc			829
Ile Glu Ala Leu Pro Ser Lys Lys Thr Ala Arg Tyr Gln Ser			
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<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 14

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 Arg Ser Leu Thr Pro Gly Gly Leu Phe Leu Ala Leu Pro Gly Ala Arg
 35 40 45
 Val Asp Gly His Asp Phe Ala Ala Thr Ala Ile Glu Lys Gly Ala Val
 50 55 60
 Ala Val Leu Ala Ala Arg Glu Val Asp Val Pro Ala Ile Val Val Pro
 65 70 75 80
 Pro Val Lys Ile Gln Glu Ser Asn Ala Asp Ile Tyr Ala His Asp Pro
 85 90 95
 Asp Gly His Gly Ala Ala Val Val Glu Ala Leu Ser Arg Leu Ala Arg
 100 105 110
 His Val Val Asp Ile Cys Val Ala Gly His Gln Leu Asn Val Val Ala
 115 120 125
 Ile Thr Gly Ser Ala Gly Lys Thr Ser Thr Lys Asp Phe Ile Ala Thr
 130 135 140
 Val Leu Asp Gln Asp Gly Pro Thr Val Ala Pro Pro Gly Ser Phe Asn
 145 150 155 160
 Asn Glu Leu Gly Leu Pro His Thr Ala Leu Arg Cys Thr Thr Asp Thr
 165 170 175
 Lys Tyr Leu Val Ala Glu Met Ser Ala Arg Gly Ile Gly His Ile Lys
 180 185 190
 His Leu Thr Glu Ile Ala Pro Pro Arg Ile Ala Ala Val Leu Asn Val
 195 200 205
 Gly His Ala His Leu Gly Glu Phe Gly Ser Arg Glu Asn Ile Ala Gln
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 Ala Lys Gly Glu Ile Ile Glu Ala Leu Pro Ser Lys Lys Thr Ala Arg
 225 230 235 240
 Tyr Gln Ser

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 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(1663)
 <223> RXA02710

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												1				5	
ctg	gac	ctc	acc	aaa	ctt	atc	gat	ggc	atc	ctc	aag	ggc	tct	gcc	cag		163
Leu	Asp	Leu	Thr	Lys	Leu	Ile	Asp	Gly	Ile	Leu	Lys	Gly	Ser	Ala	Gln		
				10					15					20			
ggc	gtt	ccc	gct	cac	gca	gta	ggg	gaa	caa	gca	atc	gcg	gct	att	ggg		211
Gly	Val	Pro	Ala	His	Ala	Val	Gly	Glu	Gln	Ala	Ile	Ala	Ala	Ile	Gly		
			25					30					35				
ctt	gac	tcc	tcc	agc	tta	cct	acc	tcg	gac	gct	att	ttt	gct	gca	gtt		259
Leu	Asp	Ser	Ser	Ser	Leu	Pro	Thr	Ser	Asp	Ala	Ile	Phe	Ala	Ala	Val		
		40					45					50					
cca	gga	acc	cgc	act	cac	ggc	gca	cag	ttt	gca	ggg	acg	gat	aac	gct		307
Pro	Gly	Thr	Arg	Thr	His	Gly	Ala	Gln	Phe	Ala	Gly	Thr	Asp	Asn	Ala		
	55					60					65						
gcg	aaa	gct	gtg	gcc	att	ttg	act	gac	gca	gct	gga	ctt	gag	gtg	ctc		355
Ala	Lys	Ala	Val	Ala	Ile	Leu	Thr	Asp	Ala	Ala	Gly	Leu	Glu	Val	Leu		
70					75					80					85		
aac	gaa	gca	gga	gag	acc	cgc	cca	gtc	atc	gtt	gtt	gat	gat	gtc	cgc		403
Asn	Glu	Ala	Gly	Glu	Thr	Arg	Pro	Val	Ile	Val	Val	Asp	Asp	Val	Arg		
				90					95					100			
gca	gta	ctt	ggc	gca	gca	tca	tca	agc	att	tat	ggc	gat	cct	tca	aaa		451
Ala	Val	Leu	Gly	Ala	Ala	Ser	Ser	Ser	Ile	Tyr	Gly	Asp	Pro	Ser	Lys		
			105					110					115				
gat	ttc	acg	ctc	att	gga	gtc	act	gga	acc	tca	ggg	aaa	acc	acc	acc		499
Asp	Phe	Thr	Leu	Ile	Gly	Val	Thr	Gly	Thr	Ser	Gly	Lys	Thr	Thr	Thr		
		120					125					130					
agc	tac	ctc	ttg	gaa	aaa	gga	ctc	atg	gag	gca	ggc	cac	aaa	gtt	ggg		547
Ser	Tyr	Leu	Leu	Glu	Lys	Gly	Leu	Met	Glu	Ala	Gly	His	Lys	Val	Gly		
	135					140					145						
ttg	atc	ggc	acc	aca	ggg	aca	cgt	att	gac	ggg	gaa	gaa	gta	ccc	aca		595
Leu	Ile	Gly	Thr	Thr	Gly	Thr	Arg	Ile	Asp	Gly	Glu	Glu	Val	Pro	Thr		
150					155					160					165		
aag	ctc	acc	act	cca	gaa	gcg	ccg	act	ctg	cag	gca	ttg	ttt	gct	cga		643
Lys	Leu	Thr	Thr	Pro	Glu	Ala	Pro	Thr	Leu	Gln	Ala	Leu	Phe	Ala	Arg		
				170					175					180			
atg	cgc	gat	cac	ggg	gtc	acc	cac	gtg	gtg	atg	gaa	gta	tcc	agc	cat		691
Met	Arg	Asp	His	Gly	Val	Thr	His	Val	Val	Met	Glu	Val	Ser	Ser	His		
			185					190					195				
gca	ttg	tca	ttg	ggc	aga	gtt	gcg	ggg	tcc	cac	ttt	gat	gta	gct	gcg		739
Ala	Leu	Ser	Leu	Gly	Arg	Val	Ala	Gly	Ser	His	Phe	Asp	Val	Ala	Ala		
		200					205					210					
ttt	acc	aac	ctg	tcg	cag	gat	cac	ctt	gat	ttc	cac	ccc	acc	atg	gat		787
Phe	Thr	Asn	Leu	Ser	Gln	Asp	His	Leu	Asp	Phe	His	Pro	Thr	Met	Asp		
	215					220					225						
gat	tac	ttt	gac	gcg	aag	gca	ttg	ttc	ttc	cgc	gca	gat	tct	cca	ctt		835
Asp	Tyr	Phe	Asp	Ala	Lys	Ala	Leu	Phe	Phe	Arg	Ala	Asp	Ser	Pro	Leu		

230	235	240	245	
gtg gct gac aaa cag gtc gtg tgc gtg gat gat tct tgg ggt cag cgc 883 Val Ala Asp Lys Gln Val Val Cys Val Asp Asp Ser Trp Gly Gln Arg 250 255 260				
atg gcc agc gtg gca gcg gat gtg caa aca gta tcc acc ctt ggg caa 931 Met Ala Ser Val Ala Ala Asp Val Gln Thr Val Ser Thr Leu Gly Gln 265 270 275				
gaa gca gac ttc agc gct aca gac atc aat gtc agc gac tct ggc gcc 979 Glu Ala Asp Phe Ser Ala Thr Asp Ile Asn Val Ser Asp Ser Gly Ala 280 285 290				
cag agt ttt aag atc aac gcc ccc tca aac cag tcc tac cag gtc gag 1027 Gln Ser Phe Lys Ile Asn Ala Pro Ser Asn Gln Ser Tyr Gln Val Glu 295 300 305				
cta gct ctt cca ggt gcg ttc aac gtt gct aac gcc acg ttg gca ttt 1075 Leu Ala Leu Pro Gly Ala Phe Asn Val Ala Asn Ala Thr Leu Ala Phe 310 315 320 325				
gcc gct gcg gca cgc gtg ggt gtt gat ggc gaa gcg ttt gct cga ggc 1123 Ala Ala Ala Ala Arg Val Gly Val Asp Gly Glu Ala Phe Ala Arg Gly 330 335 340				
atg tcc aag gtc gcg gtt cca ggc cgt atg gaa cgc att gat gag gga 1171 Met Ser Lys Val Ala Val Pro Gly Arg Met Glu Arg Ile Asp Glu Gly 345 350 355				
caa gac ttc ctt gca gtg gtg gat tat gcc cac aag cct gct gca gtg 1219 Gln Asp Phe Leu Ala Val Val Asp Tyr Ala His Lys Pro Ala Ala Val 360 365 370				
gct gct gtg ttg gat acg ttg agg acc cag att gac ggg cgc ctc gga 1267 Ala Ala Val Leu Asp Thr Leu Arg Thr Gln Ile Asp Gly Arg Leu Gly 375 380 385				
gtg gtt atc ggt gct ggt gga gac cgc gat tcc acc aag cgt ggc ccc 1315 Val Val Ile Gly Ala Gly Gly Asp Arg Asp Ser Thr Lys Arg Gly Pro 390 395 400 405				
atg ggg cag ttg tcc gca cag cgt gct gat cta gtt att gtc act gat 1363 Met Gly Gln Leu Ser Ala Gln Arg Ala Asp Leu Val Ile Val Thr Asp 410 415 420				
gac aac cct cgt tca gag gtg cct gcc acg att cgc gca gca gtc act 1411 Asp Asn Pro Arg Ser Glu Val Pro Ala Thr Ile Arg Ala Ala Val Thr 425 430 435				
gca gga gca cag cag ggt gct tca gag tcc gaa cga ccg gtg gaa gtc 1459 Ala Gly Ala Gln Gln Gly Ala Ser Glu Ser Glu Arg Pro Val Glu Val 440 445 450				
cta gaa att ggt gac cgt gca gaa gca att cgc gtt ttg gtc gag tgg 1507 Leu Glu Ile Gly Asp Arg Ala Glu Ala Ile Arg Val Leu Val Glu Trp 455 460 465				
gca cag cct gga gat ggc att gta gta gct gga aaa ggc cat gaa gtt 1555 Ala Gln Pro Gly Asp Gly Ile Val Val Ala Gly Lys Gly His Glu Val 470 475 480 485				

gga caa cta gtt gct ggt gtc acc cac cat ttt gat gac cgc gaa gaa 1603
 Gly Gln Leu Val Ala Gly Val Thr His His Phe Asp Asp Arg Glu Glu
 490 495 500

gtt cgc gct gct ttg aca gaa aag ctc aac aat aaa ctt ccc ctt act 1651
 Val Arg Ala Ala Leu Thr Glu Lys Leu Asn Asn Lys Leu Pro Leu Thr
 505 510 515

acg gaa gaa gga taggccacag tcatgatcac aat 1686
 Thr Glu Glu Gly
 520

<210> 16

<211> 521

<212> PRT

<213> Corynebacterium glutamicum

<400> 16

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 20 25 30

Ile Ala Ala Ile Gly Leu Asp Ser Ser Ser Leu Pro Thr Ser Asp Ala
 35 40 45

Ile Phe Ala Ala Val Pro Gly Thr Arg Thr His Gly Ala Gln Phe Ala
 50 55 60

Gly Thr Asp Asn Ala Ala Lys Ala Val Ala Ile Leu Thr Asp Ala Ala
 65 70 75 80

Gly Leu Glu Val Leu Asn Glu Ala Gly Glu Thr Arg Pro Val Ile Val
 85 90 95

Val Asp Asp Val Arg Ala Val Leu Gly Ala Ala Ser Ser Ser Ile Tyr
 100 105 110

Gly Asp Pro Ser Lys Asp Phe Thr Leu Ile Gly Val Thr Gly Thr Ser
 115 120 125

Gly Lys Thr Thr Thr Ser Tyr Leu Leu Glu Lys Gly Leu Met Glu Ala
 130 135 140

Gly His Lys Val Gly Leu Ile Gly Thr Thr Gly Thr Arg Ile Asp Gly
 145 150 155 160

Glu Glu Val Pro Thr Lys Leu Thr Thr Pro Glu Ala Pro Thr Leu Gln
 165 170 175

Ala Leu Phe Ala Arg Met Arg Asp His Gly Val Thr His Val Val Met
 180 185 190

Glu Val Ser Ser His Ala Leu Ser Leu Gly Arg Val Ala Gly Ser His
 195 200 205

Phe Asp Val Ala Ala Phe Thr Asn Leu Ser Gln Asp His Leu Asp Phe
 210 215 220

His Pro Thr Met Asp Asp Tyr Phe Asp Ala Lys Ala Leu Phe Phe Arg
 225 230 235 240
 Ala Asp Ser Pro Leu Val Ala Asp Lys Gln Val Val Cys Val Asp Asp
 245 250 255
 Ser Trp Gly Gln Arg Met Ala Ser Val Ala Ala Asp Val Gln Thr Val
 260 265 270
 Ser Thr Leu Gly Gln Glu Ala Asp Phe Ser Ala Thr Asp Ile Asn Val
 275 280 285
 Ser Asp Ser Gly Ala Gln Ser Phe Lys Ile Asn Ala Pro Ser Asn Gln
 290 295 300
 Ser Tyr Gln Val Glu Leu Ala Leu Pro Gly Ala Phe Asn Val Ala Asn
 305 310 315 320
 Ala Thr Leu Ala Phe Ala Ala Ala Ala Arg Val Gly Val Asp Gly Glu
 325 330 335
 Ala Phe Ala Arg Gly Met Ser Lys Val Ala Val Pro Gly Arg Met Glu
 340 345 350
 Arg Ile Asp Glu Gly Gln Asp Phe Leu Ala Val Val Asp Tyr Ala His
 355 360 365
 Lys Pro Ala Ala Val Ala Ala Val Leu Asp Thr Leu Arg Thr Gln Ile
 370 375 380
 Asp Gly Arg Leu Gly Val Val Ile Gly Ala Gly Gly Asp Arg Asp Ser
 385 390 395 400
 Thr Lys Arg Gly Pro Met Gly Gln Leu Ser Ala Gln Arg Ala Asp Leu
 405 410 415
 Val Ile Val Thr Asp Asp Asn Pro Arg Ser Glu Val Pro Ala Thr Ile
 420 425 430
 Arg Ala Ala Val Thr Ala Gly Ala Gln Gln Gly Ala Ser Glu Ser Glu
 435 440 445
 Arg Pro Val Glu Val Leu Glu Ile Gly Asp Arg Ala Glu Ala Ile Arg
 450 455 460
 Val Leu Val Glu Trp Ala Gln Pro Gly Asp Gly Ile Val Val Ala Gly
 465 470 475 480
 Lys Gly His Glu Val Gly Gln Leu Val Ala Gly Val Thr His His Phe
 485 490 495
 Asp Asp Arg Glu Glu Val Arg Ala Ala Leu Thr Glu Lys Leu Asn Asn
 500 505 510
 Lys Leu Pro Leu Thr Thr Glu Glu Gly
 515 520

<210> 17

<211> 618

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(595)

<223> RXN00531

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ggccggtgac aatttatcaa gcagtgctat aataggggtc atg gca aac tac aca 115
 Met Ala Asn Tyr Thr
 1 5

gtc cct gga atc aac gag aat gac gca aag cag ctt att gat gga ctg 163
 Val Pro Gly Ile Asn Glu Asn Asp Ala Lys Gln Leu Ile Asp Gly Leu
 10 15 20

cag gag cgt ctc acc gac tac aac gat ctt cac ctc atc ttg aag cac 211
 Gln Glu Arg Leu Thr Asp Tyr Asn Asp Leu His Leu Ile Leu Lys His
 25 30 35

gtg cac tgg aac gtc act ggc ccc aac ttc att gct gtt cac gaa atg 259
 Val His Trp Asn Val Thr Gly Pro Asn Phe Ile Ala Val His Glu Met
 40 45 50

ctc gac cca cag gtt gac ctt gtt cgt ggc tat gct gac gaa gtt gca 307
 Leu Asp Pro Gln Val Asp Leu Val Arg Gly Tyr Ala Asp Glu Val Ala
 55 60 65

gag cgc att ttc acc ctc gga ggc gca cca gtt gga acc cca gaa ggc 355
 Glu Arg Ile Phe Thr Leu Gly Gly Ala Pro Val Gly Thr Pro Glu Gly
 70 75 80 85

cac gtt gct gac cgc acc cca ctg caa tat gag cgc aat gcc gga aat 403
 His Val Ala Asp Arg Thr Pro Leu Gln Tyr Glu Arg Asn Ala Gly Asn
 90 95 100

gtc caa gca cac ctc act gac ctc aat cgc gtg tac acc caa gtg ctg 451
 Val Gln Ala His Leu Thr Asp Leu Asn Arg Val Tyr Thr Gln Val Leu
 105 110 115

acc gga gtt cgc gag tcc atg gca tca gcc ggc cca gtg gat cca gta 499
 Thr Gly Val Arg Glu Ser Met Ala Ser Ala Gly Pro Val Asp Pro Val
 120 125 130

act gaa gac atc tac atc agc cag gcc gcg gag ctg gag aaa ttc cag 547
 Thr Glu Asp Ile Tyr Ile Ser Gln Ala Ala Glu Leu Glu Lys Phe Gln
 135 140 145

tgg ttc atc cgc gca cac att gtt gat gta gac gga aac atc caa gag 595
 Trp Phe Ile Arg Ala His Ile Val Asp Val Asp Gly Asn Ile Gln Glu
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taaaacgtcg aaaagcgta agg 618

<210> 18

<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 18

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Leu Ile Asp Gly Leu Gln Glu Arg Leu Thr Asp Tyr Asn Asp Leu His
          20           25           30
Leu Ile Leu Lys His Val His Trp Asn Val Thr Gly Pro Asn Phe Ile
          35           40           45
Ala Val His Glu Met Leu Asp Pro Gln Val Asp Leu Val Arg Gly Tyr
          50           55           60
Ala Asp Glu Val Ala Glu Arg Ile Phe Thr Leu Gly Gly Ala Pro Val
          65           70           75           80
Gly Thr Pro Glu Gly His Val Ala Asp Arg Thr Pro Leu Gln Tyr Glu
          85           90           95
Arg Asn Ala Gly Asn Val Gln Ala His Leu Thr Asp Leu Asn Arg Val
          100          105          110
Tyr Thr Gln Val Leu Thr Gly Val Arg Glu Ser Met Ala Ser Ala Gly
          115          120          125
Pro Val Asp Pro Val Thr Glu Asp Ile Tyr Ile Ser Gln Ala Ala Glu
          130          135          140
Leu Glu Lys Phe Gln Trp Phe Ile Arg Ala His Ile Val Asp Val Asp
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Gly Asn Ile Gln Glu
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<211> 1095

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1072)

<223> RXA00944

<400> 19

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atcaattgac ttctgctg gttgaatcag cgcaaggatt gtg gat ttt tgg act 115
          Val Asp Phe Trp Thr
          1           5
att ctc gac acc atg act tcc ctc ctt act ccc att gca atc cgt gga 163
Ile Leu Asp Thr Met Thr Ser Leu Leu Thr Pro Ile Ala Ile Arg Gly
          10           15           20
tta gaa att ccc aat agg atg tgg ctc gcg ccc atg tgc cag tac caa 211
Leu Glu Ile Pro Asn Arg Met Trp Leu Ala Pro Met Cys Gln Tyr Gln
          25           30           35

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gcc aat aac ctc gat ggg gtt cca ctt gat tgg cac ctc gtg cat tac	259
Ala Asn Asn Leu Asp Gly Val Pro Leu Asp Trp His Leu Val His Tyr	
40 45 50	
gga gcc cga gct gtt ggc ggc ttc gga ctc ctc atc gcg gaa tcc acc	307
Gly Ala Arg Ala Val Gly Gly Phe Gly Leu Leu Ile Ala Glu Ser Thr	
55 60 65	
ggc att agt cca gag gga aga atc tca tcg cgt tgc act ggc cta tgg	355
Gly Ile Ser Pro Glu Gly Arg Ile Ser Ser Arg Cys Thr Gly Leu Trp	
70 75 80 85	
aat gag gcc caa gtt gag gca tgg gag aga att aca aat ttt gtc cac	403
Asn Glu Ala Gln Val Glu Ala Trp Glu Arg Ile Thr Asn Phe Val His	
90 95 100	
gct caa ggt gga ctg atc ggt gtg caa ctt aac cat gca ggc cgc aaa	451
Ala Gln Gly Gly Leu Ile Gly Val Gln Leu Asn His Ala Gly Arg Lys	
105 110 115	
gcg agc aca tat ccg gcc ctt cct aac ttc cct act ggt act caa tca	499
Ala Ser Thr Tyr Pro Ala Leu Pro Asn Phe Pro Thr Gly Thr Gln Ser	
120 125 130	
gtt gac gag ggt gga tgg gaa acc ttt ggg cct agt gct gtc gct cag	547
Val Asp Glu Gly Gly Trp Glu Thr Phe Gly Pro Ser Ala Val Ala Gln	
135 140 145	
ccg ggg ctt gca gat ccg acc gaa ttg acc cgc gaa ggt att gaa aag	595
Pro Gly Leu Ala Asp Pro Thr Glu Leu Thr Arg Glu Gly Ile Glu Lys	
150 155 160 165	
gtt att cag gat ttc gct gct gct gca gag cgc gcg gtg cgt gca ggg	643
Val Ile Gln Asp Phe Ala Ala Ala Glu Arg Ala Val Arg Ala Gly	
170 175 180	
ttt gat gct gtg gag gtc cat ggt gcc cac ggt tac ctg ttg cat cag	691
Phe Asp Ala Val Glu Val His Gly Ala His Gly Tyr Leu Leu His Gln	
185 190 195	
ttc ctc act ccc ctc gca aat aaa cgt act gat att tat gga ggt tcg	739
Phe Leu Thr Pro Leu Ala Asn Lys Arg Thr Asp Ile Tyr Gly Gly Ser	
200 205 210	
ttt gag aat cgc aca cga cta ttt agg gaa gta gcc cag gcg atc cgt	787
Phe Glu Asn Arg Thr Arg Leu Phe Arg Glu Val Ala Gln Ala Ile Arg	
215 220 225	
gca gtg att ccg ggc tcg atg cca ctg att gcc cgg atc tct gcc acg	835
Ala Val Ile Pro Gly Ser Met Pro Leu Ile Ala Arg Ile Ser Ala Thr	
230 235 240 245	
gac tgg att gat gat gaa cct tcg tgg gat gac gat caa acc gtc tcg	883
Asp Trp Ile Asp Glu Pro Ser Trp Asp Asp Asp Gln Thr Val Ser	
250 255 260	
ctt gtg tca gga tct gaa aaa gct ggg tgt gga tgc agt cga tat ttc	931
Leu Val Ser Gly Ser Glu Lys Ala Gly Cys Gly Cys Ser Arg Tyr Phe	
265 270 275	

cac cgg agg tgc agt acc cgc gac aat ccc tgt gga gcc gag cta tca 979
 His Arg Arg Cys Ser Thr Arg Asp Asn Pro Cys Gly Ala Glu Leu Ser
 280 285 290
 agt gaa att tgc tcg tcg tgt gaa gca aga ggt ggg tat ccc tac ctc 1027
 Ser Glu Ile Cys Ser Ser Cys Glu Ala Arg Gly Gly Tyr Pro Tyr Leu
 295 300 305
 cgc ggt tgg att aat tac tca tgt ggg tca ggc gca ggg gca tct 1072
 Arg Gly Trp Ile Asn Tyr Ser Cys Gly Ser Gly Ala Gly Ala Ser
 310 315 320
 tgatcgtgga gatgcggaca tta 1095

<210> 20

<211> 324

<212> PRT

<213> Corynebacterium glutamicum

<400> 20

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 20 25 30
 Met Cys Gln Tyr Gln Ala Asn Asn Leu Asp Gly Val Pro Leu Asp Trp
 35 40 45
 His Leu Val His Tyr Gly Ala Arg Ala Val Gly Gly Phe Gly Leu Leu
 50 55 60
 Ile Ala Glu Ser Thr Gly Ile Ser Pro Glu Gly Arg Ile Ser Ser Arg
 65 70 75 80
 Cys Thr Gly Leu Trp Asn Glu Ala Gln Val Glu Ala Trp Glu Arg Ile
 85 90 95
 Thr Asn Phe Val His Ala Gln Gly Gly Leu Ile Gly Val Gln Leu Asn
 100 105 110
 His Ala Gly Arg Lys Ala Ser Thr Tyr Pro Ala Leu Pro Asn Phe Pro
 115 120 125
 Thr Gly Thr Gln Ser Val Asp Glu Gly Gly Trp Glu Thr Phe Gly Pro
 130 135 140
 Ser Ala Val Ala Gln Pro Gly Leu Ala Asp Pro Thr Glu Leu Thr Arg
 145 150 155 160
 Glu Gly Ile Glu Lys Val Ile Gln Asp Phe Ala Ala Ala Ala Glu Arg
 165 170 175
 Ala Val Arg Ala Gly Phe Asp Ala Val Glu Val His Gly Ala His Gly
 180 185 190
 Tyr Leu Leu His Gln Phe Leu Thr Pro Leu Ala Asn Lys Arg Thr Asp
 195 200 205
 Ile Tyr Gly Gly Ser Phe Glu Asn Arg Thr Arg Leu Phe Arg Glu Val

210	215	220
Ala Gln Ala Ile Arg	Ala Val Ile Pro Gly	Ser Met Pro Leu Ile Ala
225	230	235
Arg Ile Ser Ala Thr	Asp Trp Ile Asp	Asp Glu Pro Ser Trp Asp Asp
	245	250
Asp Gln Thr Val Ser	Leu Val Ser Gly	Ser Glu Lys Ala Gly Cys Gly
	260	265
Cys Ser Arg Tyr Phe	His Arg Arg Cys	Ser Thr Arg Asp Asn Pro Cys
	275	280
Gly Ala Glu Leu Ser	Ser Glu Ile Cys	Ser Ser Cys Glu Ala Arg Gly
	290	295
Gly Tyr Pro Tyr Leu	Arg Gly Trp Ile	Asn Tyr Ser Cys Gly Ser Gly
	305	310
Ala Gly Ala Ser		

<210> 21
 <211> 990
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(967)
 <223> RXS02560

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 Met Gln Gly Asn Ser 1 5
 ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca 163
 Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro 10 15 20
 gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca 211
 Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro 25 30 35
 ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt 259
 Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val 40 45 50
 cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att 307
 Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile 55 60 65
 att tcc gcc gca caa tcg gct gga acc tct tcc aat aag cag gtc att 355
 Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser Asn Lys Gln Val Ile 70 75 80 85

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tct gtc atc gtg gtt aaa gat cct gag ctg agg aaa ggc ctc gcg ggg 403
Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg Lys Gly Leu Ala Gly
          90          95          100

atc act cgc cag atg ttt ccg cac ctt gag cag gtt ccc gcg gtg ctg 451
Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln Val Pro Ala Val Leu
          105          110          115

att tgg ttg att gat tat tcc cga atc agt gcg gtg gca gcc aga gaa 499
Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu
          120          125          130

gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg 547
Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly
          135          140          145

ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag 595
Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu
          150          155          160          165

tca ctt gga ttg gga acg ctc tat ttg ggt tcg gtg cgc aac gat gcg 643
Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser Val Arg Asn Asp Ala
          170          175          180

gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc 691
Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val
          185          190          195

gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att 739
Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile
          200          205          210

aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc 787
Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr
          215          220          225

gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act 835
Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr
          230          235          240          245

tac tat tct cgc tac ggc cag cac cag ctc tgg tcg aag cag acg gcg 883
Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala
          250          255          260

cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt 931
His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu
          265          270          275

agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg 977
Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg
          280          285

attatggacg cct 990

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<210> 22

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 22

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 20 25 30
 Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His
 35 40 45
 Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
 50 55 60
 Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
 65 70 75 80
 Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
 85 90 95
 Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
 100 105 110
 Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
 115 120 125
 Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
 130 135 140
 Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
 145 150 155 160
 Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
 165 170 175
 Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
 180 185 190
 Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
 195 200 205
 Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
 210 215 220
 Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp
 225 230 235 240
 Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp
 245 250 255
 Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr
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 Asn Arg Gln Phe Leu Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu
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<212> DNA

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Met Ala Val Tyr Glu
1 5

ctc cca gaa ctc gac tac gca tac gac gct ctc gag cca cac atc gtc 163
Leu Pro Glu Leu Asp Tyr Ala Tyr Asp Ala Leu Glu Pro His Ile Val
10 15 20

gct gaa atc atg gag ctt gac cag tcc aag gac cac gca acc tac gtt 211
Ala Glu Ile Met Glu Leu Asp Gln Ser Lys Asp His Ala Thr Tyr Val
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<212> PRT

<213> Corynebacterium glutamicum

<400> 24

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His Ala Thr Tyr Val Ala Gly Ala Asn Ala Ala Leu
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<223> RXS03120

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Met Leu Asp Met Trp
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										gtg	tct	aaa	gtc	ctg			115
										Val	Ser	Lys	Val	Leu			
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aga gtt ggc gat cgc agc ccg cgc gtg gca gaa gtg cgc act acg ctc																	163
Arg	Val	Gly	Asp	Arg	Ser	Pro	Arg	Val	Ala	Glu	Val	Arg	Thr	Thr	Leu		
				10					15					20			
gct cgc ctc ggt gtg att gaa ggc tat tcc agg gag atg tct gca aag																	211
Ala	Arg	Leu	Gly	Val	Ile	Glu	Gly	Tyr	Ser	Arg	Glu	Met	Ser	Ala	Lys		
			25					30					35				
aca gaa tcc cag aag ttc cac gaa gaa gag acg ctt ttc gac gaa gaa																	259
Thr	Glu	Ser	Gln	Lys	Phe	His	Glu	Glu	Glu	Thr	Leu	Phe	Asp	Glu	Glu		
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ctc agc ctc agc atc aag tca ttc cag caa gct cga gga gtc gtt ccc																	307
Leu	Ser	Leu	Ser	Ile	Lys	Ser	Phe	Gln	Gln	Ala	Arg	Gly	Val	Val	Pro		
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Ser Gly Leu Ile Asp Asp Pro Thr Leu Arg Ala Ile Arg Glu Ala Ser	
70 75 80 85	
tac acc ctg gga acc cgc gtg ctg gcc tac cag ccc ggc aac cag ctt	403
Tyr Thr Leu Gly Thr Arg Val Leu Ala Tyr Gln Pro Gly Asn Gln Leu	
90 95 100	
gtt ggt gac gac gtt gta gaa atc caa tcc cat ctc caa gag ctc ggc	451
Val Gly Asp Asp Val Val Glu Ile Gln Ser His Leu Gln Glu Leu Gly	
105 110 115	
ttc tac gcc gac cgt gtg gat gga cat ttt ggc gag ctc aca cac aaa	499
Phe Tyr Ala Asp Arg Val Asp Gly His Phe Gly Glu Leu Thr His Lys	
120 125 130	
gct gtg atg aac tac caa ctc aac tac ggc atg cag gta gac ggc atc	547
Ala Val Met Asn Tyr Gln Leu Asn Tyr Gly Met Gln Val Asp Gly Ile	
135 140 145	
tgt ggc cct gac acc atc cgt gcg ctg tcc cga ctt ggt ctg cgc atc	595
Cys Gly Pro Asp Thr Ile Arg Ala Leu Ser Arg Leu Gly Leu Arg Ile	
150 155 160 165	
aag ggt ggc tct gct caa gct atc cgt gaa cgc gaa cgc atg cgc aat	643
Lys Gly Gly Ser Ala Gln Ala Ile Arg Glu Arg Glu Arg Met Arg Asn	
170 175 180	
gca ggc cca cgt ctt gct ggc aag cgt gtg gtc att gat cct gcg ctt	691
Ala Gly Pro Arg Leu Ala Gly Lys Arg Val Val Ile Asp Pro Ala Leu	
185 190 195	
ggg ggc tcc aac aag ggt cag atc gtg aaa ggc ccc tac ggt gag atc	739
Gly Gly Ser Asn Lys Gly Gln Ile Val Lys Gly Pro Tyr Gly Glu Ile	
200 205 210	
tct gag gaa gaa atc ctc tgg gat ttg gcc acc cgc ctg gaa ggt cgc	787
Ser Glu Glu Glu Ile Leu Trp Asp Leu Ala Thr Arg Leu Glu Gly Arg	
215 220 225	
atg atc gca aca ggc atg gaa acc att ctg tcg cgc ccg cac atg gat	835
Met Ile Ala Thr Gly Met Glu Thr Ile Leu Ser Arg Pro His Met Asp	
230 235 240 245	
gat ccc agc agc cgt gat cgc gcg tcg atc gcg aat gct ttc ggc gct	883
Asp Pro Ser Ser Arg Asp Arg Ala Ser Ile Ala Asn Ala Phe Gly Ala	
250 255 260	
gac ctc atg ctg agc ctg cac tgc gat tcc tac ccg aat gaa aaa gct	931
Asp Leu Met Leu Ser Leu His Cys Asp Ser Tyr Pro Asn Glu Lys Ala	
265 270 275	
aac ggc gtg gcc agc ttc tac ttc ggt tcg gaa aac ggc acc aac tcc	979
Asn Gly Val Ala Ser Phe Tyr Phe Gly Ser Glu Asn Gly Thr Asn Ser	
280 285 290	
ttg acc ggt gaa acg ctc tcc gcg tac atc caa aaa gag atc gtt gcc	1027
Leu Thr Gly Glu Thr Leu Ser Ala Tyr Ile Gln Lys Glu Ile Val Ala	
295 300 305	
cgc acc cca ctg aac aac tgt ggc agc cat gcc cgt acc tgg gat ctg	1075

Arg Thr Pro Leu Asn Asn Cys Gly Ser His Ala Arg Thr Trp Asp Leu
 310 315 320 325
 ctg cgc ctc acg cgc atg ccc atg gtg gaa gtt gtc acc ggt tac ctc 1123
 Leu Arg Leu Thr Arg Met Pro Met Val Glu Val Val Thr Gly Tyr Leu
 330 335 340
 acc aac ccc gat gac ctg gca gtt ctg act gat cca caa atg cgt gat 1171
 Thr Asn Pro Asp Asp Leu Ala Val Leu Thr Asp Pro Gln Met Arg Asp
 345 350 355
 cac att gcc gaa gcc atc gtt gtc gcc gtc aag cgc ctg tac ctc ctt 1219
 His Ile Ala Glu Ala Ile Val Val Ala Val Lys Arg Leu Tyr Leu Leu
 360 365 370
 gat gag gaa gca cag ccc aag acc gga acc ttc aag ttc tct gag ctg 1267
 Asp Glu Glu Ala Gln Pro Lys Thr Gly Thr Phe Lys Phe Ser Glu Leu
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 Leu Gln Ser Glu Gln Ala Gly
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<213> Corynebacterium glutamicum

<400> 28

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 Glu Met Ser Ala Lys Thr Glu Ser Gln Lys Phe His Glu Glu Glu Thr
 35 40 45
 Leu Phe Asp Glu Glu Leu Ser Leu Ser Ile Lys Ser Phe Gln Gln Ala
 50 55 60
 Arg Gly Val Val Pro Ser Gly Leu Ile Asp Asp Pro Thr Leu Arg Ala
 65 70 75 80
 Ile Arg Glu Ala Ser Tyr Thr Leu Gly Thr Arg Val Leu Ala Tyr Gln
 85 90 95
 Pro Gly Asn Gln Leu Val Gly Asp Asp Val Val Glu Ile Gln Ser His
 100 105 110
 Leu Gln Glu Leu Gly Phe Tyr Ala Asp Arg Val Asp Gly His Phe Gly
 115 120 125
 Glu Leu Thr His Lys Ala Val Met Asn Tyr Gln Leu Asn Tyr Gly Met
 130 135 140
 Gln Val Asp Gly Ile Cys Gly Pro Asp Thr Ile Arg Ala Leu Ser Arg
 145 150 155 160
 Leu Gly Leu Arg Ile Lys Gly Gly Ser Ala Gln Ala Ile Arg Glu Arg

165										170					175				
Glu	Arg	Met	Arg	Asn	Ala	Gly	Pro	Arg	Leu	Ala	Gly	Lys	Arg	Val	Val				
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Ile	Asp	Pro	Ala	Leu	Gly	Gly	Ser	Asn	Lys	Gly	Gln	Ile	Val	Lys	Gly				
		195					200					205							
Pro	Tyr	Gly	Glu	Ile	Ser	Glu	Glu	Glu	Ile	Leu	Trp	Asp	Leu	Ala	Thr				
	210					215					220								
Arg	Leu	Glu	Gly	Arg	Met	Ile	Ala	Thr	Gly	Met	Glu	Thr	Ile	Leu	Ser				
225					230					235					240				
Arg	Pro	His	Met	Asp	Asp	Pro	Ser	Ser	Arg	Asp	Arg	Ala	Ser	Ile	Ala				
				245					250					255					
Asn	Ala	Phe	Gly	Ala	Asp	Leu	Met	Leu	Ser	Leu	His	Cys	Asp	Ser	Tyr				
			260					265					270						
Pro	Asn	Glu	Lys	Ala	Asn	Gly	Val	Ala	Ser	Phe	Tyr	Phe	Gly	Ser	Glu				
		275					280						285						
Asn	Gly	Thr	Asn	Ser	Leu	Thr	Gly	Glu	Thr	Leu	Ser	Ala	Tyr	Ile	Gln				
	290					295					300								
Lys	Glu	Ile	Val	Ala	Arg	Thr	Pro	Leu	Asn	Asn	Cys	Gly	Ser	His	Ala				
305					310					315					320				
Arg	Thr	Trp	Asp	Leu	Leu	Arg	Leu	Thr	Arg	Met	Pro	Met	Val	Glu	Val				
				325					330					335					
Val	Thr	Gly	Tyr	Leu	Thr	Asn	Pro	Asp	Asp	Leu	Ala	Val	Leu	Thr	Asp				
			340					345					350						
Pro	Gln	Met	Arg	Asp	His	Ile	Ala	Glu	Ala	Ile	Val	Val	Ala	Val	Lys				
		355					360					365							
Arg	Leu	Tyr	Leu	Leu	Asp	Glu	Glu	Ala	Gln	Pro	Lys	Thr	Gly	Thr	Phe				
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 <223> RXA02641

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 Met Leu Ala Ile Ile
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ttg acc gcc gta ttg ggc gca tct ggc ctt gca gcc gct ggc act cag	163
Leu Thr Ala Val Leu Gly Ala Ser Gly Leu Ala Ala Ala Gly Thr Gln	
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tac ctc aat act cag ggc gaa ggc atc ggt ccg gtc gcc gtc caa aac	211
Tyr Leu Asn Thr Gln Gly Glu Gly Ile Gly Pro Val Ala Val Gln Asn	
25 30 35	
gac agt gaa tcg ttt aat tcc ggc acc aac gtg gtt gtt gaa gac gca	259
Asp Ser Glu Ser Phe Asn Ser Gly Thr Asn Val Val Glu Asp Ala	
40 45 50	
gca gtc acc gcc cag ggt gaa ggc gga ggc gct cgc acc gtc aag gaa	307
Ala Val Thr Ala Gln Gly Glu Gly Gly Gly Ala Arg Thr Val Lys Glu	
55 60 65	
ttc cag cgt gac cag caa ttc tct agt ttt gct ctt acc tgg acc ggt	355
Phe Gln Arg Asp Gln Gln Phe Ser Ser Phe Ala Leu Thr Trp Thr Gly	
70 75 80 85	
aaa aaa gac atc act gct ttt gtt cgc gca gaa cag gaa gac ggc acc	403
Lys Lys Asp Ile Thr Ala Phe Val Arg Ala Glu Gln Glu Asp Gly Thr	
90 95 100	
tgg tca cag tgg tac gac ttg gag cca atg gtc aat gaa gat caa ggc	451
Trp Ser Gln Trp Tyr Asp Leu Glu Pro Met Val Asn Glu Asp Gln Gly	
105 110 115	
acc aac gga act gag ctg atc tgg cac ggc cct acc aac aag atc cag	499
Thr Asn Gly Thr Glu Leu Ile Trp His Gly Pro Thr Asn Lys Ile Gln	
120 125 130	
gtt tcc acc ctc aac gtg gat ctc ttt gga gca gat gct gca gcc gct	547
Val Ser Thr Leu Asn Val Asp Leu Phe Gly Ala Asp Ala Ala Ala Ala	
135 140 145	
gat gaa aac ggt caa gac att cca gca gta gat gca gcc gag gca gcg	595
Asp Glu Asn Gly Gln Asp Ile Pro Ala Val Asp Ala Ala Glu Ala Ala	
150 155 160 165	
cca gca gca gaa cct gca cca gct gaa gca cca gtc gag gaa gct cct	643
Pro Ala Ala Glu Pro Ala Pro Ala Glu Ala Pro Val Glu Glu Ala Pro	
170 175 180	
gca cct gtc gca gaa cca gca cca gct gct gaa cct atc gct gag cca	691
Ala Pro Val Ala Glu Pro Ala Pro Ala Ala Glu Pro Ile Ala Glu Pro	
185 190 195	
gtc gct gat tac tca gca aat gac ggc ctc gct ccc ctg cca tcc aac	739
Val Ala Asp Tyr Ser Ala Asn Asp Gly Leu Ala Pro Leu Pro Ser Asn	
200 205 210	
tat ggc gac atc cag cct gtt gcc gat gtt gat gac ggc cta aac gca	787
Tyr Gly Asp Ile Gln Pro Val Ala Asp Val Asp Gly Leu Asn Ala	
215 220 225	
gta ttt atc gat ggc aac gct gat gca ggc gtg ggt atc gct aac gtt	835
Val Phe Ile Asp Gly Asn Ala Asp Ala Gly Val Gly Ile Ala Asn Val	
230 235 240 245	

gct gac acc gat ggc atg cca aag gtg att tct cgt gct ggt tgg ggt	883
Ala Asp Thr Asp Gly Met Pro Lys Val Ile Ser Arg Ala Gly Trp Gly	
250 255 260	
gcg gac gaa agt ctg cgc tgc tca aac cca act att gat gat ggc gtt	931
Ala Asp Glu Ser Leu Arg Cys Ser Asn Pro Thr Ile Asp Asp Gly Val	
265 270 275	
tct gcg atc acc att cac cac act gcg ggt tcc aac aac tac acc gag	979
Ser Ala Ile Thr Ile His His Thr Ala Gly Ser Asn Asn Tyr Thr Glu	
280 285 290	
gcg cag gct gca gcc cag gtt cgt agt gct tac agc tac cac gcc aag	1027
Ala Gln Ala Ala Ala Gln Val Arg Ser Ala Tyr Ser Tyr His Ala Lys	
295 300 305	
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Asn Leu Gly Trp Cys Asp Ile Gly Tyr Gln Ser Leu Val Asp Lys Tyr	
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ggc aac atc tac gaa ggc cgt gcc ggc ggc atg acc aat gct gtt cag	1123
Gly Asn Ile Tyr Glu Gly Arg Ala Gly Gly Met Thr Asn Ala Val Gln	
330 335 340	
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Gly Ala His Ala Gly Gly Phe Asn Gln Asn Thr Trp Ala Ile Ser Met	
345 350 355	
att ggc gac tat tcc tac aac gct ccc cct cag gaa acc atc aat gct	1219
Ile Gly Asp Tyr Ser Tyr Asn Ala Pro Pro Gln Glu Thr Ile Asn Ala	
360 365 370	
gtc ggt gag ctt gct ggt tgg cgt gca aag gtt gcc ggt ttc gac cca	1267
Val Gly Glu Leu Ala Gly Trp Arg Ala Lys Val Ala Gly Phe Asp Pro	
375 380 385	
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Thr Gly Thr Asp Thr His Tyr Ser Glu Gly Thr Ser Tyr Ala Lys Tyr	
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Ser Tyr Gly Thr Arg Val Ser Leu Pro Asn Ile Leu Ala His Arg Asn	
410 415 420	
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Val Gly Leu Thr Ala Cys Pro Gly Asp Ala Gly Tyr Ala Gln Met Glu	
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Asn Ile Arg Gln Ile Val Lys Ala Lys Tyr Thr Ser Leu Gln Asn Gly	
440 445 450	
aac aca ggt ggc acg act acc acc ccg gcg aca acg ccg aag gag acg	1507
Asn Thr Gly Gly Thr Thr Thr Pro Ala Thr Thr Pro Lys Glu Thr	
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tcg aca agc aat gct cct tcg acg acc act gcc cag ctt gta act ccc	1555
Ser Thr Ser Asn Ala Pro Ser Thr Thr Thr Ala Gln Leu Val Thr Pro	
470 475 480 485	
gct gaa cct cag cag tac agc gaa tcc gat gcc ctg gca gct ctg ctg	1603

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Thr	Gly	Gly	Ser	Ser	Gly	Gly	Thr	Asp	Leu	Leu	Asn	Gly	Ala	Asn	Ser		
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gag	cag	ctc	ctg	act	ggc	ctg	ggt	tcc	att	gcg	gct	gtg	ctg	att	gct	1699	
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			520				525					530					
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Ala	Ser	Leu	Ala	Asp	Gly	Gly	Leu	Asn	Gly	Leu	Ile	Ser	Asn	Val	Gly		
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agc	aac	aac	ggc	gtc	cca	gtg	ctt	ggc	gat	atc	aag	atc	act	gac	gtc	1795	
Ser	Asn	Asn	Gly	Val	Pro	Val	Leu	Gly	Asp	Ile	Lys	Ile	Thr	Asp	Val		
550					555				560					565			
atc	cca	atc	gtt	gat	acc	gcg	atc	aac	cta	acc	gga	gac	aat	aag	tac	1843	
Ile	Pro	Ile	Val	Asp	Thr	Ala	Ile	Asn	Leu	Thr	Gly	Asp	Asn	Lys	Tyr		
				570					575					580			
tct	cgc	ggt	tgg	aac	gac	ctg	aac	aac	acg	ctt	gga	cca	gtg	ctt	ggc	1891	
Ser	Arg	Gly	Trp	Asn	Asp	Leu	Asn	Asn	Thr	Leu	Gly	Pro	Val	Leu	Gly		
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gct	gcc	act	ggt	ggc	gaa	acc	acc	gtg	aag	tac	acc	agc	gac	cag	aac	1939	
Ala	Ala	Thr	Gly	Gly	Glu	Thr	Thr	Val	Lys	Tyr	Thr	Ser	Asp	Gln	Asn		
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tct	gag	gtt	act	ttc	gtg	ccg	ttt	gaa	aat	ggc	atc	atg	gtg	tct	tcc	1987	
Ser	Glu	Val	Thr	Phe	Val	Pro	Phe	Glu	Asn	Gly	Ile	Met	Val	Ser	Ser		
	615					620					625						
cct	gag	gct	gga	act	cac	ggc	ctg	tgg	ggc	gca	atc	ggt	gac	gcg	tgg	2035	
Pro	Glu	Ala	Gly	Thr	His	Gly	Leu	Trp	Gly	Ala	Ile	Gly	Asp	Ala	Trp		
630					635					640					645		
gct	cag	cag	ggc	gct	gac	ctt	ggc	cct	ctg	gga	ctt	cca	acc	agt	aat	2083	
Ala	Gln	Gln	Gly	Ala	Asp	Leu	Gly	Pro	Leu	Gly	Leu	Pro	Thr	Ser	Asn		
				650					655					660			
gaa	tac	acc	gtt	ggc	gaa	cag	ctt	cgt	gtt	gat	ttc	cag	aat	ggt	tac	2131	
Glu	Tyr	Thr	Val	Gly	Glu	Gln	Leu	Arg	Val	Asp	Phe	Gln	Asn	Gly	Tyr		
			665					670					675				
atc	act	tac	gat	tct	gcg	act	ggc	cag	gca	agc	att	cag	ctg	aac		2176	
Ile	Thr	Tyr	Asp	Ser	Ala	Thr	Gly	Gln	Ala	Ser	Ile	Gln	Leu	Asn			
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<211> 692

<212> PRT

<213> Corynebacterium glutamicum

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Val Ala Val Gln	Asn Asp Ser Glu	Ser Phe Asn Ser	Gly Thr Asn Val
35	40	45	
Val Val Glu Asp	Ala Ala Val Thr	Ala Gln Gly Glu	Gly Gly Gly Ala
50	55	60	
Arg Thr Val Lys	Glu Phe Gln Arg	Asp Gln Gln Phe	Ser Ser Phe Ala
65	70	75	80
Leu Thr Trp Thr	Gly Lys Lys Asp	Ile Thr Ala Phe	Val Arg Ala Glu
85	90	95	
Gln Glu Asp Gly	Thr Trp Ser Gln	Trp Tyr Asp Leu	Glu Pro Met Val
100	105	110	
Asn Glu Asp Gln	Gly Thr Asn Gly	Thr Glu Leu Ile	Trp His Gly Pro
115	120	125	
Thr Asn Lys Ile	Gln Val Ser Thr	Leu Asn Val Asp	Leu Phe Gly Ala
130	135	140	
Asp Ala Ala Ala	Ala Asp Glu Asn	Gly Gln Asp Ile	Pro Ala Val Asp
145	150	155	160
Ala Ala Glu Ala	Ala Pro Ala Ala	Glu Pro Ala Pro	Ala Glu Ala Pro
165	170	175	
Val Glu Glu Ala	Pro Ala Pro Val	Ala Glu Pro Ala	Pro Ala Ala Glu
180	185	190	
Pro Ile Ala Glu	Pro Val Ala Asp	Tyr Ser Ala Asn	Asp Gly Leu Ala
195	200	205	
Pro Leu Pro Ser	Asn Tyr Gly Asp	Ile Gln Pro Val	Ala Asp Val Asp
210	215	220	
Asp Gly Leu Asn	Ala Val Phe Ile	Asp Gly Asn Ala	Asp Ala Gly Val
225	230	235	240
Gly Ile Ala Asn	Val Ala Asp Thr	Asp Gly Met Pro	Lys Val Ile Ser
245	250	255	
Arg Ala Gly Trp	Gly Ala Asp Glu	Ser Leu Arg Cys	Ser Asn Pro Thr
260	265	270	
Ile Asp Asp Gly	Val Ser Ala Ile	Thr Ile His His	Thr Ala Gly Ser
275	280	285	
Asn Asn Tyr Thr	Glu Ala Gln Ala	Ala Ala Gln Val	Arg Ser Ala Tyr
290	295	300	
Ser Tyr His Ala	Lys Asn Leu Gly	Trp Cys Asp Ile	Gly Tyr Gln Ser
305	310	315	320
Leu Val Asp Lys	Tyr Gly Asn Ile	Tyr Glu Gly Arg	Ala Gly Gly Met
325	330	335	

Thr Asn Ala Val Gln Gly Ala His Ala Gly Gly Phe Asn Gln Asn Thr
 340 345 350
 Trp Ala Ile Ser Met Ile Gly Asp Tyr Ser Tyr Asn Ala Pro Pro Gln
 355 360 365
 Glu Thr Ile Asn Ala Val Gly Glu Leu Ala Gly Trp Arg Ala Lys Val
 370 375 380
 Ala Gly Phe Asp Pro Thr Gly Thr Asp Thr His Tyr Ser Glu Gly Thr
 385 390 395 400
 Ser Tyr Ala Lys Tyr Ser Tyr Gly Thr Arg Val Ser Leu Pro Asn Ile
 405 410 415
 Leu Ala His Arg Asn Val Gly Leu Thr Ala Cys Pro Gly Asp Ala Gly
 420 425 430
 Tyr Ala Gln Met Glu Asn Ile Arg Gln Ile Val Lys Ala Lys Tyr Thr
 435 440 445
 Ser Leu Gln Asn Gly Asn Thr Gly Gly Thr Thr Thr Thr Pro Ala Thr
 450 455 460
 Thr Pro Lys Glu Thr Ser Thr Ser Asn Ala Pro Ser Thr Thr Thr Ala
 465 470 475 480
 Gln Leu Val Thr Pro Ala Glu Pro Gln Gln Tyr Ser Glu Ser Asp Ala
 485 490 495
 Leu Ala Ala Leu Leu Thr Gly Gly Ser Ser Gly Gly Thr Asp Leu Leu
 500 505 510
 Asn Gly Ala Asn Ser Glu Gln Leu Leu Thr Gly Leu Gly Ser Ile Ala
 515 520 525
 Ala Val Leu Ile Ala Ala Ser Leu Ala Asp Gly Gly Leu Asn Gly Leu
 530 535 540
 Ile Ser Asn Val Gly Ser Asn Asn Gly Val Pro Val Leu Gly Asp Ile
 545 550 555 560
 Lys Ile Thr Asp Val Ile Pro Ile Val Asp Thr Ala Ile Asn Leu Thr
 565 570 575
 Gly Asp Asn Lys Tyr Ser Arg Gly Trp Asn Asp Leu Asn Asn Thr Leu
 580 585 590
 Gly Pro Val Leu Gly Ala Ala Thr Gly Gly Glu Thr Thr Val Lys Tyr
 595 600 605
 Thr Ser Asp Gln Asn Ser Glu Val Thr Phe Val Pro Phe Glu Asn Gly
 610 615 620
 Ile Met Val Ser Ser Pro Glu Ala Gly Thr His Gly Leu Trp Gly Ala
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 Ile Gly Asp Ala Trp Ala Gln Gln Gly Ala Asp Leu Gly Pro Leu Gly
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Leu Pro Thr Ser Asn Glu Tyr Thr Val Gly Glu Gln Leu Arg Val Asp
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Ile Gln Leu Asn
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 Val Lys Asp Lys Phe
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tta gtc act ggt gga gca cag ctg cag ggc gct gta aaa gtt tac ggc 163
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gca aaa aac agc gtt ttg aag ctc atg gca gca gca ctt ctc gct gaa 211
 Ala Lys Asn Ser Val Leu Lys Leu Met Ala Ala Ala Leu Leu Ala Glu
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 Gly Thr Thr Thr Leu Thr Asn Cys Pro Glu Ile Leu Asp Val Pro Leu
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atg cgc gac gtc ctc gtt ggt ctt ggc tgc gat gtc acc atc gac ggc 307
 Met Arg Asp Val Leu Val Gly Leu Gly Cys Asp Val Thr Ile Asp Gly
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tca acc gta acc att act acc cct gca gaa ctc agc tcc aat gct gac 355
 Ser Thr Val Thr Ile Thr Thr Pro Ala Glu Leu Ser Ser Asn Ala Asp
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gcc att gga tcc cgt cca ctc gac atg cat caa agc ggc ctg gaa aag 499
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Cys Val Leu Gly Pro Leu Thr Ala Arg Cys Gly Arg Ala Val Val Ser
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Leu Pro Gly Gly Asp Ala Ile Gly Ser Arg Pro Leu Asp Met His Gln
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Ser Gly Leu Glu Lys Leu Gly Ala Thr Thr Arg Ile Ser His Gly Ala
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Val Val Ala Glu Ala Glu Lys Leu Val Gly Ala Asn Ile Thr Leu Asp
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Phe Pro Ser Val Gly Ala Thr Glu Asn Ile Leu Thr Ala Ser Val Met
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Ala Glu Gly Arg Thr Val Leu Asp Asn Ala Ala Arg Glu Pro Glu Ile
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Val Asp Leu Cys Arg Met Leu Arg Ser Met Gly Ala Asn Ile Glu Gly
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Met Gln Gln Ile Met
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Gly Leu Asn Lys Thr Ala Lys Leu Val Ser Gln Leu Ala Ile Ala Leu	
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Ile Phe Gly Phe Leu Val Leu Gln Phe Pro Asp Glu Asn Gly Leu Thr	
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Pro Ala Ser Thr His Leu Ser Phe Ile Arg Asp Ile Asp Thr Ile Asp	

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Asp Phe Ser Gly Ser Met Ile Glu Arg Pro Val Pro Gly Ala Asp Ala

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Pro	Arg	Phe	Val	Asp 165	Phe	Val	Glu	Arg	Gly 170	Ile	Thr	Ser	Gly	Arg 175	Gln
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Glu 225	Glu	Thr	Ala	Lys	Asp 230	Val	Leu	Arg	Ile	Leu 235	Ser	Gln	Gln	Asp	Leu 240

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cgt gat cgt acc gag ctg acc gag gca gaa aag aac ctg ctg ggc ctg			643
Arg Asp Arg Thr Glu Leu Thr Glu Ala Glu Lys Asn Leu Leu Gly Leu			
	170	175	180
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Gly Phe Thr Pro Ile Ser Met Tyr Pro Gln Met Phe Thr Ala Ser Gly			
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gtg gct tat gag gaa ttg ttg gat gtg ttg gtg cag cag gca ttg cac			1171
Val Ala Tyr Glu Glu Leu Leu Asp Val Leu Val Gln Gln Ala Leu His			
	345	350	355
cgc gac aac tagcatcaaaa taaaaacagc ccc			1203
Arg Asp Asn			
	360		

<210> 38

<211> 360

<213> Corynebacterium glutamicum

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Gly	Arg	Ser	Ser 20	Glu	His	Ser	Val	Ser 25	Cys	Val	Ser	Ala	Gly 30	Ala	Ile
Met	Ala	His 35	Leu	Asp	Pro	Glu	Lys 40	Tyr	Asp	Val	Ile	Pro 45	Val	Gly	Ile
Thr	Val 50	Asp	Gly	Ala	Trp	Val 55	Val	Gly	Glu	Thr	Asp 60	Pro	Gln	Lys	Leu
Thr 65	Leu	Ile	Asp	Arg	Thr 70	Met	Pro	Glu	Val	Glu 75	His	His	Glu	Glu	Val 80
Arg	Pro	Ser	Leu	Asp 85	Pro	Ala	His	Arg	Gly 90	Glu	Phe	His	Phe	Ser 95	Asp
Gly	Ser	Leu	Tyr 100	Ala	Thr	Ala	Asp	Val 105	Ile	Phe	Pro	Val	Leu 110	His	Gly
Arg	Phe	Gly 115	Glu	Asp	Gly	Thr	Val 120	Gln	Gly	Leu	Phe	Ala 125	Leu	Ser	Asp
Ile	Pro 130	Val	Val	Gly	Pro	Gly 135	Val	Leu	Ala	Ser	Ala 140	Ala	Gly	Met	Asp
Lys 145	Glu	Tyr	Thr	Lys	Lys 150	Leu	Met	Ala	Ala	Glu 155	Gly	Leu	Pro	Val	Gly 160
Arg	Glu	Val	Ile 165	Leu	Arg	Asp	Arg	Thr	Glu 170	Leu	Thr	Glu	Ala	Glu 175	Lys
Asn	Leu	Leu	Gly 180	Leu	Pro	Val	Phe	Val 185	Lys	Pro	Ala	Arg	Gly 190	Gly	Ser
Ser	Ile	Gly 195	Ile	Ser	Arg	Val	Thr 200	Ala	Trp	Glu	Asp	Phe 205	Asn	Lys	Ala
Val	Gly 210	Leu	Ala	Arg	Ala	His 215	Asp	Glu	Lys	Val	Ile 220	Val	Glu	Ser	Glu
Ile 225	Val	Gly	Ser	Glu	Val 230	Glu	Cys	Gly	Val	Leu 235	Gln	Tyr	Pro	Asp	Gly 240
Arg	Ile	Val	Ala 245	Ser	Val	Pro	Ala	Leu	Leu 250	Ser	Gly	Thr	Glu	Ser 255	Gly
Ala	Gly	Gly	Phe 260	Tyr	Asp	Phe	Asp	Thr 265	Lys	Tyr	Leu	Asp	Asn 270	Val	Val
Thr	Ala	Glu	Ile 275	Pro	Ala	Pro	Leu	Asp	Glu	Lys	Thr	Thr 285	Glu	Leu	Ile
Gln	Ser 290	Leu	Ala	Val	Glu	Ser 295	Phe	Gln	Ala	Leu	Ala 300	Cys	Glu	Gly	Leu

Ala Arg Val Asp Phe Phe Val Thr Ala Asn Gly Pro Val Leu Asn Glu
305 310 315 320

Ile Asn Thr Met Pro Gly Phe Thr Pro Ile Ser Met Tyr Pro Gln Met
325 330 335

Phe Thr Ala Ser Gly Val Ala Tyr Glu Glu Leu Leu Asp Val Leu Val
340 345 350

Gln Gln Ala Leu His Arg Asp Asn
355 360

<210> 39

<211> 827

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(804)

<223> FRXA01022

<400> 39

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gtg ctg cat ggt cgt ttt ggt gaa gac ggc act gtg cag ggt ctg ttt	96
Val Leu His Gly Arg Phe Gly Glu Asp Gly Thr Val Gln Gly Leu Phe	
20 25 30	
gca ctg tct gat att ccg gtc gtt ggc cca ggt gtg ctg gcc tct gct	144
Ala Leu Ser Asp Ile Pro Val Val Gly Pro Gly Val Leu Ala Ser Ala	
35 40 45	
gcg gga atg gac aag gaa tac act aag aag ctc atg gca gcg gaa ggg	192
Ala Gly Met Asp Lys Glu Tyr Thr Lys Lys Leu Met Ala Ala Glu Gly	
50 55 60	
ctg ccc gtt ggc cgt gag gtg att cta cgt gat cgt acc gag ctg acc	240
Leu Pro Val Gly Arg Glu Val Ile Leu Arg Asp Arg Thr Glu Leu Thr	
65 70 75 80	
gag gca gaa aag aac ctg ctg ggc ctg cct gta ttt gtg aag cct gcg	288
Glu Ala Glu Lys Asn Leu Leu Gly Leu Pro Val Phe Val Lys Pro Ala	
85 90 95	
cgt ggt ggc tca tcg att ggt atc tct cgt gtt act gcg tgg gag gat	336
Arg Gly Gly Ser Ser Ile Gly Ile Ser Arg Val Thr Ala Trp Glu Asp	
100 105 110	
ttt aat aag gct gtg ggg ctt gct cgt gcc cat gat gag aag gtc att	384
Phe Asn Lys Ala Val Gly Leu Ala Arg Ala His Asp Glu Lys Val Ile	
115 120 125	
gtg gaa tca gag atc gtt ggc tct gag gtg gag tgt ggc gtg ctg cag	432
Val Glu Ser Glu Ile Val Gly Ser Glu Val Glu Cys Gly Val Leu Gln	
130 135 140	
tat cca gac ggt cgt atc gtg gcg tct gtt cct gcg ttg ctg tct ggc	480

Tyr Pro Asp Gly Arg Ile Val Ala Ser Val Pro Ala Leu Leu Ser Gly
 145 150 155 160
 acc gaa tca ggc gct ggt gga ttc tat gac ttt gat acc aag tac ttg 528
 Thr Glu Ser Gly Ala Gly Gly Phe Tyr Asp Phe Asp Thr Lys Tyr Leu
 165 170 175
 gac aac gtt gtt act gca gag atc cca gca ccg ctt gat gag aag acc 576
 Asp Asn Val Val Thr Ala Glu Ile Pro Ala Pro Leu Asp Glu Lys Thr
 180 185 190
 acg gaa ctg atc cag tct ttg gct gtg gaa tct ttc cag gct ctt gcg 624
 Thr Glu Leu Ile Gln Ser Leu Ala Val Glu Ser Phe Gln Ala Leu Ala
 195 200 205
 tgt gaa ggc ctt gct cgc gtg gac ttc ttt gtt acc gcc aat ggt cct 672
 Cys Glu Gly Leu Ala Arg Val Asp Phe Phe Val Thr Ala Asn Gly Pro
 210 215 220
 gtg ctc aat gag atc aac acc atg cca gga ttt acc ccc att tcc atg 720
 Val Leu Asn Glu Ile Asn Thr Met Pro Gly Phe Thr Pro Ile Ser Met
 225 230 235 240
 tac cca cag atg ttc act gca tca ggc gtg gct tat gag gaa ttg ttg 768
 Tyr Pro Gln Met Phe Thr Ala Ser Gly Val Ala Tyr Glu Glu Leu Leu
 245 250 255
 gat gtg ttg gtg cag cag gca ttg cac cgc gac aac tagcatcaaa 814
 Asp Val Leu Val Gln Gln Ala Leu His Arg Asp Asn
 260 265
 taaaaacagc ccc 827

<210> 40

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 40

His Phe Ser Asp Gly Ser Leu Tyr Ala Thr Ala Asp Val Ile Phe Pro
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Val Leu His Gly Arg Phe Gly Glu Asp Gly Thr Val Gln Gly Leu Phe
 20 25 30

Ala Leu Ser Asp Ile Pro Val Val Gly Pro Gly Val Leu Ala Ser Ala
 35 40 45

Ala Gly Met Asp Lys Glu Tyr Thr Lys Lys Leu Met Ala Ala Glu Gly
 50 55 60

Leu Pro Val Gly Arg Glu Val Ile Leu Arg Asp Arg Thr Glu Leu Thr
 65 70 75 80

Glu Ala Glu Lys Asn Leu Leu Gly Leu Pro Val Phe Val Lys Pro Ala
 85 90 95

Arg Gly Gly Ser Ser Ile Gly Ile Ser Arg Val Thr Ala Trp Glu Asp
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<210> 41
<211> 1212
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1189)
<223> RXA02703
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accgcagata aatgtgaaat caggagaact acgaataaag atg gct aac tcc cca															115	
Met Ala Asn Ser Pro																
1 5																
aaa ccc atg cgg gtt gtc gtt gct ggt ggc ggt acc gca gga cat att															163	
Lys	Pro	Met	Arg	Val	Val	Val	Ala	Gly	Gly	Gly	Thr	Ala	Gly	His	Ile	
10 15 20																
gag cct gcg ttg gca gtg gct gaa gcg ctg cgc gat aag cac ggt gca															211	
Glu	Pro	Ala	Leu	Ala	Val	Ala	Glu	Ala	Leu	Arg	Asp	Lys	His	Gly	Ala	
25 30 35																
aca gtt tcg gct tta ggt act gct cgt ggt ttg gaa aca acc ctg gtg															259	
Thr	Val	Ser	Ala	Leu	Gly	Thr	Ala	Arg	Gly	Leu	Glu	Thr	Thr	Leu	Val	
40 45 50																
cct gat cgt ggg ttt gag ctt cat ctc atc gag ccg gtt cca gtc cca															307	

Pro	Asp	Arg	Gly	Phe	Glu	Leu	His	Leu	Ile	Glu	Pro	Val	Pro	Val	Pro	
	55					60					65					
cgc	aag	ccc	aat	atg	gat	ttg	ttg	aag	ctc	cca	ttc	cgg	gta	gct	aag	355
Arg	Lys	Pro	Asn	Met	Asp	Leu	Leu	Lys	Leu	Pro	Phe	Arg	Val	Ala	Lys	
	70				75					80					85	
gca	tta	ggc	caa	gca	cgc	aag	gca	ctg	aag	gac	aca	gac	gct	caa	gcg	403
Ala	Leu	Gly	Gln	Ala	Arg	Lys	Ala	Leu	Lys	Asp	Thr	Asp	Ala	Gln	Ala	
			90						95					100		
gtc	atc	ggc	ttt	ggc	ggg	tat	gta	tct	gct	ccg	gct	tat	atg	gcg	gcg	451
Val	Ile	Gly	Phe	Gly	Gly	Tyr	Val	Ser	Ala	Pro	Ala	Tyr	Met	Ala	Ala	
			105					110					115			
aag	tct	ttg	ggc	ttg	cca	ttt	ttt	gtc	cac	gaa	gcc	aac	gcc	cgt	gca	499
Lys	Ser	Leu	Gly	Leu	Pro	Phe	Phe	Val	His	Glu	Ala	Asn	Ala	Arg	Ala	
		120				125						130				
ggc	atg	gcc	aac	aaa	ttg	ggc	gtc	aag	ctc	ggg	ggc	gtt	ggc	ctt	aat	547
Gly	Met	Ala	Asn	Lys	Leu	Gly	Val	Lys	Leu	Gly	Gly	Val	Gly	Leu	Asn	
	135				140					145						
gct	gtt	gct	ggg	tcc	ggc	atg	gac	ggc	gac	gtg	gtg	ggc	att	ccg	att	595
Ala	Val	Ala	Gly	Ser	Gly	Met	Asp	Gly	Asp	Val	Val	Gly	Ile	Pro	Ile	
	150				155					160					165	
cgt	gct	gtt	tta	agt	ggc	gcg	cgg	gat	gag	tcc	gca	gct	gac	cga	gcc	643
Arg	Ala	Val	Leu	Ser	Gly	Ala	Arg	Asp	Glu	Ser	Ala	Ala	Asp	Arg	Ala	
			170						175					180		
agg	gac	act	tgg	ggg	ttg	gac	aag	gac	cgc	caa	acc	att	ttt	gtc	acc	691
Arg	Asp	Thr	Trp	Gly	Leu	Asp	Lys	Asp	Arg	Gln	Thr	Ile	Phe	Val	Thr	
			185					190					195			
ggg	ggg	tcc	cag	ggc	tct	gtg	agt	atc	aac	aag	gcc	gtc	gag	caa	gct	739
Gly	Gly	Ser	Gln	Gly	Ser	Val	Ser	Ile	Asn	Lys	Ala	Val	Glu	Gln	Ala	
		200				205						210				
gta	gat	cag	ctg	gtg	gag	gca	ggg	ttc	cag	gtg	ctc	cac	gcc	gtg	ggg	787
Val	Asp	Gln	Leu	Val	Glu	Ala	Gly	Phe	Gln	Val	Leu	His	Ala	Val	Gly	
	215				220						225					
aag	aaa	aac	gag	ttg	cct	gca	gcg	aaa	ccc	ggc	tac	cat	ccc	gtt	ccg	835
Lys	Lys	Asn	Glu	Leu	Pro	Ala	Ala	Lys	Pro	Gly	Tyr	His	Pro	Val	Pro	
	230				235					240					245	
ttt	atc	gac	gat	atg	cag	gct	gcc	tac	acc	gtt	gct	gat	ctt	atc	gtg	883
Phe	Ile	Asp	Asp	Met	Gln	Ala	Ala	Tyr	Thr	Val	Ala	Asp	Leu	Ile	Val	
				250					255					260		
tgc	cgc	tcc	ggc	gcg	atg	acg	gtt	gca	gag	gtc	acc	gcc	gcc	ggc	gtc	931
Cys	Arg	Ser	Gly	Ala	Met	Thr	Val	Ala	Glu	Val	Thr	Ala	Ala	Gly	Val	
			265					270					275			
ccc	gcg	att	tat	gtc	ccg	ctg	cct	cac	ggc	aac	ggg	gag	cag	gct	ctc	979
Pro	Ala	Ile	Tyr	Val	Pro	Leu	Pro	His	Gly	Asn	Gly	Glu	Gln	Ala	Leu	
		280					285					290				
aac	gcc	cag	gct	gtc	att	aaa	gct	ggg	gcc	gca	cgc	cag	atc	gac	gac	1027
Asn	Ala	Gln	Ala	Val	Ile	Lys	Ala	Gly	Ala	Ala	Arg	Gln	Ile	Asp	Asp	

295	300	305	
gcg gac ttc acc gcc cag acg ctt atc gac gcc acc ctt gac att ctc			1075
Ala Asp Phe Thr Ala Gln Thr Leu Ile Asp Ala Thr Leu Asp Ile Leu			
310	315	320	325
ctt cat ccc tcc aca cac caa tcg atg tcg gac gca gct aaa acc tcc			1123
Leu His Pro Ser Thr His Gln Ser Met Ser Asp Ala Ala Lys Thr Ser			
	330	335	340
acc gca ggt aac gcc tcc acg gtg att gca gac atg att gct gca act			1171
Thr Ala Gly Asn Ala Ser Thr Val Ile Ala Asp Met Ile Ala Ala Thr			
	345	350	355
atc aat agc caa cac aac taaaacgacc agctcaacgc aaa			1212
Ile Asn Ser Gln His Asn			
360			

<210> 42

<211> 363

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 42

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Thr Ala Gly His Ile Glu Pro Ala Leu Ala Val Ala Glu Ala Leu Arg			
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Asp Lys His Gly Ala Thr Val Ser Ala Leu Gly Thr Ala Arg Gly Leu			
	35	40	45
Glu Thr Thr Leu Val Pro Asp Arg Gly Phe Glu Leu His Leu Ile Glu			
	50	55	60
Pro Val Pro Val Pro Arg Lys Pro Asn Met Asp Leu Leu Lys Leu Pro			
	65	70	75
Phe Arg Val Ala Lys Ala Leu Gly Gln Ala Arg Lys Ala Leu Lys Asp			
	85	90	95
Thr Asp Ala Gln Ala Val Ile Gly Phe Gly Gly Tyr Val Ser Ala Pro			
	100	105	110
Ala Tyr Met Ala Ala Lys Ser Leu Gly Leu Pro Phe Phe Val His Glu			
	115	120	125
Ala Asn Ala Arg Ala Gly Met Ala Asn Lys Leu Gly Val Lys Leu Gly			
	130	135	140
Gly Val Gly Leu Asn Ala Val Ala Gly Ser Gly Met Asp Gly Asp Val			
	145	150	155
Val Gly Ile Pro Ile Arg Ala Val Leu Ser Gly Ala Arg Asp Glu Ser			
	165	170	175
Ala Ala Asp Arg Ala Arg Asp Thr Trp Gly Leu Asp Lys Asp Arg Gln			
	180	185	190

Thr Ile Phe Val Thr Gly Gly Ser Gln Gly Ser Val Ser Ile Asn Lys
 195 200 205
 Ala Val Glu Gln Ala Val Asp Gln Leu Val Glu Ala Gly Phe Gln Val
 210 215 220
 Leu His Ala Val Gly Lys Lys Asn Glu Leu Pro Ala Ala Lys Pro Gly
 225 230 235 240
 Tyr His Pro Val Pro Phe Ile Asp Asp Met Gln Ala Ala Tyr Thr Val
 245 250 255
 Ala Asp Leu Ile Val Cys Arg Ser Gly Ala Met Thr Val Ala Glu Val
 260 265 270
 Thr Ala Ala Gly Val Pro Ala Ile Tyr Val Pro Leu Pro His Gly Asn
 275 280 285
 Gly Glu Gln Ala Leu Asn Ala Gln Ala Val Ile Lys Ala Gly Ala Ala
 290 295 300
 Arg Gln Ile Asp Asp Ala Asp Phe Thr Ala Gln Thr Leu Ile Asp Ala
 305 310 315 320
 Thr Leu Asp Ile Leu Leu His Pro Ser Thr His Gln Ser Met Ser Asp
 325 330 335
 Ala Ala Lys Thr Ser Thr Ala Gly Asn Ala Ser Thr Val Ile Ala Asp
 340 345 350
 Met Ile Ala Ala Thr Ile Asn Ser Gln His Asn
 355 360

<210> 43
 <211> 2235
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2212)
 <223> RXA02711

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 Val Thr Phe Pro Ser
 1 5
 aat ggc aga agt cgg ggc gag cgt gcg gga cgt gaa gat acg tcc cgc 163
 Asn Gly Arg Ser Arg Gly Glu Arg Ala Gly Arg Glu Asp Thr Ser Arg
 10 15 20
 cgt tcg gcg tat cag gac gaa agc aga aga gcc gct aga gag cgc gaa 211
 Arg Ser Ala Tyr Gln Asp Glu Ser Arg Arg Ala Ala Arg Glu Arg Glu
 25 30 35
 ctt acg cga cgc agc ggt aaa gct aaa ggc gta aac caa gaa gaa gga 259
 Leu Thr Arg Arg Ser Gly Lys Ala Lys Gly Val Asn Gln Glu Glu Gly

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Val	Thr	Tyr	Arg	Pro	Lys	Ser	Ser	Thr	Gln	Gly	Gly	Ala	Arg	Lys	Arg	
55					60					65						
cgt	gtg	aac	atg	gtt	acc	gct	atc	gca	ttg	gtc	atc	gct	ggc	gta	ctg	355
Arg	Val	Asn	Met	Val	Thr	Ala	Ile	Ala	Leu	Val	Ile	Ala	Gly	Val	Leu	
70					75					80					85	
atc	att	cgc	ctc	ggc	tgg	gtc	caa	gtt	gtc	tgg	gga	cca	gaa	ctg	tcc	403
Ile	Ile	Arg	Leu	Gly	Trp	Val	Gln	Val	Val	Trp	Gly	Pro	Glu	Leu	Ser	
90					95					100						
ctc	aat	gct	tcg	gaa	cag	cgc	acc	cgc	gtg	tac	gta	gat	cct	gca	cgt	451
Leu	Asn	Ala	Ser	Glu	Gln	Arg	Thr	Arg	Val	Tyr	Val	Asp	Pro	Ala	Arg	
105					110					115						
cgt	gga	agc	atc	gtg	gac	cgc	gaa	gga	aac	cag	atg	gcg	tac	acg	atg	499
Arg	Gly	Ser	Ile	Val	Asp	Arg	Glu	Gly	Asn	Gln	Met	Ala	Tyr	Thr	Met	
120					125					130						
cag	gca	cgt	tcg	ctg	acg	gtt	tct	ccg	aac	atc	atg	cgt	gag	gaa	tta	547
Gln	Ala	Arg	Ser	Leu	Thr	Val	Ser	Pro	Asn	Ile	Met	Arg	Glu	Glu	Leu	
135					140					145						
aag	acc	gga	act	gat	ttg	gcc	ttg	cgt	ttg	gcg	gct	gaa	gaa	acc	gat	595
Lys	Thr	Gly	Thr	Asp	Leu	Ala	Leu	Arg	Leu	Ala	Ala	Glu	Glu	Thr	Asp	
150					155					160					165	
ccg	gaa	aac	gtg	gcc	agc	tat	gtg	acc	atc	gaa	gaa	ggc	aac	gcg	tat	643
Pro	Glu	Asn	Val	Ala	Ser	Tyr	Val	Thr	Ile	Glu	Glu	Gly	Asn	Ala	Tyr	
170					175					180						
gtt	ttt	gcg	tct	gaa	gaa	cag	cgc	gaa	acc	att	ctg	tcc	gac	aag	gta	691
Val	Phe	Ala	Ser	Glu	Glu	Gln	Arg	Glu	Thr	Ile	Leu	Ser	Asp	Lys	Val	
185					190					195						
gaa	gag	cgc	att	caa	agc	att	gcg	gat	cgg	atc	cct	gag	atc	atc	aaa	739
Glu	Glu	Arg	Ile	Gln	Ser	Ile	Ala	Asp	Arg	Ile	Pro	Glu	Ile	Ile	Lys	
200					205					210						
tcc	cat	gac	caa	gat	gtc	act	gga	att	tcc	tct	gag	gag	atc	ctg	gac	787
Ser	His	Asp	Gln	Asp	Val	Thr	Gly	Ile	Ser	Ser	Glu	Glu	Ile	Leu	Asp	
215					220					225						
aag	ctc	aat	gct	gat	agc	cag	tat	gag	gtg	ctc	gtc	cgc	aat	gtt	gat	835
Lys	Leu	Asn	Ala	Asp	Ser	Gln	Tyr	Glu	Val	Leu	Val	Arg	Asn	Val	Asp	
230					235					240					245	
ccc	gat	gta	gcg	tca	gaa	atc	acc	gat	gag	atg	ccc	agc	gtc	gca	gct	883
Pro	Asp	Val	Ala	Ser	Glu	Ile	Thr	Asp	Glu	Met	Pro	Ser	Val	Ala	Ala	
250					255					260						
gat	cat	caa	gac	atc	cgc	caa	tac	cca	aac	ggc	gcg	att	ggt	gaa	aac	931
Asp	His	Gln	Asp	Ile	Arg	Gln	Tyr	Pro	Asn	Gly	Ala	Ile	Gly	Glu	Asn	
265					270					275						
atc	atc	ggg	cga	atc	agc	atg	gac	ggc	gaa	ggc	cag	ttc	ggc	ttt	gag	979
Ile	Ile	Gly	Arg	Ile	Ser	Met	Asp	Gly	Glu	Gly	Gln	Phe	Gly	Phe	Glu	
280					285					290						

gct tcc aac gat tcc ctg ttg gca gga aac aac ggt cgc tca acc cag	1027
Ala Ser Asn Asp Ser Leu Leu Ala Gly Asn Asn Gly Arg Ser Thr Gln	
295 300 305	
gac atg tcc att ttg gga caa gca ata ccg ggc acg ttg agg gat caa	1075
Asp Met Ser Ile Leu Gly Gln Ala Ile Pro Gly Thr Leu Arg Asp Gln	
310 315 320 325	
att cca gcc att gat ggt gcc agc gtt gaa ctc acc gtt gat ctg gat	1123
Ile Pro Ala Ile Asp Gly Ala Ser Val Glu Leu Thr Val Asp Leu Asp	
330 335 340	
ctg caa acc tat gtg cag cag gca ttg gag cag gcg aaa gct aac tcc	1171
Leu Gln Thr Tyr Val Gln Gln Ala Leu Glu Gln Ala Lys Ala Asn Ser	
345 350 355	
ggt gca gaa aac gcc tcc gct gtg gtt ctt gat gcc aag acc gct gag	1219
Gly Ala Glu Asn Ala Ser Ala Val Val Leu Asp Ala Lys Thr Ala Glu	
360 365 370	
gtt ttg gcg atg gca aac acc gat acc atc aac ccc aac gaa gac acg	1267
Val Leu Ala Met Ala Asn Thr Asp Thr Ile Asn Pro Asn Glu Asp Thr	
375 380 385	
gga aag cag att gag cag ggc aag agc ttt gac aat cct tct gtc acc	1315
Gly Lys Gln Ile Glu Gln Gly Lys Ser Phe Asp Asn Pro Ser Val Thr	
390 395 400 405	
cac ccc ttc gag cct ggt tct gta gcc aag gtg att act gca gca ggc	1363
His Pro Phe Glu Pro Gly Ser Val Ala Lys Val Ile Thr Ala Ala Gly	
410 415 420	
gta att caa gag ggc ttg act act cca gat gaa gtg ttg cag gta ccg	1411
Val Ile Gln Glu Gly Leu Thr Thr Pro Asp Glu Val Leu Gln Val Pro	
425 430 435	
ggc agt att gaa atg gcc ggt gtt tct gtc ggt gat gcg tgg gac cac	1459
Gly Ser Ile Glu Met Ala Gly Val Ser Val Gly Asp Ala Trp Asp His	
440 445 450	
ggt gtc gtt ccc tac acc act gca gga att ttt ggt aag tcc tcg aat	1507
Gly Val Val Pro Tyr Thr Thr Ala Gly Ile Phe Gly Lys Ser Ser Asn	
455 460 465	
gta ggc act ctg atg ctt gcg cag cgt ctt ggt gaa gat aaa ttt gct	1555
Val Gly Thr Leu Met Leu Ala Gln Arg Leu Gly Glu Asp Lys Phe Ala	
470 475 480 485	
gat tac ctg gaa cga ttc ggt gtg gga cag cca acg ggt att gag ctt	1603
Asp Tyr Leu Glu Arg Phe Gly Val Gly Gln Pro Thr Gly Ile Glu Leu	
490 495 500	
ccg agc gaa tcc caa ggc ctg ctg ccc gca cgt gag cag tgg tct ggc	1651
Pro Ser Glu Ser Gln Gly Leu Leu Pro Ala Arg Glu Gln Trp Ser Gly	
505 510 515	
ggt act ttt gct aac ctg ccc atc ggt cag ggt atg tcg atc acc acg	1699
Gly Thr Phe Ala Asn Leu Pro Ile Gly Gln Gly Met Ser Ile Thr Thr	
520 525 530	

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 Leu Gln Met Ala Gly Ile Tyr Gln Ala Leu Ala Asn Asp Gly Glu Arg
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att caa ccg cgg atc atc aag agc gtg act gat tct gac gga aca gtc 1795
 Ile Gln Pro Arg Ile Ile Lys Ser Val Thr Asp Ser Asp Gly Thr Val
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cta gag cag cca gaa ccc gat aaa atc cag gtt gtc agc gct gaa gct 1843
 Leu Glu Gln Pro Glu Pro Asp Lys Ile Gln Val Val Ser Ala Glu Ala
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gcc cgc acc acg gtg gat atg ttt agg tct gtc acc cag gtt gat cca 1891
 Ala Arg Thr Thr Val Asp Met Phe Arg Ser Val Thr Gln Val Asp Pro
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 Gln Ile Ser Gly Lys Thr Gly Thr Ala Gln Lys Val Asp Pro Asn Thr
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ggc gcg tac tct aac tcg caa tac tgg att acc ttc gcg ggt att gca 2035
 Gly Ala Tyr Ser Asn Ser Gln Tyr Trp Ile Thr Phe Ala Gly Ile Ala
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ccc gct gat gat cct cga ttt gtt gta gcc atc atg ctt gat gag cca 2083
 Pro Ala Asp Asp Pro Arg Phe Val Val Ala Ile Met Leu Asp Glu Pro
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 Glu Arg Gly Val His Gly Gly Gly Gly Gln Thr Ala Ala Pro Leu Phe
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aaa gac atc gcc acc tgg ttg ctc aac cgc gac aac atc cca ctg tct 2179
 Lys Asp Ile Ala Thr Trp Leu Leu Asn Arg Asp Asn Ile Pro Leu Ser
 680 685 690

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Asn Gln Glu Glu Gly Val Thr Tyr Arg Pro Lys Ser Ser Thr Gln Gly
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 Gly Ala Arg Lys Arg Arg Val Asn Met Val Thr Ala Ile Ala Leu Val
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 Gly Pro Glu Leu Ser Leu Asn Ala Ser Glu Gln Arg Thr Arg Val Tyr
 100 105 110
 Val Asp Pro Ala Arg Arg Gly Ser Ile Val Asp Arg Glu Gly Asn Gln
 115 120 125
 Met Ala Tyr Thr Met Gln Ala Arg Ser Leu Thr Val Ser Pro Asn Ile
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 Glu Gly Asn Ala Tyr Val Phe Ala Ser Glu Glu Gln Arg Glu Thr Ile
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 Pro Glu Ile Ile Lys Ser His Asp Gln Asp Val Thr Gly Ile Ser Ser
 210 215 220
 Glu Glu Ile Leu Asp Lys Leu Asn Ala Asp Ser Gln Tyr Glu Val Leu
 225 230 235 240
 Val Arg Asn Val Asp Pro Asp Val Ala Ser Glu Ile Thr Asp Glu Met
 245 250 255
 Pro Ser Val Ala Ala Asp His Gln Asp Ile Arg Gln Tyr Pro Asn Gly
 260 265 270
 Ala Ile Gly Glu Asn Ile Ile Gly Arg Ile Ser Met Asp Gly Glu Gly
 275 280 285
 Gln Phe Gly Phe Glu Ala Ser Asn Asp Ser Leu Leu Ala Gly Asn Asn
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 Gly Arg Ser Thr Gln Asp Met Ser Ile Leu Gly Gln Ala Ile Pro Gly
 305 310 315 320
 Thr Leu Arg Asp Gln Ile Pro Ala Ile Asp Gly Ala Ser Val Glu Leu
 325 330 335
 Thr Val Asp Leu Asp Leu Gln Thr Tyr Val Gln Gln Ala Leu Glu Gln
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 Ala Lys Ala Asn Ser Gly Ala Glu Asn Ala Ser Ala Val Val Leu Asp
 355 360 365

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 Pro Asn Glu Asp Thr Gly Lys Gln Ile Glu Gln Gly Lys Ser Phe Asp
 385 390 395 400
 Asn Pro Ser Val Thr His Pro Phe Glu Pro Gly Ser Val Ala Lys Val
 405 410 415
 Ile Thr Ala Ala Gly Val Ile Gln Glu Gly Leu Thr Thr Pro Asp Glu
 420 425 430
 Val Leu Gln Val Pro Gly Ser Ile Glu Met Ala Gly Val Ser Val Gly
 435 440 445
 Asp Ala Trp Asp His Gly Val Val Pro Tyr Thr Thr Ala Gly Ile Phe
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 Gly Lys Ser Ser Asn Val Gly Thr Leu Met Leu Ala Gln Arg Leu Gly
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 Glu Asp Lys Phe Ala Asp Tyr Leu Glu Arg Phe Gly Val Gly Gln Pro
 485 490 495
 Thr Gly Ile Glu Leu Pro Ser Glu Ser Gln Gly Leu Leu Pro Ala Arg
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 Glu Gln Trp Ser Gly Gly Thr Phe Ala Asn Leu Pro Ile Gly Gln Gly
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 Met Ser Ile Thr Thr Leu Gln Met Ala Gly Ile Tyr Gln Ala Leu Ala
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 Ser Asp Gly Thr Val Leu Glu Gln Pro Glu Pro Asp Lys Ile Gln Val
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 Val Ser Ala Glu Ala Ala Arg Thr Thr Val Asp Met Phe Arg Ser Val
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 Phe Ala Gly Ile Ala Pro Ala Asp Asp Pro Arg Phe Val Val Ala Ile
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 Met Leu Asp Glu Pro Glu Arg Gly Val His Gly Gly Gly Gly Gln Thr
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 Thr Leu Glu Lys Val Asn Ala Leu Ala Lys Glu Leu Gly Thr Gln Asp
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acc ttc gtt gcc act tat tcc ggt ttg gat gcg ccg gga atg tcg acc 192
 Thr Phe Val Ala Thr Tyr Ser Gly Leu Asp Ala Pro Gly Met Ser Thr
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 Ser Ala Tyr Asp Met Ser Leu Ile Tyr Gln His Ala Trp Gln Asn Pro
 65 70 75 80

gtt ttc gag tcg att atc tcc acc gat cac att gat ttc cct ggt tgg 288
 Val Phe Glu Ser Ile Ile Ser Thr Asp His Ile Asp Phe Pro Gly Trp
 85 90 95

ggc gac aat gag ggt ttc caa gtc tgg aac gat aac gcc ttg ttc atg 336
 Gly Asp Asn Glu Gly Phe Gln Val Trp Asn Asp Asn Ala Leu Phe Met
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aac gat cct gat ggc atc ggc ggc aag acc ggc tac acc gac gac gcg 384
 Asn Asp Pro Asp Gly Ile Gly Gly Lys Thr Gly Tyr Thr Asp Asp Ala
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aac cac acc ttt gtc ggc ggt ctc gat cgg ggt ggt cgc cgc ctc gcc 432
 Asn His Thr Phe Val Gly Gly Leu Asp Arg Gly Gly Arg Arg Leu Ala
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 Ala Val Leu Leu Asp Ser Thr Val Ser Asp Ile Arg Pro Trp Glu Gln
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 Ala Arg Leu Leu Ile Asp Ala Ser Leu Pro Ile Thr Pro Gly Ser Gly
 165 170 175

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 Val Gly Gln Leu Gly Ser Gly Ser Ala Asn Asp Val Ala Pro Ala Thr
 180 185 190

cca gaa tta cca gaa ccc acc gac aac ctg act tca ggt gag ggt ggg 624
 Pro Glu Leu Pro Glu Pro Thr Asp Asn Leu Thr Ser Gly Glu Gly Gly
 195 200 205

tcg cag aac acg ctg ctt aag ctc gtg gtg ccc atc gga atc atc gtg 672
 Ser Gln Asn Thr Leu Leu Lys Leu Val Val Pro Ile Gly Ile Ile Val
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ctg ttg cta atc gcc gca cta gcg tgg aca ttc aga tct ccc aag aaa 720
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 <213> Corynebacterium glutamicum

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Thr Leu Glu Lys Val Asn Ala Leu Ala Lys Glu Leu Gly Thr Gln Asp
 35 40 45

Thr Phe Val Ala Thr Tyr Ser Gly Leu Asp Ala Pro Gly Met Ser Thr
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Ser Ala Tyr Asp Met Ser Leu Ile Tyr Gln His Ala Trp Gln Asn Pro
 65 70 75 80

Val Phe Glu Ser Ile Ile Ser Thr Asp His Ile Asp Phe Pro Gly Trp
 85 90 95

Gly Asp Asn Glu Gly Phe Gln Val Trp Asn Asp Asn Ala Leu Phe Met
 100 105 110

Asn Asp Pro Asp Gly Ile Gly Gly Lys Thr Gly Tyr Thr Asp Asp Ala
 115 120 125

Asn His Thr Phe Val Gly Gly Leu Asp Arg Gly Gly Arg Arg Leu Ala
 130 135 140

Ala Val Leu Leu Asp Ser Thr Val Ser Asp Ile Arg Pro Trp Glu Gln
 145 150 155 160

Ala Arg Leu Leu Ile Asp Ala Ser Leu Pro Ile Thr Pro Gly Ser Gly
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Val Gly Gln Leu Gly Ser Gly Ser Ala Asn Asp Val Ala Pro Ala Thr
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Pro Glu Leu Pro Glu Pro Thr Asp Asn Leu Thr Ser Gly Glu Gly Gly

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Lys Asn

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 Met Arg Leu Lys Lys
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cag ctt ctt ggc agc ctg tta gtt gtc atc gtg gtt ttg tcc atc gcc 163
 Gln Leu Leu Gly Ser Leu Leu Val Val Ile Val Val Leu Ser Ile Ala
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gta gca acc acc aaa caa caa aaa ggc ttc gtc aca ggt cag ccc acc 211
 Val Ala Thr Thr Lys Gln Gln Lys Gly Phe Val Thr Gly Gln Pro Thr
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 Gly Ala Leu Asn Leu Ser Asp Ile Leu Asp Ser Glu Glu Leu Gly Glu
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tat cac ctc atg tca gcc gcc atc atc act ggt aac act gta gat ttc 307
 Tyr His Leu Met Ser Ala Ala Ile Ile Thr Gly Asn Thr Val Asp Phe
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agc ggg ctc ggc gca ggt cca gac gac cct ttt gaa atc gca tcg att 355
 Ser Gly Leu Gly Ala Gly Pro Asp Asp Pro Phe Glu Ile Ala Ser Ile
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 Thr Lys Ile Phe Thr Gly Glu Leu Leu Arg Leu Gln Ile Glu Arg Gly
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 Glu Ile Thr Glu Ser Thr Ala Val Gly Asp Val Leu Gly Glu Arg Val
 105 110 115

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 120 125 130

acc agc gga cta ccc cgt cta ggc aat gta gga ctt aga cct ttt atg 547
 Thr Ser Gly Leu Pro Arg Leu Gly Asn Val Gly Leu Arg Pro Phe Met
 135 140 145

gct acg ttc ttt gac aag aat cct tac aaa gac ctc tct gca gat cga 595
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gtc atc tct atc agc aca acg tcc aaa ttg aat tcg cgc gga gaa ttt 643
 Val Ile Ser Ile Ser Thr Thr Ser Lys Leu Asn Ser Arg Gly Glu Phe
 170 175 180

cac tac tca aat ctt ggt ttt gct ctg ctt ggc caa gtc ctt gcc cgc 691
 His Tyr Ser Asn Leu Gly Phe Ala Leu Leu Gly Gln Val Leu Ala Arg
 185 190 195

aat gcc ggt tta acg ttt gac cag ctc tta gac cgt gat tta ctg gca 739
 Asn Ala Gly Leu Thr Phe Asp Gln Leu Leu Asp Arg Asp Leu Leu Ala
 200 205 210

cca ctc aac ctc aat aac acc aag ctc atg acc cca gaa tcc ctc gct 787
 Pro Leu Asn Leu Asn Asn Thr Lys Leu Met Thr Pro Glu Ser Leu Ala
 215 220 225

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 Gln Asp Ala Pro Gln Gly Phe Ser Thr Pro Gly Lys Gln Val Glu Ala
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 Trp Glu Met Asp Gly Phe Leu Pro Ala Ala Gly Leu Arg Ser Thr Ala
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cgc gac atg gca gtt ttc tgt cag tac tta ttc aca aaa ggc ccc gcc 931
 Arg Asp Met Ala Val Phe Cys Gln Tyr Leu Phe Thr Lys Gly Pro Ala
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cct ttc acc tgg caa tcc ctt gaa tcg gcc cct gaa atc gtc tgg cat 979
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 Asn Gly Glu Ser Phe Gly Tyr Ser Ser Val Leu Phe Phe Asn Thr Ala
 295 300 305

aca act act gcc atc ttc gtt gct gcc gac gtt gcc aca tct gtc ttc 1075
 Thr Thr Thr Ala Ile Phe Val Ala Ala Asp Val Ala Thr Ser Val Phe
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cca att ggt cac gag ctt tta atg gca aac tcc act agg cag gaa tca 1123
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<211> 342

<212> PRT

<213> Corynebacterium glutamicum

<400> 48

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Thr	Gly	Gln	Pro	Thr	Gly	Ala	Leu	Asn	Leu	Ser	Asp	Ile	Leu	Asp	Ser
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Glu	Glu	Leu	Gly	Glu	Tyr	His	Leu	Met	Ser	Ala	Ala	Ile	Ile	Thr	Gly
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Asn	Thr	Val	Asp	Phe	Ser	Gly	Leu	Gly	Ala	Gly	Pro	Asp	Asp	Pro	Phe
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Glu	Ile	Ala	Ser	Ile	Thr	Lys	Ile	Phe	Thr	Gly	Glu	Leu	Leu	Arg	Leu
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Gln	Ile	Glu	Arg	Gly	Glu	Ile	Thr	Glu	Ser	Thr	Ala	Val	Gly	Asp	Val
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Glu	Leu	Ala	Asn	His	Thr	Ser	Gly	Leu	Pro	Arg	Leu	Gly	Asn	Val	Gly
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Leu	Arg	Pro	Phe	Met	Ala	Thr	Phe	Phe	Asp	Lys	Asn	Pro	Tyr	Lys	Asp
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Leu	Ser	Ala	Asp	Arg	Val	Ile	Ser	Ile	Ser	Thr	Thr	Ser	Lys	Leu	Asn
				165					170					175	
Ser	Arg	Gly	Glu	Phe	His	Tyr	Ser	Asn	Leu	Gly	Phe	Ala	Leu	Leu	Gly
			180					185					190		
Gln	Val	Leu	Ala	Arg	Asn	Ala	Gly	Leu	Thr	Phe	Asp	Gln	Leu	Leu	Asp
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Arg	Asp	Leu	Leu	Ala	Pro	Leu	Asn	Leu	Asn	Asn	Thr	Lys	Leu	Met	Thr
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Pro	Glu	Ser	Leu	Ala	Gln	Asp	Ala	Pro	Gln	Gly	Phe	Ser	Thr	Pro	Gly
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Lys	Gln	Val	Glu	Ala	Trp	Glu	Met	Asp	Gly	Phe	Leu	Pro	Ala	Ala	Gly
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Leu	Arg	Ser	Thr	Ala	Arg	Asp	Met	Ala	Val	Phe	Cys	Gln	Tyr	Leu	Phe
			260					265					270		
Thr	Lys	Gly	Pro	Ala	Pro	Phe	Thr	Trp	Gln	Ser	Leu	Glu	Ser	Ala	Pro
		275					280					285			
Glu	Ile	Val	Trp	His	Asn	Gly	Glu	Ser	Phe	Gly	Tyr	Ser	Ser	Val	Leu
	290					295					300				
Phe	Phe	Asn	Thr	Ala	Thr	Thr	Thr	Ala	Ile	Phe	Val	Ala	Ala	Asp	Val
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Thr Arg Gln Glu Ser Lys
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<211> 1008

<212> DNA

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<223> RXN03092

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 Val Ser Thr Thr Asn
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tct ctg aca aag ctc gtt gca tct aca gtc gcc gct ggc gtc ctt ggt 163
 Ser Leu Thr Lys Leu Val Ala Ser Thr Val Ala Ala Gly Val Leu Gly
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gcg ctc gca ctt gtg cct ttc gct agt ctt tct ggc gtt gcg gtt gcg 211
 Ala Leu Ala Leu Val Pro Phe Ala Ser Leu Ser Gly Val Ala Val Ala
 25 30 35

cgt acc aat gac acg atg cag acc aac ctt tca gat ctg acg gat ggt 259
 Arg Thr Asn Asp Thr Met Gln Thr Asn Leu Ser Asp Leu Thr Asp Gly
 40 45 50

cgc ggg ccg ggc gtc acg acg att act gat tcc act gac cag ccg att 307
 Arg Gly Pro Gly Val Thr Thr Ile Thr Asp Ser Thr Asp Gln Pro Ile
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gct tat att tat gcg cag ccg ccg ttt gag gtt ggg ggt gat cag att 355
 Ala Tyr Ile Tyr Ala Gln Arg Arg Phe Glu Val Gly Gly Asp Gln Ile
 70 75 80 85

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 Ser Thr Ser Met Lys Asp Ala Ile Val Ser Ile Glu Asp Arg Arg Phe
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 Tyr Glu His Asp Gly Val Asp Leu Gln Gly Phe Gly Arg Ala Ile Leu
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 Thr Asn Leu Ala Ala Gly Gly Val Glu Gln Gly Ala Ser Thr Ile Asn
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cag cag tat gtg aag aac ttc ttg ctg ttg gtg gaa gct gat gat gag 547
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 135 140 145

gcg gag cag gct gct gct gtg gaa acc tcc atc cct cgt aag ctc cgt 595
 Ala Glu Gln Ala Ala Val Glu Thr Ser Ile Pro Arg Lys Leu Arg
 150 155 160 165

 gag atg aag atg gcg tct gat ttg gaa aag acg ttg tcg aag gat gag 643
 Glu Met Lys Met Ala Ser Asp Leu Glu Lys Thr Leu Ser Lys Asp Glu
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 Ile Leu Thr Arg Tyr Leu Asn Ile Val Pro Phe Gly Asn Gly Ala Tyr
 185 190 195

 ggt gtt gag gct gcg gcg cgg acg tat ttc ggt acg tcg gct gcc gag 739
 Gly Val Glu Ala Ala Ala Arg Thr Tyr Phe Gly Thr Ser Ala Ala Glu
 200 205 210

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 Leu Thr Ile Pro Gln Ser Ala Met Leu Ala Gly Ile Val Gln Ser Ser
 215 220 225

 tct tat ctc aat cca tac acc aat cac gat gct gtg ttt gag cgt cgt 835
 Ser Tyr Leu Asn Pro Tyr Thr Asn His Asp Ala Val Phe Glu Arg Arg
 230 235 240 245

 aat act gtt ttg ggc gct atg gct gat gct ggc gcg att tcc cca gac 883
 Asn Thr Val Leu Gly Ala Met Ala Asp Ala Gly Ala Ile Ser Pro Asp
 250 255 260

 gag gct tcg gct ttc cag cag gaa cct ttg ggt gtc ctg gaa acc ccg 931
 Glu Ala Ser Ala Phe Gln Gln Glu Pro Leu Gly Val Leu Glu Thr Pro
 265 270 275

 caa ggc tta tcc aat ggt tgt atc ggc gct ggc gat cgg tgg ttt ttt 979
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 Leu Gln
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<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 50

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 20 25 30

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Asp Leu Thr Asp Gly Arg Gly Pro Gly Val Thr Thr Ile Thr Asp Ser
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Thr Asp Gln Pro Ile Ala Tyr Ile Tyr Ala Gln Arg Arg Phe Glu Val
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Val Ser Thr Thr Asn
1 5
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Ala	Leu	Ala	Leu	Val	Pro	Phe	Ala	Ser	Leu	Ser	Gly	Val	Ala	Val	Ala	
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cgt	acc	aat	gac	acg	atg	cag	acc	aac	ctt	tca	gat	ctg	acg	gat	ggg	259
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Ser	Thr	Ser	Met	Lys	Asp	Ala	Ile	Val	Ser	Ile	Glu	Asp	Arg	Arg	Phe	
				90					95					100		
tat	gag	cat	gat	ggg	gtg	gat	ttg	cag	ggc	ttt	ggg	cgt	gca	atc	ctg	451
Tyr	Glu	His	Asp	Gly	Val	Asp	Leu	Gln	Gly	Phe	Gly	Arg	Ala	Ile	Leu	
			105					110					115			
acg	aac	ctg	gct	gcg	ggg	ggc	gtg	gag	cag	ggg	gct	tcg	acg	att	aac	499
Thr	Asn	Leu	Ala	Ala	Gly	Gly	Val	Glu	Gln	Gly	Ala	Ser	Thr	Ile	Asn	
		120					125					130				
cag	cag	tat	gtg	aag	aac	ttc	ttg	ctg	ttg	gtg	gaa	gct	gat	gat	gag	547
Gln	Gln	Tyr	Val	Lys	Asn	Phe	Leu	Leu	Leu	Val	Glu	Ala	Asp	Asp	Glu	
		135				140					145					
gcg	gag	cag	gct	gct	gct	gtg	gaa	acc	tcc	atc	cct	cgt	aag	ctc	cgt	595
Ala	Glu	Gln	Ala	Ala	Ala	Val	Glu	Thr	Ser	Ile	Pro	Arg	Lys	Leu	Arg	
	150				155					160					165	
gag	atg	aag	atg	gcg	tct	gat	ttg	gaa	aag	acg	ttg	tcg	aag	gat	gag	643
Glu	Met	Lys	Met	Ala	Ser	Asp	Leu	Glu	Lys	Thr	Leu	Ser	Lys	Asp	Glu	
				170					175					180		
att	ctg	act	cgt	tat	ctc	aac	att	gtt	cct	ttt	ggg	aat	ggg	gct	tat	691
Ile	Leu	Thr	Arg	Tyr	Leu	Asn	Ile	Val	Pro	Phe	Gly	Asn	Gly	Ala	Tyr	
			185					190					195			
ggg	gtt	gag	gct	gcg	gcg	cgg	acg	tat	ttc	ggg	acg	tcg	gct	gcc	gag	739
Gly	Val	Glu	Ala	Ala	Ala	Arg	Thr	Tyr	Phe	Gly	Thr	Ser	Ala	Ala	Glu	
		200					205					210				
tta	acc	att	cca	cag	tct	gcg	atg	ctc	gcg	ggc	att	gtg	cag	tct	tcg	787
Leu	Thr	Ile	Pro	Gln	Ser	Ala	Met	Leu	Ala	Gly	Ile	Val	Gln	Ser	Ser	
		215				220					225					
tct	tat	ctc	aat	cca	tac	acc	aat	cac	gat	gct	gtg	ttt	gag	cgt	cgt	835
Ser	Tyr	Leu	Asn	Pro	Tyr	Thr	Asn	His	Asp	Ala	Val	Phe	Glu	Arg	Arg	
	230				235					240					245	
aat	act	gtt	ttg	ggc	gct	atg	gct	gat	gct	ggc	gcg	att	tcc	cca	gac	883

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<211> 311
<212> PRT
<213> Corynebacterium glutamicum
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Ala	Gly	Val	Leu	Gly	Ala	Leu	Ala	Leu	Val	Pro	Phe	Ala	Ser	Leu	Ser
			20					25					30		
Gly	Val	Ala	Val	Ala	Arg	Thr	Asn	Asp	Thr	Met	Gln	Thr	Asn	Leu	Ser
		35					40					45			
Asp	Leu	Thr	Asp	Gly	Arg	Gly	Pro	Gly	Val	Thr	Thr	Ile	Thr	Asp	Ser
	50					55					60				
Thr	Asp	Gln	Pro	Ile	Ala	Tyr	Ile	Tyr	Ala	Gln	Arg	Arg	Phe	Glu	Val
65					70					75					80
Gly	Gly	Asp	Gln	Ile	Ser	Thr	Ser	Met	Lys	Asp	Ala	Ile	Val	Ser	Ile
				85					90					95	
Glu	Asp	Arg	Arg	Phe	Tyr	Glu	His	Asp	Gly	Val	Asp	Leu	Gln	Gly	Phe
			100					105					110		
Gly	Arg	Ala	Ile	Leu	Thr	Asn	Leu	Ala	Ala	Gly	Gly	Val	Glu	Gln	Gly
		115					120					125			
Ala	Ser	Thr	Ile	Asn	Gln	Gln	Tyr	Val	Lys	Asn	Phe	Leu	Leu	Leu	Val
	130					135					140				
Glu	Ala	Asp	Asp	Glu	Ala	Glu	Gln	Ala	Ala	Ala	Val	Glu	Thr	Ser	Ile
145					150					155					160
Pro	Arg	Lys	Leu	Arg	Glu	Met	Lys	Met	Ala	Ser	Asp	Leu	Glu	Lys	Thr
				165					170					175	
Leu	Ser	Lys	Asp	Glu	Ile	Leu	Thr	Arg	Tyr	Leu	Asn	Ile	Val	Pro	Phe
			180					185					190		

Gly Asn Gly Ala Tyr Gly Val Glu Ala Ala Ala Arg Thr Tyr Phe Gly
 195 200 205
 Thr Ser Ala Ala Glu Leu Thr Ile Pro Gln Ser Ala Met Leu Ala Gly
 210 215 220
 Ile Val Gln Ser Ser Ser Tyr Leu Asn Pro Tyr Thr Asn His Asp Ala
 225 230 235 240
 Val Phe Glu Arg Arg Asn Thr Val Leu Gly Ala Met Ala Asp Ala Gly
 245 250 255
 Ala Ile Ser Pro Asp Glu Ala Ser Ala Phe Gln Gln Glu Pro Leu Gly
 260 265 270
 Val Leu Glu Thr Pro Gln Gly Leu Ser Asn Gly Cys Ile Gly Ala Gly
 275 280 285
 Asp Arg Gly Phe Phe Cys Asp Tyr Ala Leu Gln Tyr Leu Ser Glu Gln
 290 295 300
 Gly Ile Thr Gln Asp Met Leu
 305 310

<210> 53
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1522)
 <223> RXA01828

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 gccgacctgt catgtccaag caagcatcgg aggtggctgc gtg aac cgc tcg att 115
 Val Asn Arg Ser Ile
 1 5
 cga atc aca tcc ctc ttc tct ttg ctc ctg atc ttg gtg ctc gta gca 163
 Arg Ile Thr Ser Leu Phe Ser Leu Leu Leu Ile Leu Val Leu Val Ala
 10 15 20
 aac ctc acc tgg att cag gct ttt agg gac gat gat ctt gct cag aac 211
 Asn Leu Thr Trp Ile Gln Ala Phe Arg Asp Asp Asp Leu Ala Gln Asn
 25 30 35
 cca ctg aac gca cgt ggt ttc ctg gag gcg aag tcc act ccg cgt gga 259
 Pro Leu Asn Ala Arg Gly Phe Leu Glu Ala Lys Ser Thr Pro Arg Gly
 40 45 50
 cag att tca act ggt ggc caa gta ctc gca gag tcc tcc cag gac gat 307
 Gln Ile Ser Thr Gly Gly Gln Val Leu Ala Glu Ser Ser Gln Asp Asp
 55 60 65
 cag ggt ttt tac cag cgc agc tac atc acc aac ccg act gcc tac gca 355
 Gln Gly Phe Tyr Gln Arg Ser Tyr Ile Thr Asn Pro Thr Ala Tyr Ala

70	75	80	85	
ccg gtg gtt ggt tac ctc tct gat gtt tat gga gca gct ggc ctg gaa	403			
Pro Val Val Gly Tyr 90		95	100	
ttg gga tac aac tct atc ctc aac ggc agt gac tct tcc ctg ttt acc	451			
Leu Gly Tyr Asn Ser Ile Leu Asn Gly Ser Asp Ser Ser Leu Phe Thr	105	110	115	
tcc cag tgg ctg gat gtc att tct ggc agc cct acc cat ggc gca aac	499			
Ser Gln Trp Leu Asp Val Ile Ser Gly Ser Pro Thr His Gly Ala Asn	120	125	130	
att gag ctg acc ttg gat ccc aat gcg cag caa act gct tat gaa cag	547			
Ile Glu Leu Thr Leu Asp Pro Asn Ala Gln Gln Thr Ala Tyr Glu Gln	135	140	145	
ctg agc caa agc ggc tac gag ggt gct gtg gtg gcg ctt cgc cca agc	595			
Leu Ser Gln Ser Gly Tyr Glu Gly Ala Val Val Ala Leu Arg Pro Ser	150	155	160	165
act ggt gag gtg ctg gcc atg gcg tca tcg cca agc tat gac ccc aac	643			
Thr Gly Glu Val Leu Ala Met Ala Ser Ser Pro Ser Tyr Asp Pro Asn	170	175	180	
cag atc gtg gat cca gca acc gca gag gac gct tgg gct gag tac acc	691			
Gln Ile Val Asp Pro Ala Thr Ala Glu Asp Ala Trp Ala Glu Tyr Thr	185	190	195	
tcc act gaa ggt gca ccg ctg ctc aac cat gca acg cag gaa tca ctg	739			
Ser Thr Glu Gly Ala Pro Leu Leu Asn His Ala Thr Gln Glu Ser Leu	200	205	210	
cct cct gga tct att ttc aag atc atc act act gcg gca gct ttg gaa	787			
Pro Pro Gly Ser Ile Phe Lys Ile Ile Thr Thr Ala Ala Ala Leu Glu	215	220	225	
aac ggc tac tct gct gat tcc acc gtg act gca gag gca gca gtg acc	835			
Asn Gly Tyr Ser Ala Asp Ser Thr Val Thr Ala Glu Ala Ala Val Thr	230	235	240	245
ctg cct ggc acc aac acc acc ttg acc aac tac ggc ggt cag aca tgt	883			
Leu Pro Gly Thr Asn Thr Thr Leu Thr Asn Tyr Gly Gly Gln Thr Cys	250	255	260	
gcg ggc ggt ggc acc act acc ctg ctc acc gct ttc cag ctc tcc tgc	931			
Ala Gly Gly Gly Thr Thr Thr Leu Leu Thr Ala Phe Gln Leu Ser Cys	265	270	275	
aat act gcg ttt gtg gag acc ggc att gat gtt ggc gcg gat gct ttg	979			
Asn Thr Ala Phe Val Glu Thr Gly Ile Asp Val Gly Ala Asp Ala Leu	280	285	290	
cgc gcg tct gcc gag gac ttc gga gtg gga caa acc tac agc ttg gga	1027			
Arg Ala Ser Ala Glu Asp Phe Gly Val Gly Gln Thr Tyr Ser Leu Gly	295	300	305	
cta gat aac gtt cct ggc ggc ttg ggt gaa atc ccc gac gat gcc gcc	1075			
Leu Asp Asn Val Pro Gly Gly Leu Gly Glu Ile Pro Asp Asp Ala Ala	310	315	320	325

ctt gga caa tcc agc att ggc cag cgc gac gtg caa atg aac gtg ctg 1123
 Leu Gly Gln Ser Ser Ile Gly Gln Arg Asp Val Gln Met Asn Val Leu
 330 335 340

cag gcc gct gtc atg gca gga acc gta tcc aac ggt ggc gta cgc atg 1171
 Gln Ala Ala Val Met Ala Gly Thr Val Ser Asn Gly Gly Val Arg Met
 345 350 355

gaa cca tat ttg gta tcc cgc gtc acc ggt cag gac ctg agc gaa ctg 1219
 Glu Pro Tyr Leu Val Ser Arg Val Thr Gly Gln Asp Leu Ser Glu Leu
 360 365 370

agc acc cac aag ccg aaa tca gtt ggt gga gtc gag cca gaa att gca 1267
 Ser Thr His Lys Pro Lys Ser Val Gly Gly Val Glu Pro Glu Ile Ala
 375 380 385

gaa cag ttg aag act ttg atg gaa gcc tca gag cgc aat act tcg ggc 1315
 Glu Gln Leu Lys Thr Leu Met Glu Ala Ser Glu Arg Asn Thr Ser Gly
 390 395 400 405

tac acc gga att cag atc gct tcc aag act ggt acc gcg gaa cat ggt 1363
 Tyr Thr Gly Ile Gln Ile Ala Ser Lys Thr Gly Thr Ala Glu His Gly
 410 415 420

gat gaa aac aca cca cca cac acc tgg tac gtg gca ttc aac aac gac 1411
 Asp Glu Asn Thr Pro Pro His Thr Trp Tyr Val Ala Phe Asn Asn Asp
 425 430 435

att gct gtt gct gtg ttg gtg aaa gac ggc ggt gga ttt ggc acc agt 1459
 Ile Ala Val Ala Val Leu Val Lys Asp Gly Gly Gly Phe Gly Thr Ser
 440 445 450

gca act ggt ggt cag gtc gca gcc cca att ggc cga gct gtg ctt cag 1507
 Ala Thr Gly Gly Gln Val Ala Ala Pro Ile Gly Arg Ala Val Leu Gln
 455 460 465

gca gcc gga gga ttt taaaatatga gtcaagaaga cat 1545
 Ala Ala Gly Gly Phe
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<210> 54

<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 54

Val Asn Arg Ser Ile Arg Ile Thr Ser Leu Phe Ser Leu Leu Leu Ile
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Leu Val Leu Val Ala Asn Leu Thr Trp Ile Gln Ala Phe Arg Asp Asp
 20 25 30

Asp Leu Ala Gln Asn Pro Leu Asn Ala Arg Gly Phe Leu Glu Ala Lys
 35 40 45

Ser Thr Pro Arg Gly Gln Ile Ser Thr Gly Gly Gln Val Leu Ala Glu
 50 55 60

Ser Ser Gln Asp Asp Gln Gly Phe Tyr Gln Arg Ser Tyr Ile Thr Asn

65	70	75	80
Pro Thr Ala Tyr	Ala Pro Val Val Gly Tyr	Leu Ser Asp Val Tyr Gly	
	85	90	95
Ala Ala Gly Leu Glu	Leu Gly Tyr Asn Ser Ile Leu Asn Gly Ser Asp		
	100	105	110
Ser Ser Leu Phe Thr	Ser Gln Trp Leu Asp Val Ile Ser Gly Ser Pro		
	115	120	125
Thr His Gly Ala Asn Ile	Glu Leu Thr Leu Asp Pro Asn Ala Gln Gln		
	130	135	140
Thr Ala Tyr Glu Gln	Leu Ser Gln Ser Gly Tyr Glu Gly Ala Val Val		
	145	150	155
Ala Leu Arg Pro Ser Thr	Gly Glu Val Leu Ala Met Ala Ser Ser Pro		
	165	170	175
Ser Tyr Asp Pro Asn Gln Ile Val	Asp Pro Ala Thr Ala Glu Asp Ala		
	180	185	190
Trp Ala Glu Tyr Thr Ser Thr	Glu Gly Ala Pro Leu Leu Asn His Ala		
	195	200	205
Thr Gln Glu Ser Leu Pro Pro	Gly Ser Ile Phe Lys Ile Ile Thr Thr		
	210	215	220
Ala Ala Ala Leu Glu Asn Gly Tyr Ser Ala	Asp Ser Thr Val Thr Ala		
	225	230	235
Glu Ala Ala Val Thr Leu Pro Gly Thr	Asn Thr Thr Leu Thr Asn Tyr		
	245	250	255
Gly Gly Gln Thr Cys Ala Gly Gly Gly	Thr Thr Thr Leu Leu Thr Ala		
	260	265	270
Phe Gln Leu Ser Cys Asn Thr Ala Phe Val	Glu Thr Gly Ile Asp Val		
	275	280	285
Gly Ala Asp Ala Leu Arg Ala Ser Ala Glu Asp	Phe Gly Val Gly Gln		
	290	295	300
Thr Tyr Ser Leu Gly Leu Asp Asn Val Pro Gly Gly	Leu Gly Glu Ile		
	305	310	315
Pro Asp Asp Ala Ala Leu Gly Gln Ser Ser Ile Gly Gln Arg Asp Val			
	325	330	335
Gln Met Asn Val Leu Gln Ala Ala Val Met Ala Gly Thr Val Ser Asn			
	340	345	350
Gly Gly Val Arg Met Glu Pro Tyr Leu Val Ser Arg Val Thr Gly Gln			
	355	360	365
Asp Leu Ser Glu Leu Ser Thr His Lys Pro Lys Ser Val Gly Gly Val			
	370	375	380
Glu Pro Glu Ile Ala Glu Gln Leu Lys Thr Leu Met Glu Ala Ser Glu			
	385	390	395
			400

Arg Asn Thr Ser Gly Tyr Thr Gly Ile Gln Ile Ala Ser Lys Thr Gly
 405 410 415

Thr Ala Glu His Gly Asp Glu Asn Thr Pro Pro His Thr Trp Tyr Val
 420 425 430

Ala Phe Asn Asn Asp Ile Ala Val Ala Val Leu Val Lys Asp Gly Gly
 435 440 445

Gly Phe Gly Thr Ser Ala Thr Gly Gly Gln Val Ala Ala Pro Ile Gly
 450 455 460

Arg Ala Val Leu Gln Ala Ala Gly Gly Phe
 465 470

<210> 55

<211> 1208

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1185)

<223> RXA00612

<400> 55

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 Ala Ala Ala Ala Ile Gln Gln Gly Ala Gly Leu Asp Thr Met Leu Asp
 1 5 10 15

gtt cct tct cga tat gag gtc aag ggc atg ggc tcc ggc ggt gcc gcg 96
 Val Pro Ser Arg Tyr Glu Val Lys Gly Met Gly Ser Gly Gly Ala Ala
 20 25 30

aac tgt ccc gca aat act tac tgc gtg gaa aac gca gga tcc tac gcg 144
 Asn Cys Pro Ala Asn Thr Tyr Cys Val Glu Asn Ala Gly Ser Tyr Ala
 35 40 45

cct cgc atg act ctg cag gac gct ctc gcg cag tcc ccc aac act gca 192
 Pro Arg Met Thr Leu Gln Asp Ala Leu Ala Gln Ser Pro Asn Thr Ala
 50 55 60

ttc gtt gaa atg atc gag cag gtt ggc gtg gac acc gtt gtg gat ctt 240
 Phe Val Glu Met Ile Glu Gln Val Gly Val Asp Thr Val Val Asp Leu
 65 70 75 80

tca gta aag ctg ggc ctg cga agc tac acc gat gaa ggt tcc ttc gac 288
 Ser Val Lys Leu Gly Leu Arg Ser Tyr Thr Asp Glu Gly Ser Phe Asp
 85 90 95

ggc gaa agc tca atc gcg gac tac atg aag gac aac aac ctc ggt tct 336
 Gly Glu Ser Ser Ile Ala Asp Tyr Met Lys Asp Asn Asn Leu Gly Ser
 100 105 110

tac act ctt gga cct acc gct gtt aac cct ctt gaa ttg tcc aat gtt 384
 Tyr Thr Leu Gly Pro Thr Ala Val Asn Pro Leu Glu Leu Ser Asn Val
 115 120 125

gct gca acc att gca tcc ggt ggc atg tgg tgc gaa ccc aat ccc atc 432

Ala	Ala	Thr	Ile	Ala	Ser	Gly	Gly	Met	Trp	Cys	Glu	Pro	Asn	Pro	Ile		
130						135					140						
gcc	agc	gtc	cat	gac	cgt	gaa	ggc	aac	gaa	gtc	tac	att	gac	cgc	cct	480	
Ala	Ser	Val	His	Asp	Arg	Glu	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Pro		
145					150					155					160		
gca	tgt	gag	cgc	gcc	atc	gat	gcc	gaa	acg	gct	tca	gct	ttg	gcc	gtc	528	
Ala	Cys	Glu	Arg	Ala	Ile	Asp	Ala	Glu	Thr	Ala	Ser	Ala	Leu	Ala	Val		
				165					170					175			
ggc	atg	agc	aag	gat	acg	gtc	agc	gga	act	gcg	gcc	tct	gca	gcc	agc	576	
Gly	Met	Ser	Lys	Asp	Thr	Val	Ser	Gly	Thr	Ala	Ala	Ser	Ala	Ala	Ser		
			180					185					190				
atg	tac	gga	tgg	tcc	ttg	cca	acc	gca	gcg	aag	acc	ggt	acc	acc	gag	624	
Met	Tyr	Gly	Trp	Ser	Leu	Pro	Thr	Ala	Ala	Lys	Thr	Gly	Thr	Thr	Glu		
		195					200					205					
tcc	aac	cag	tcc	tca	gca	ttt	atg	ggc	ttc	aac	agc	aac	ttt	gcc	gca	672	
Ser	Asn	Gln	Ser	Ser	Ala	Phe	Met	Gly	Phe	Asn	Ser	Asn	Phe	Ala	Ala		
	210					215					220						
gct	cca	tac	atc	tac	aat	gac	ggc	acc	tcc	acc	acc	cca	ctg	tgc	agc	720	
Ala	Pro	Tyr	Ile	Tyr	Asn	Asp	Gly	Thr	Ser	Thr	Thr	Pro	Leu	Cys	Ser		
225					230					235					240		
ggc	ccc	gtc	cgc	cag	tgc	agc	agc	ggt	aac	ctc	ttc	ggc	ggt	aac	gaa	768	
Gly	Pro	Val	Arg	Gln	Cys	Ser	Ser	Gly	Asn	Leu	Phe	Gly	Gly	Asn	Glu		
				245					250					255			
cca	gct	caa	aca	tgg	ttt	aac	atg	gca	agc	aac	gtc	ccc	gca	gct	tcg	816	
Pro	Ala	Gln	Thr	Trp	Phe	Asn	Met	Ala	Ser	Asn	Val	Pro	Ala	Ala	Ser		
			260					265					270				
caa	gga	aca	ctg	cca	tcc	agc	agc	gat	tca	ttc	cgc	ctc	ggc	act	tcc	864	
Gln	Gly	Thr	Leu	Pro	Ser	Ser	Ser	Asp	Ser	Phe	Arg	Leu	Gly	Thr	Ser		
		275					280					285					
ggc	gaa	ctc	ctc	aac	cag	gtt	gtc	ggc	caa	agc	gaa	gcc	tcc	gct	cga	912	
Gly	Glu	Leu	Leu	Asn	Gln	Val	Val	Gly	Gln	Ser	Glu	Ala	Ser	Ala	Arg		
	290					295					300						
cgc	acc	ctc	gaa	gcc	aaa	ggc	tac	aag	gtc	acc	acg	cgt	tca	gtc	tcc	960	
Arg	Thr	Leu	Glu	Ala	Lys	Gly	Tyr	Lys	Val	Thr	Thr	Arg	Ser	Val	Ser		
305					310					315					320		
ggc	gcc	ggc	agc	gcg	cgc	ggc	acc	gta	gtc	agc	gca	acc	cct	cag	ggt	1008	
Gly	Ala	Gly	Ser	Ala	Arg	Gly	Thr	Val	Val	Ser	Ala	Thr	Pro	Gln	Gly		
				325					330					335			
gca	gtg	ctt	atc	gac	ggt	gga	acc	gtc	att	ttg	gac	atc	tcc	gac	ggc	1056	
Ala	Val	Leu	Ile	Asp	Gly	Gly	Thr	Val	Ile	Leu	Asp	Ile	Ser	Asp	Gly		
			340					345					350				
aca	agc	cct	gcc	ccc	gct	gcc	acc	aac	aat	gat	gac	agc	gac	gat	gga	1104	
Thr	Ser	Pro	Ala	Pro	Ala	Ala	Thr	Asn	Asn	Asp	Asp	Ser	Asp	Asp	Gly		
		355					360					365					
gac	acc	cct	gct	cca	tca	aca	aac	aac	cgc	gga	aca	acc	att	gaa	gac	1152	
Asp	Thr	Pro	Ala	Pro	Ser	Thr	Asn	Asn	Arg	Gly	Thr	Thr	Ile	Glu	Asp		

370 375 380
gcc atc aat gac gcc atc aac cag ttc ttc cgc tagaaatacc tagttgctca 1205
Ala Ile Asn Asp Ala Ile Asn Gln Phe Phe Arg
385 390 395

aac 1208

<210> 56

<211> 395

<212> PRT

<213> Corynebacterium glutamicum

<400> 56

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Val Pro Ser Arg Tyr Glu Val Lys Gly Met Gly Ser Gly Gly Ala Ala
20 25 30

Asn Cys Pro Ala Asn Thr Tyr Cys Val Glu Asn Ala Gly Ser Tyr Ala
35 40 45

Pro Arg Met Thr Leu Gln Asp Ala Leu Ala Gln Ser Pro Asn Thr Ala
50 55 60

Phe Val Glu Met Ile Glu Gln Val Gly Val Asp Thr Val Val Asp Leu
65 70 75 80

Ser Val Lys Leu Gly Leu Arg Ser Tyr Thr Asp Glu Gly Ser Phe Asp
85 90 95

Gly Glu Ser Ser Ile Ala Asp Tyr Met Lys Asp Asn Asn Leu Gly Ser
100 105 110

Tyr Thr Leu Gly Pro Thr Ala Val Asn Pro Leu Glu Leu Ser Asn Val
115 120 125

Ala Ala Thr Ile Ala Ser Gly Gly Met Trp Cys Glu Pro Asn Pro Ile
130 135 140

Ala Ser Val His Asp Arg Glu Gly Asn Glu Val Tyr Ile Asp Arg Pro
145 150 155 160

Ala Cys Glu Arg Ala Ile Asp Ala Glu Thr Ala Ser Ala Leu Ala Val
165 170 175

Gly Met Ser Lys Asp Thr Val Ser Gly Thr Ala Ala Ser Ala Ala Ser
180 185 190

Met Tyr Gly Trp Ser Leu Pro Thr Ala Ala Lys Thr Gly Thr Thr Glu
195 200 205

Ser Asn Gln Ser Ser Ala Phe Met Gly Phe Asn Ser Asn Phe Ala Ala
210 215 220

Ala Pro Tyr Ile Tyr Asn Asp Gly Thr Ser Thr Thr Pro Leu Cys Ser
225 230 235 240

Gly Pro Val Arg Gln Cys Ser Ser Gly Asn Leu Phe Gly Gly Asn Glu

245										250					255				
Pro	Ala	Gln	Thr	Trp	Phe	Asn	Met	Ala	Ser	Asn	Val	Pro	Ala	Ala	Ser				
			260					265					270						
Gln	Gly	Thr	Leu	Pro	Ser	Ser	Ser	Asp	Ser	Phe	Arg	Leu	Gly	Thr	Ser				
		275					280					285							
Gly	Glu	Leu	Leu	Asn	Gln	Val	Val	Gly	Gln	Ser	Glu	Ala	Ser	Ala	Arg				
	290					295					300								
Arg	Thr	Leu	Glu	Ala	Lys	Gly	Tyr	Lys	Val	Thr	Thr	Arg	Ser	Val	Ser				
305					310					315					320				
Gly	Ala	Gly	Ser	Ala	Arg	Gly	Thr	Val	Val	Ser	Ala	Thr	Pro	Gln	Gly				
				325					330					335					
Ala	Val	Leu	Ile	Asp	Gly	Gly	Thr	Val	Ile	Leu	Asp	Ile	Ser	Asp	Gly				
			340					345					350						
Thr	Ser	Pro	Ala	Pro	Ala	Ala	Thr	Asn	Asn	Asp	Asp	Ser	Asp	Asp	Gly				
		355					360					365							
Asp	Thr	Pro	Ala	Pro	Ser	Thr	Asn	Asn	Arg	Gly	Thr	Thr	Ile	Glu	Asp				
	370					375					380								
Ala	Ile	Asn	Asp	Ala	Ile	Asn	Gln	Phe	Phe	Arg									
385					390					395									

<210> 57

<211> 1404

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1381)

<223> RXA01510

<400> 57

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				Met	Lys	Asn	Ala	Trp		
				1				5		

tgg	gtt	ggc	tca	tcg	gtt	ggt	gta	ctg	att	gca	gtg	ggg	gct	gtc	atc	163
Trp	Val	Gly	Ser	Ser	Val	Gly	Val	Leu	Ile	Ala	Val	Gly	Ala	Val	Ile	
			10					15						20		

ggt	ggt	ggc	gtg	tgg	gtg	aat	cat	tct	ggt	ttt	ggt	ttg	gat	cac	ccg	211
Gly	Gly	Gly	Val	Trp	Val	Asn	His	Ser	Gly	Phe	Gly	Leu	Asp	His	Pro	
			25					30					35			

gag	ccc	atg	tcg	gtg	gag	atg	cct	gag	cag	ctg	ttt	tct	tct	gcg	att	259
Glu	Pro	Met	Ser	Val	Glu	Met	Pro	Glu	Gln	Leu	Phe	Ser	Ser	Ala	Ile	
		40					45					50				

gat	ccg	gat	gct	ttg	gaa	gcc	cca	gat	ttt	gcc	act	ttg	gag	aag	gat	307
Asp	Pro	Asp	Ala	Leu	Glu	Ala	Pro	Asp	Phe	Ala	Thr	Leu	Glu	Lys	Asp	

55	60	65	
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gcc agg gat gtg gaa tct ggt gag gtg gtg tgg gag cag aat cag ggg Ala Arg Asp Val Glu Ser Gly Glu Val Val Trp Glu Gln Asn Gln Gly 90 95 100			403
act gcg gtg agg ccg gcg tcg gcg acg aag att ttg acg gcg gcg gtg Thr Ala Val Arg Pro Ala Ser Ala Thr Lys Ile Leu Thr Ala Ala Val 105 110 115			451
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gag ggg gag cag ccg gga acg gtg gtg att aag gcg ggt ggt gat gtc Glu Gly Glu Gln Pro Gly Thr Val Val Ile Lys Ala Gly Gly Asp Val 135 140 145			547
acg ttg agt gag gag atg ctc gat gat ttg gcc acc cag ctt gag ggg Thr Leu Ser Glu Glu Met Leu Asp Asp Leu Ala Thr Gln Leu Glu Gly 150 155 160 165			595
caa gat att ggc act gtg ttg atc gat acg tct att tgg cct gat gag Gln Asp Ile Gly Thr Val Leu Ile Asp Thr Ser Ile Trp Pro Asp Glu 170 175 180			643
ggc ttt gct agt acg tgg gat cca gtg gat gtt gat gct ggt tat atc Gly Phe Ala Ser Thr Trp Asp Pro Val Asp Val Asp Ala Gly Tyr Ile 185 190 195			691
gct gat gtg gag ccc gcg atg att gag gct gcc cgc att ggt ggg tcg Ala Asp Val Glu Pro Ala Met Ile Glu Ala Ala Arg Ile Gly Gly Ser 200 205 210			739
gag ggg gat ctg ccg agg tct cat act ccg gcg tta gat gtt gcg cag Glu Gly Asp Leu Pro Arg Ser His Thr Pro Ala Leu Asp Val Ala Gln 215 220 225			787
gcg ttg gcg gat cgt gtc ggc gcg gac acc gta gat gag ggc agc gct Ala Leu Ala Asp Arg Val Gly Ala Asp Thr Val Asp Glu Gly Ser Ala 230 235 240 245			835
ccg gac aaa acc gtg ctg gca tcc gtg gag tct gac acg ttg gat cag Pro Asp Lys Thr Val Leu Ala Ser Val Glu Ser Asp Thr Leu Asp Gln 250 255 260			883
cgt ctt gct cgg atg atg aag gat tct gac aat gtg atg gca gag ggt Arg Leu Ala Arg Met Met Lys Asp Ser Asp Asn Val Met Ala Glu Gly 265 270 275			931
atc gct aag gaa gtg gcc gcg tcg aag gat ttg gct acc gat tcg gcg Ile Ala Lys Glu Val Ala Ala Ser Lys Asp Leu Ala Thr Asp Ser Ala 280 285 290			979
agt acc tcg aag atg acg ttg gag att ctc aag gac aag ggc ttc gat Ser Thr Ser Lys Met Thr Leu Glu Ile Leu Lys Asp Lys Gly Phe Asp 295 300 305			1027

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 Leu Ser Gly Val Ser Ile Val Asp Asn Ser Gly Leu Ser Phe Asp Asn
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 ctc att acg ccc cgc ctg ctt gat gat att ttg acc cgc gcc gcc acg 1123
 Leu Ile Thr Pro Arg Leu Leu Asp Asp Ile Leu Thr Arg Ala Ala Thr
 330 335 340
 gaa cct gag ttg agt tca cta ttg aca tcg ctg cct atc gcg cat gga 1171
 Glu Pro Glu Leu Ser Ser Leu Leu Thr Ser Leu Pro Ile Ala His Gly
 345 350 355
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 Thr Gly Thr Leu Glu Asp Arg Tyr Asp Gly Leu Ser Gly Ala Gly Trp
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 gtg cgg gcg aaa act ggc act ctg acg gat aca tcg gca ttg gca ggg 1267
 Val Arg Ala Lys Thr Gly Thr Leu Thr Asp Thr Ser Ala Leu Ala Gly
 375 380 385
 gtg gtg acc tcg gag tcg ggg cgt gtg ttt acc ttt gct ttt gtg tct 1315
 Val Val Thr Ser Glu Ser Gly Arg Val Phe Thr Phe Ala Phe Val Ser
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 aat ggt tcc gcg att gtg ccg gcg cgt gag gct ttg gat gag atg gcg 1363
 Asn Gly Ser Ala Ile Val Pro Ala Arg Glu Ala Leu Asp Glu Met Ala
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<210> 58

<211> 427

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 58

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 35 40 45
 Phe Ser Ser Ala Ile Asp Pro Asp Ala Leu Glu Ala Pro Asp Phe Ala
 50 55 60
 Thr Leu Glu Lys Asp Leu Thr Ser Gln Ala Ala Asp Ser Arg Leu Gly
 65 70 75 80
 Thr Phe Val Gly Val Ala Arg Asp Val Glu Ser Gly Glu Val Val Trp
 85 90 95
 Glu Gln Asn Gln Gly Thr Ala Val Arg Pro Ala Ser Ala Thr Lys Ile
 100 105 110

Leu Thr Ala Ala Val Ala Leu Tyr Glu Leu Gly Arg Glu Asp Thr Ile
 115 120 125
 Thr Thr Lys Val Val Glu Gly Glu Gln Pro Gly Thr Val Val Ile Lys
 130 135 140
 Ala Gly Gly Asp Val Thr Leu Ser Glu Glu Met Leu Asp Asp Leu Ala
 145 150 155 160
 Thr Gln Leu Glu Gly Gln Asp Ile Gly Thr Val Leu Ile Asp Thr Ser
 165 170 175
 Ile Trp Pro Asp Glu Gly Phe Ala Ser Thr Trp Asp Pro Val Asp Val
 180 185 190
 Asp Ala Gly Tyr Ile Ala Asp Val Glu Pro Ala Met Ile Glu Ala Ala
 195 200 205
 Arg Ile Gly Gly Ser Glu Gly Asp Leu Pro Arg Ser His Thr Pro Ala
 210 215 220
 Leu Asp Val Ala Gln Ala Leu Ala Asp Arg Val Gly Ala Asp Thr Val
 225 230 235 240
 Asp Glu Gly Ser Ala Pro Asp Lys Thr Val Leu Ala Ser Val Glu Ser
 245 250 255
 Asp Thr Leu Asp Gln Arg Leu Ala Arg Met Met Lys Asp Ser Asp Asn
 260 265 270
 Val Met Ala Glu Gly Ile Ala Lys Glu Val Ala Ala Ser Lys Asp Leu
 275 280 285
 Ala Thr Asp Ser Ala Ser Thr Ser Lys Met Thr Leu Glu Ile Leu Lys
 290 295 300
 Asp Lys Gly Phe Asp Leu Ser Gly Val Ser Ile Val Asp Asn Ser Gly
 305 310 315 320
 Leu Ser Phe Asp Asn Leu Ile Thr Pro Arg Leu Leu Asp Asp Ile Leu
 325 330 335
 Thr Arg Ala Ala Thr Glu Pro Glu Leu Ser Ser Leu Leu Thr Ser Leu
 340 345 350
 Pro Ile Ala His Gly Thr Gly Thr Leu Glu Asp Arg Tyr Asp Gly Leu
 355 360 365
 Ser Gly Ala Gly Trp Val Arg Ala Lys Thr Gly Thr Leu Thr Asp Thr
 370 375 380
 Ser Ala Leu Ala Gly Val Val Thr Ser Glu Ser Gly Arg Val Phe Thr
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Met Ala Leu Cys Met 5																
acg gtg gca ttt gct gga gga agc ctg acc gcg tgc aca cct cgt cct 163																
Thr Val Ala Phe Ala Gly Gly Ser Leu Thr Ala Cys Thr Pro Arg Pro 20																
gat acc gca gac ccc atc gca gag gaa ttc ctt caa gct tgg gca tcg 211																
Asp Thr Ala Asp Pro Ile Ala Glu Glu Phe Leu Gln Ala Trp Ala Ser 35																
caa gat ttc gac act att gcg gac atc acc gac caa gct gac ctt gcc 259																
Gln Asp Phe Asp Thr Ile Ala Asp Ile Thr Asp Gln Ala Asp Leu Ala 50																
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Thr Glu Met Leu Ser Thr Ser Phe Asp Gly Leu Gln Ala Asp Ser Val 65																
gaa ctg act ttg gat tcc gtg gat tcc cgg gac acc atc gcc acc gcc 355																
Glu Leu Thr Leu Asp Ser Val Asp Ser Arg Asp Thr Ile Ala Thr Ala 85																
aat ttc tcc gtg gtg tgg aag ctt ccc cga gac aga gaa gtt tcc tac 403																
Asn Phe Ser Val Val Trp Lys Leu Pro Arg Asp Arg Glu Val Ser Tyr 100																
gac tca tcg atg acg ctg acc aag atg cgc aac gaa tgg aca gtg cgt 451																
Asp Ser Ser Met Thr Leu Thr Lys Met Arg Asn Glu Trp Thr Val Arg 115																
tgg gaa cct tcc ctc gtg cac ccc aaa ctg ggc gcc aac cag cac ctg 499																
Trp Glu Pro Ser Leu Val His Pro Lys Leu Gly Ala Asn Gln His Leu 130																
gaa ttg cgc gcc att gaa gcg cag cga gcc aac gta att tcc tcc gat 547																
Glu Leu Arg Ala Ile Glu Ala Gln Arg Ala Asn Val Ile Ser Ser Asp 145																
gga gct ccg gtt ctc gcg ccg gga agt atc tac cga gtt ttg gtt gat 595																
Gly Ala Pro Val Leu Ala Pro Gly Ser Ile Tyr Arg Val Leu Val Asp 165																
ccc agc gca ggg gat gcc gat gtg gtg gtc aag agg gtg gca gat tat 643																
Pro Ser Ala Gly Asp Ala Asp Val Val Val Lys Arg Val Ala Asp Tyr 180																

ttg aat gaa gcc cat gcg act gat gag aat gtg aac acc ctt gat gtc	691
Leu Asn Glu Ala His Ala Thr Asp Glu Asn Val Asn Thr Leu Asp Val	
185 190 195	
gaa gac att atg agc aat ctt ggc gat tcc acc tat tca ctc acc aca	739
Glu Asp Ile Met Ser Asn Leu Gly Asp Ser Thr Tyr Ser Leu Thr Thr	
200 205 210	
gtt gat gcc aat ttg ggt gcc cgc atg gaa cag gat cta gcg ggg att	787
Val Asp Ala Asn Leu Gly Ala Arg Met Glu Gln Asp Leu Ala Gly Ile	
215 220 225	
ccg ggg ctg acg ttc aat gag gaa gca tcc atg gta gcc acc gac cca	835
Pro Gly Leu Thr Phe Asn Glu Glu Ala Ser Met Val Ala Thr Asp Pro	
230 235 240 245	
ggg ttt gct ccg gat att gtg tct cgc gtt gcg cgc att gtg gaa gat	883
Gly Phe Ala Pro Asp Ile Val Ser Arg Val Ala Arg Ile Val Glu Asp	
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gaa tta gaa gga tcc aat ggt tgg cgc gcc tcc att gtc act tcc aat	931
Glu Leu Glu Gly Ser Asn Gly Trp Arg Ala Ser Ile Val Thr Ser Asn	
265 270 275	
ggg gcg gtg att gat gat atc gcc tac gac gcc cca gag ctt gcc ccc	979
Gly Ala Val Ile Asp Asp Ile Ala Tyr Asp Ala Pro Glu Leu Ala Pro	
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Ser Val Arg Ile Ser Leu Asp His Asn Val Gln Arg Ala Ala Glu Glu	
295 300 305	
gcc gta gac ctg cgc gct gag atg aaa gcc atg atg gtg gtc atg agg	1075
Ala Val Asp Leu Arg Ala Glu Met Lys Ala Met Met Val Val Met Arg	
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Pro Ser Thr Gly Glu Ile Leu Ala Val Ala Gln Thr Asp Glu Ala Asp	
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Lys Asp Gly Asp Val Ala Leu Met Gly Gln Tyr Pro Pro Gly Ser Thr	
345 350 355	
ttc aag atc atc act gca gcc gcg ggg ttg gcg cat gaa gga tta act	1219
Phe Lys Ile Ile Thr Ala Ala Ala Gly Leu Ala His Glu Gly Leu Thr	
360 365 370	
cca gac agc att gtg cca tgc cct ggc acc atg aat atc tac ggc cga	1267
Pro Asp Ser Ile Val Pro Cys Pro Gly Thr Met Asn Ile Tyr Gly Arg	
375 380 385	
att gtc acc aac tac aac agc ttc tcc ttg ggc aac acc tca ttg gat	1315
Ile Val Thr Asn Tyr Asn Ser Phe Ser Leu Gly Asn Thr Ser Leu Asp	
390 395 400 405	
gat gct ttt gcc aat tca tgc aac acc act ttc gcg gat att ttc cac	1363
Asp Ala Phe Ala Asn Ser Cys Asn Thr Thr Phe Ala Asp Ile Phe His	
410 415 420	
cac ttg gag cca ggc caa ctg aaa aat gtg gct aag cag ttt ggc ctc	1411

His Leu Glu Pro Gly Gln Leu Lys Asn Val Ala Lys Gln Phe Gly Leu
 425 430 435

 gga att gat tat caa atc cca ggc ctt gac acc atg acg gga tcg gtg 1459
 Gly Ile Asp Tyr Gln Ile Pro Gly Leu Asp Thr Met Thr Gly Ser Val
 440 445 450

 cct gaa ggt gac atc gtg ttg gac cgt acc gaa tct ggt tac ggc cag 1507
 Pro Glu Gly Asp Ile Val Leu Asp Arg Thr Glu Ser Gly Tyr Gly Gln
 455 460 465

 ggt ctt gac cta gca agt ccc ttt ggc atg gcg ttg gtc gcc tcc act 1555
 Gly Leu Asp Leu Ala Ser Pro Phe Gly Met Ala Leu Val Ala Ser Thr
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 gca gcc acc ggt tca gtt ccc acg cca acg ctg att tct gga cat gaa 1603
 Ala Ala Thr Gly Ser Val Pro Thr Pro Thr Leu Ile Ser Gly His Glu
 490 495 500

 act gtt gcc agt gaa gaa gtt ctg gcg ctt gat cca gaa gtc ctt gcc 1651
 Thr Val Ala Ser Glu Glu Val Leu Ala Leu Asp Pro Glu Val Leu Ala
 505 510 515

 aat gtg cag cgg atg atg aaa tcc gtg gtc aat gac ggt acc gct cgt 1699
 Asn Val Gln Arg Met Met Lys Ser Val Val Asn Asp Gly Thr Ala Arg
 520 525 530

 ggc atg cgc caa acc ggt ggc cag atc tac gca aag aca ggt gaa gcc 1747
 Gly Met Arg Gln Thr Gly Gly Gln Ile Tyr Ala Lys Thr Gly Glu Ala
 535 540 545

 gaa atc aac gaa ggc tcc cat gcg tgg ttc acc ggc tac cgc gaa gat 1795
 Glu Ile Asn Glu Gly Ser His Ala Trp Phe Thr Gly Tyr Arg Glu Asp
 550 555 560 565

 gac atc gct ttt gcc acc ctc gtg gtg ttg ggc gga ggc tcc gaa gcg 1843
 Asp Ile Ala Phe Ala Thr Leu Val Val Leu Gly Gly Gly Ser Glu Ala
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 gct gcc gct gtg aca gat cag ttc ttt gtg aaa ctc gat gag ctt cgc 1891
 Ala Ala Ala Val Thr Asp Gln Phe Phe Val Lys Leu Asp Glu Leu Arg
 585 590 595

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<211> 613

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

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 35 40 45
 Gln Ala Asp Leu Ala Thr Glu Met Leu Ser Thr Ser Phe Asp Gly Leu
 50 55 60
 Gln Ala Asp Ser Val Glu Leu Thr Leu Asp Ser Val Asp Ser Arg Asp
 65 70 75 80
 Thr Ile Ala Thr Ala Asn Phe Ser Val Val Trp Lys Leu Pro Arg Asp
 85 90 95
 Arg Glu Val Ser Tyr Asp Ser Ser Met Thr Leu Thr Lys Met Arg Asn
 100 105 110
 Glu Trp Thr Val Arg Trp Glu Pro Ser Leu Val His Pro Lys Leu Gly
 115 120 125
 Ala Asn Gln His Leu Glu Leu Arg Ala Ile Glu Ala Gln Arg Ala Asn
 130 135 140
 Val Ile Ser Ser Asp Gly Ala Pro Val Leu Ala Pro Gly Ser Ile Tyr
 145 150 155 160
 Arg Val Leu Val Asp Pro Ser Ala Gly Asp Ala Asp Val Val Val Lys
 165 170 175
 Arg Val Ala Asp Tyr Leu Asn Glu Ala His Ala Thr Asp Glu Asn Val
 180 185 190
 Asn Thr Leu Asp Val Glu Asp Ile Met Ser Asn Leu Gly Asp Ser Thr
 195 200 205
 Tyr Ser Leu Thr Thr Val Asp Ala Asn Leu Gly Ala Arg Met Glu Gln
 210 215 220
 Asp Leu Ala Gly Ile Pro Gly Leu Thr Phe Asn Glu Glu Ala Ser Met
 225 230 235 240
 Val Ala Thr Asp Pro Gly Phe Ala Pro Asp Ile Val Ser Arg Val Ala
 245 250 255
 Arg Ile Val Glu Asp Glu Leu Glu Gly Ser Asn Gly Trp Arg Ala Ser
 260 265 270
 Ile Val Thr Ser Asn Gly Ala Val Ile Asp Asp Ile Ala Tyr Asp Ala
 275 280 285
 Pro Glu Leu Ala Pro Ser Val Arg Ile Ser Leu Asp His Asn Val Gln
 290 295 300
 Arg Ala Ala Glu Glu Ala Val Asp Leu Arg Ala Glu Met Lys Ala Met
 305 310 315 320
 Met Val Val Met Arg Pro Ser Thr Gly Glu Ile Leu Ala Val Ala Gln
 325 330 335
 Thr Asp Glu Ala Asp Lys Asp Gly Asp Val Ala Leu Met Gly Gln Tyr
 340 345 350

Pro Pro Gly Ser Thr Phe Lys Ile Ile Thr Ala Ala Ala Gly Leu Ala
 355 360 365
 His Glu Gly Leu Thr Pro Asp Ser Ile Val Pro Cys Pro Gly Thr Met
 370 375 380
 Asn Ile Tyr Gly Arg Ile Val Thr Asn Tyr Asn Ser Phe Ser Leu Gly
 385 390 395 400
 Asn Thr Ser Leu Asp Asp Ala Phe Ala Asn Ser Cys Asn Thr Thr Phe
 405 410 415
 Ala Asp Ile Phe His His Leu Glu Pro Gly Gln Leu Lys Asn Val Ala
 420 425 430
 Lys Gln Phe Gly Leu Gly Ile Asp Tyr Gln Ile Pro Gly Leu Asp Thr
 435 440 445
 Met Thr Gly Ser Val Pro Glu Gly Asp Ile Val Leu Asp Arg Thr Glu
 450 455 460
 Ser Gly Tyr Gly Gln Gly Leu Asp Leu Ala Ser Pro Phe Gly Met Ala
 465 470 475 480
 Leu Val Ala Ser Thr Ala Ala Thr Gly Ser Val Pro Thr Pro Thr Leu
 485 490 495
 Ile Ser Gly His Glu Thr Val Ala Ser Glu Glu Val Leu Ala Leu Asp
 500 505 510
 Pro Glu Val Leu Ala Asn Val Gln Arg Met Met Lys Ser Val Val Asn
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 Asp Gly Thr Ala Arg Gly Met Arg Gln Thr Gly Gly Gln Ile Tyr Ala
 530 535 540
 Lys Thr Gly Glu Ala Glu Ile Asn Glu Gly Ser His Ala Trp Phe Thr
 545 550 555 560
 Gly Tyr Arg Glu Asp Asp Ile Ala Phe Ala Thr Leu Val Val Leu Gly
 565 570 575
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 Glu Gln Pro Val Gly
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<210> 61

<211> 1962

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1939)

<223> FRXA01608

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acg gtg gca ttt gct gga gga agc ctg acc gcg tgc aca cct cgt cct	163	
Thr Val Ala Phe Ala Gly Gly Ser Leu Thr Ala Cys Thr Pro Arg Pro		
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Asp Thr Ala Asp Pro Ile Ala Glu Glu Phe Leu Gln Ala Trp Ala Ser		
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caa gat ttc gac act att gcg gac atc acc gac caa gct gac ctt gcc	259	
Gln Asp Phe Asp Thr Ile Ala Asp Ile Thr Asp Gln Ala Asp Leu Ala		
	40	45 50
aca gaa atg ctc agc acc agt ttc gat ggt ctg caa gca gac agc gtt	307	
Thr Glu Met Leu Ser Thr Ser Phe Asp Gly Leu Gln Ala Asp Ser Val		
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gaa ctg act ttg gat tcc gtg gat tcc cgg gac acc atc gcc acc gcc	355	
Glu Leu Thr Leu Asp Ser Val Asp Ser Arg Asp Thr Ile Ala Thr Ala		
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aat ttc tcc gtg gtg tgg aag ctt ccc cga gac aga gaa gtt tcc tac	403	
Asn Phe Ser Val Val Trp Lys Leu Pro Arg Asp Arg Glu Val Ser Tyr		
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gac tca tcg atg acg ctg acc aag atg cgc aac gaa tgg aca gtg cgt	451	
Asp Ser Ser Met Thr Leu Thr Lys Met Arg Asn Glu Trp Thr Val Arg		
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	120	125 130
gaa ttg cgc gcc att gaa gcg cag cga gcc aac gta att tcc tcc gat	547	
Glu Leu Arg Ala Ile Glu Ala Gln Arg Ala Asn Val Ile Ser Ser Asp		
	135	140 145
gga gct ccg gtt ctc gcg ccg gga agt atc tac cga gtt ttg gtt gat	595	
Gly Ala Pro Val Leu Ala Pro Gly Ser Ile Tyr Arg Val Leu Val Asp		
	150	155 160 165
ccc agc gca ggg gat gcc gat gtg gtg gtc aag agg gtg gca gat tat	643	
Pro Ser Ala Gly Asp Ala Asp Val Val Val Lys Arg Val Ala Asp Tyr		
	170	175 180
ttg aat gaa gcc cat gcg act gat gag aat gtg aac acc ctt gat gtc	691	
Leu Asn Glu Ala His Ala Thr Asp Glu Asn Val Asn Thr Leu Asp Val		
	185	190 195
gaa gac att atg agc aat ctt ggc gat tcc acc tat tca ctc acc aca	739	
Glu Asp Ile Met Ser Asn Leu Gly Asp Ser Thr Tyr Ser Leu Thr Thr		
	200	205 210
gtt gat gcc aat ttg ggt gcc cgc atg gaa cag gat cta gcg ggg att	787	

Val	Asp	Ala	Asn	Leu	Gly	Ala	Arg	Met	Glu	Gln	Asp	Leu	Ala	Gly	Ile	
215						220					225					
ccg	ggg	ctg	acg	ttc	aat	gag	gaa	gca	tcc	atg	gta	gcc	acc	gac	cca	835
Pro	Gly	Leu	Thr	Phe	Asn	Glu	Glu	Ala	Ser	Met	Val	Ala	Thr	Asp	Pro	
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Gly	Phe	Ala	Pro	Asp	Ile	Val	Ser	Arg	Val	Ala	Arg	Ile	Val	Glu	Asp	
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gaa	tta	gaa	gga	tcc	aat	ggg	tgg	cgc	gcc	tcc	att	gtc	act	tcc	aat	931
Glu	Leu	Glu	Gly	Ser	Asn	Gly	Trp	Arg	Ala	Ser	Ile	Val	Thr	Ser	Asn	
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Gly	Ala	Val	Ile	Asp	Asp	Ile	Ala	Tyr	Asp	Ala	Pro	Glu	Leu	Ala	Pro	
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agc	gtg	agg	atc	agc	ctg	gat	cac	aac	gtt	caa	cga	gca	gcg	gaa	gaa	1027
Ser	Val	Arg	Ile	Ser	Leu	Asp	His	Asn	Val	Gln	Arg	Ala	Ala	Glu	Glu	
	295					300					305					
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Ala	Val	Asp	Leu	Arg	Ala	Glu	Met	Lys	Ala	Met	Met	Val	Val	Met	Arg	
310					315					320					325	
cca	tcc	act	ggg	gaa	atc	ctc	gca	gtg	gcc	caa	aca	gat	gaa	gct	gac	1123
Pro	Ser	Thr	Gly	Glu	Ile	Leu	Ala	Val	Ala	Gln	Thr	Asp	Glu	Ala	Asp	
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Lys	Asp	Gly	Asp	Val	Ala	Leu	Met	Gly	Gln	Tyr	Pro	Pro	Gly	Ser	Thr	
			345					350					355			
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Phe	Lys	Ile	Ile	Thr	Ala	Ala	Ala	Gly	Leu	Ala	His	Glu	Gly	Leu	Thr	
		360					365					370				
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Pro	Asp	Ser	Ile	Val	Pro	Cys	Pro	Gly	Thr	Met	Asn	Ile	Tyr	Gly	Arg	
	375					380					385					
att	gtc	acc	aac	tac	aac	agc	ttc	tcc	ttg	ggc	aac	acc	tca	ttg	gat	1315
Ile	Val	Thr	Asn	Tyr	Asn	Ser	Phe	Ser	Leu	Gly	Asn	Thr	Ser	Leu	Asp	
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Asp	Ala	Phe	Ala	Asn	Ser	Cys	Asn	Thr	Thr	Phe	Ala	Asp	Ile	Phe	His	
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Thr Ile Ala Thr Ala Asn Phe Ser Val Val Trp Lys Leu Pro Arg Asp
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 Arg Glu Val Ser Tyr Asp Ser Ser Met Thr Leu Thr Lys Met Arg Asn
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 Glu Trp Thr Val Arg Trp Glu Pro Ser Leu Val His Pro Lys Leu Gly
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 Arg Val Ala Asp Tyr Leu Asn Glu Ala His Ala Thr Asp Glu Asn Val
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 Tyr Ser Leu Thr Thr Val Asp Ala Asn Leu Gly Ala Arg Met Glu Gln
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Val	Ala	Leu	Ser	Ser	Gly	Thr	Ala	Ala	Leu	His	Leu	Gly	Leu	Leu	Ala	
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Val	Asp	Cys	Asp	Glu	Ser	Gly	Asn	Met	Asp	Pro	Asp	Leu	Leu	Glu	Lys	
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Pro	Val	Asp	Leu	Leu	Gly	Lys	Val	Val	Gln	His	Glu	Lys	Ile	Lys	Lys	
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Leu	Gly	Ala	Ile	Arg	Asn	Gly	Lys	Ser	Ala	Ala	Ala	Tyr	Gly	Val	Ala	
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gca	gcg	gtt	tcc	ttc	aac	gga	aac	aaa	att	atg	act	acc	agc	ggc	ggc	691
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Gly	Ala	Leu	Leu	Thr	Asp	Asp	Lys	Asp	Ile	Ala	Asp	Asn	Val	Arg	Tyr	
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Leu	Ala	Thr	Gln	Ala	Arg	Gln	Pro	Val	Val	His	Tyr	Glu	His	Thr	Asp	
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Val	Gly	Tyr	Asn	Tyr	Arg	Leu	Ser	Asn	Ile	Leu	Ala	Ala	Leu	Gly	Arg	
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gct	caa	ctt	tcc	cga	ctc	gac	aag	atg	att	gag	cgt	cga	cgt	caa	cac	883
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Phe	Gly	Glu	Pro	Ser	Gly	Val	Asp	Gly	Gly	Asp	Thr	Ile	Asp	Asn	Phe					
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Ile Val Pro Pro Glu Gly Asn Arg Gln Met Val Thr Ile Asp Gln Val
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Pro Asp Thr Val Lys Asn Ala Val Val Ala Ala Glu Asp Arg Glu Phe
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Tyr Thr Asn Pro Gly Phe Ser Ile Thr Gly Tyr Ala Arg Ala Ala Leu
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Gly	Asn	Val	Gly	Gly	Ser	Gly	Cys	Gly	Ser	Cys	Ser	Ile	Glu	Gln	Ala
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Leu	Leu	His	Ser	Tyr	Asn	Thr	Ser	Phe	Ile	Arg	Leu	Gln	Gln	Asp	Leu
385					390					395					400
Glu	Asn	Gly	Ser	Gln	Asp	Thr	Ala	Asp	Met	Ala	His	Ala	Leu	Gly	Ile
				405					410					415	
Ala	Lys	Ser	Leu	Pro	Thr	Ile	Pro	Glu	Thr	Leu	Thr	Glu	Asn	Gly	Glu
			420					425					430		
Thr	Pro	Tyr	Glu	Gly	Ile	Ile	Leu	Gly	Gln	Tyr	Glu	Ser	Arg	Pro	Leu
		435					440					445			

Asp Met Ala Ser Ala Met Ala Thr Ile Ala Asn Glu Gly Val Trp His
 450 455 460
 Arg Pro His Phe Val Ser Lys Val Glu Thr Val Ser Gly Glu Val Leu
 465 470 475 480
 Tyr Glu Phe Glu Asp Gly Asp Gly Glu Arg Arg Val Ser Glu Lys Val
 485 490 495
 Ala Leu Asn Leu Leu Lys Ala Met Gly Pro Ile Ala Ala Tyr Ser Asn
 500 505 510
 Gly Asn Ala Leu Ala Asp Gly Gln Val Ser Ala Ser Lys Thr Gly Thr
 515 520 525
 Thr Gln Leu Gly Asp Thr Gly Ala Asn Lys Asp Ala Trp Met Leu Gly
 530 535 540
 Ala Ala Pro Gln Leu Ala Thr Ala Val Trp Val Gly Thr Ala
 545 550 555

<210> 67

<211> 444

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(421)

<223> RXN00550

<400> 67

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 Met Tyr Gly Ser Asn
 1 5
 tcc cct gcc acg atc tgg aag cag acc atg gat aac gcc ctc gag aac 163
 Ser Pro Ala Thr Ile Trp Lys Gln Thr Met Asp Asn Ala Leu Glu Asn
 10 15 20
 tcc cct ctc gaa act tgg gat atc gct cca gca ttg ggg tac ggt aac 211
 Ser Pro Leu Glu Thr Trp Asp Ile Ala Pro Ala Leu Gly Tyr Gly Asn
 25 30 35
 cca cca gtt ccg gaa tat gtg tgg act cca agt cca aac atc gcg act 259
 Pro Pro Val Pro Glu Tyr Val Trp Thr Pro Ser Pro Asn Ile Ala Thr
 40 45 50
 aat gat cca gaa gga gca acc gag gaa gct cca gtg gag gat cca aat 307
 Asn Asp Pro Glu Gly Ala Thr Glu Glu Ala Pro Val Glu Asp Pro Asn
 55 60 65
 gca gta atc gat acc cct gct gta gat ccc act gca cct gca gag gag 355
 Ala Val Ile Asp Thr Pro Ala Val Asp Pro Thr Ala Pro Ala Glu Glu
 70 75 80 85
 acc ggt aac ggt cag gta gaa atc ctg ccg ggg ctg act atc ccg gga 403

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<400> 69
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Met Leu Ala Lys Asp
1 5

tcc tac acc atc aaa ttg act ttg gat cca gat gtt cag gat gca gcg 163
Ser Tyr Thr Ile Lys Leu Thr Leu Asp Pro Asp Val Gln Asp Ala Ala
10 15 20

cac aat gcg gtg tcc tcc cac gtt gat cca acc acc cca ggt gtc gct 211
His Asn Ala Val Ser Ser His Val Asp Pro Thr Thr Pro Gly Val Ala
25 30 35

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gaa gtt gtg aac gtc att gag cct ggc gag aac tcc cgc gat att ttg 259
 Glu Val Val Asn Val Ile Glu Pro Gly Glu Asn Ser Arg Asp Ile Leu
 40 45 50
 gct att act tct tcc cgc aac tac ggc ctt gac ctg gat gct ggt gaa 307
 Ala Ile Thr Ser Ser Arg Asn Tyr Gly Leu Asp Leu Asp Ala Gly Glu
 55 60 65
 acg atg ctg cct cag gca acg tcc cgt gtg ggt aat ggt gcc ggt tcc 355
 Thr Met Leu Pro Gln Ala Thr Ser Arg Val Gly Asn Gly Ala Gly Ser
 70 75 80 85
 att ttc aag atc ttt acc gcc gct gca gcc att cag cag ggc gct ggc 403
 Ile Phe Lys Ile Phe Thr Ala Ala Ala Ile Gln Gln Gly Ala Gly
 90 95 100
 cta gac acc atg ttg gat gtt cct tct cga tat gag gtc aag ggc atg 451
 Leu Asp Thr Met Leu Asp Val Pro Ser Arg Tyr Glu Val Lys Gly Met
 105 110 115
 ggc tcc ggc ggt gcc gcg aac tgt ccc gca aat act tac tgc gtg gaa 499
 Gly Ser Gly Gly Ala Ala Asn Cys Pro Ala Asn Thr Tyr Cys Val Glu
 120 125 130
 aac gca gga tcc tac gcg cct cgc atg act ctg cag gac gct ctc gcg 547
 Asn Ala Gly Ser Tyr Ala Pro Arg Met Thr Leu Gln Asp Ala Leu Ala
 135 140 145
 cag tcc ccc aac act gca ttc gtt gaa atg atc gag cag gtt ggc gtg 595
 Gln Ser Pro Asn Thr Ala Phe Val Glu Met Ile Glu Gln Val Gly Val
 150 155 160 165
 gac acc cgt tgt gga tct ttc agt aaa gct ggg cct gcg aag cta cac 643
 Asp Thr Arg Cys Gly Ser Phe Ser Lys Ala Gly Pro Ala Lys Leu His
 170 175 180
 cga tgaaggttcc ttcgacggcg aaa 669
 Arg

<210> 70
 <211> 182
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 70
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 Val Gln Asp Ala Ala His Asn Ala Val Ser Ser His Val Asp Pro Thr
 20 25 30
 Thr Pro Gly Val Ala Glu Val Val Asn Val Ile Glu Pro Gly Glu Asn
 35 40 45
 Ser Arg Asp Ile Leu Ala Ile Thr Ser Ser Arg Asn Tyr Gly Leu Asp
 50 55 60
 Leu Asp Ala Gly Glu Thr Met Leu Pro Gln Ala Thr Ser Arg Val Gly
 65 70 75 80

Asn Gly Ala Gly Ser Ile Phe Lys Ile Phe Thr Ala Ala Ala Ala Ile
 85 90 95
 Gln Gln Gly Ala Gly Leu Asp Thr Met Leu Asp Val Pro Ser Arg Tyr
 100 105 110
 Glu Val Lys Gly Met Gly Ser Gly Gly Ala Ala Asn Cys Pro Ala Asn
 115 120 125
 Thr Tyr Cys Val Glu Asn Ala Gly Ser Tyr Ala Pro Arg Met Thr Leu
 130 135 140
 Gln Asp Ala Leu Ala Gln Ser Pro Asn Thr Ala Phe Val Glu Met Ile
 145 150 155 160
 Glu Gln Val Gly Val Asp Thr Arg Cys Gly Ser Phe Ser Lys Ala Gly
 165 170 175
 Pro Ala Lys Leu His Arg
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<210> 71
 <211> 824
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(801)
 <223> RXN03178

<400> 71
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 Pro Thr Thr Val Val Thr Gly Thr Met Glu Ala Ala Asn Ile Glu Gly
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 Ser Arg Val Gly Val Gly Glu Ala Gly Gln Tyr Thr Val Asp Gln Leu
 20 25 30

 ctg cac ggt ctt ctt tta gcc agc ggt aac gat gcg gcg tat atg ttg 144
 Leu His Gly Leu Leu Leu Ala Ser Gly Asn Asp Ala Ala Tyr Met Leu
 35 40 45

 gct cag gaa ctt ggt ggg gat caa gca acc ctg gag aaa gta aac gcg 192
 Ala Gln Glu Leu Gly Gly Asp Gln Ala Thr Leu Glu Lys Val Asn Ala
 50 55 60

 ctg gcc aag gag ttg ggc act caa gac acc ttc gtt gcc act tat tcc 240
 Leu Ala Lys Glu Leu Gly Thr Gln Asp Thr Phe Val Ala Thr Tyr Ser
 65 70 75 80

 ggt ttg gat gcg ccg gga atg tcg acc tcc gca tac gac atg tca ttg 288
 Gly Leu Asp Ala Pro Gly Met Ser Thr Ser Ala Tyr Asp Met Ser Leu
 85 90 95

 att tat cag cat gcg tgg cag aac ccg gtt ttc gag tcg att atc tcc 336
 Ile Tyr Gln His Ala Trp Gln Asn Pro Val Phe Glu Ser Ile Ile Ser
 100 105 110

acc gat cac att gat ttc cct ggt tgg ggc gac aat gag ggt ttc caa 384
 Thr Asp His Ile Asp Phe Pro Gly Trp Gly Asp Asn Glu Gly Phe Gln
 115 120 125

gtc tgg aac gat aac gcc ttg ttc atg aac gat cct gat ggc atc ggc 432
 Val Trp Asn Asp Asn Ala Leu Phe Met Asn Asp Pro Asp Gly Ile Gly
 130 135 140

ggc aag acc ggc tac acc gac gac gcg aac cac acc ttt gtc ggc ggt 480
 Gly Lys Thr Gly Tyr Thr Asp Asp Ala Asn His Thr Phe Val Gly Gly
 145 150 155 160

ctc gat cgg ggt ggt cgc cgc ctc gcc gcc gta ctc ttg gat tcc acc 528
 Leu Asp Arg Gly Gly Arg Arg Leu Ala Ala Val Leu Leu Asp Ser Thr
 165 170 175

gtc agc gac att cgt ccg tgg gaa caa gca cga ttg ctt atc gac gcc 576
 Val Ser Asp Ile Arg Pro Trp Glu Gln Ala Arg Leu Leu Ile Asp Ala
 180 185 190

tcc ctc ccc atc acg ccg ggg tcc ggc gtg ggc cag ctg ggc tcc ggc 624
 Ser Leu Pro Ile Thr Pro Gly Ser Gly Val Gly Gln Leu Gly Ser Gly
 195 200 205

agc gcg aac gat gtg gca ccg gcg acc cca gaa tta cca gaa ccc acc 672
 Ser Ala Asn Asp Val Ala Pro Ala Thr Pro Glu Leu Pro Glu Pro Thr
 210 215 220

gac aac ctg act tca ggt gag ggt ggg tcg cag aac acg ctt ctt aag 720
 Asp Asn Leu Thr Ser Gly Glu Gly Gly Ser Gln Asn Thr Leu Leu Lys
 225 230 235 240

ctc gtg gtg ccc atc gga atc atc gtg ctg ttg cta atc gcc gca cta 768
 Leu Val Val Pro Ile Gly Ile Ile Val Leu Leu Leu Ile Ala Ala Leu
 245 250 255

gcg tgg aca ttc aga tct ccc aag aaa aag aac taggtgttct tcttcacgac 821
 Ala Trp Thr Phe Arg Ser Pro Lys Lys Lys Asn
 260 265

ctc 824

<210> 72

<211> 267

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 72

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Ser Arg Val Gly Val Gly Glu Ala Gly Gln Tyr Thr Val Asp Gln Leu
 20 25 30

Leu His Gly Leu Leu Leu Ala Ser Gly Asn Asp Ala Ala Tyr Met Leu
 35 40 45

Ala Gln Glu Leu Gly Gly Asp Gln Ala Thr Leu Glu Lys Val Asn Ala
 50 55 60

Leu Ala Lys Glu Leu Gly Thr Gln Asp Thr Phe Val Ala Thr Tyr Ser
 65 70 75 80
 Gly Leu Asp Ala Pro Gly Met Ser Thr Ser Ala Tyr Asp Met Ser Leu
 85 90 95
 Ile Tyr Gln His Ala Trp Gln Asn Pro Val Phe Glu Ser Ile Ile Ser
 100 105 110
 Thr Asp His Ile Asp Phe Pro Gly Trp Gly Asp Asn Glu Gly Phe Gln
 115 120 125
 Val Trp Asn Asp Asn Ala Leu Phe Met Asn Asp Pro Asp Gly Ile Gly
 130 135 140
 Gly Lys Thr Gly Tyr Thr Asp Asp Ala Asn His Thr Phe Val Gly Gly
 145 150 155 160
 Leu Asp Arg Gly Gly Arg Arg Leu Ala Ala Val Leu Leu Asp Ser Thr
 165 170 175
 Val Ser Asp Ile Arg Pro Trp Glu Gln Ala Arg Leu Leu Ile Asp Ala
 180 185 190
 Ser Leu Pro Ile Thr Pro Gly Ser Gly Val Gly Gln Leu Gly Ser Gly
 195 200 205
 Ser Ala Asn Asp Val Ala Pro Ala Thr Pro Glu Leu Pro Glu Pro Thr
 210 215 220
 Asp Asn Leu Thr Ser Gly Glu Gly Gly Ser Gln Asn Thr Leu Leu Lys
 225 230 235 240
 Leu Val Val Pro Ile Gly Ile Ile Val Leu Leu Leu Ile Ala Ala Leu
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 Ala Trp Thr Phe Arg Ser Pro Lys Lys Lys Asn
 260 265

<210> 73

<211> 749

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(726)

<223> FRXA02859

<400> 73

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 aac gat gcg gcg tat ctg ttg gct cag gaa ctt ggt ggg gat caa gca 96
 Asn Asp Ala Ala Tyr Leu Leu Ala Gln Glu Leu Gly Gly Asp Gln Ala
 20 25 30
 acc ctg gag aaa gta aac gcg ctg gcc aag gag ttg ggc act caa gac 144

Thr	Leu	Glu	Lys	Val	Asn	Ala	Leu	Ala	Lys	Glu	Leu	Gly	Thr	Gln	Asp		
		35					40					45					
acc	ttc	gtt	gcc	act	tat	tcc	ggt	ttg	gat	gcg	ccg	gga	atg	tcg	acc	192	
Thr	Phe	Val	Ala	Thr	Tyr	Ser	Gly	Leu	Asp	Ala	Pro	Gly	Met	Ser	Thr		
	50					55					60						
tcc	gca	tac	gac	atg	tca	ttg	att	tat	cag	cat	gcg	tgg	cag	aac	ccg	240	
Ser	Ala	Tyr	Asp	Met	Ser	Leu	Ile	Tyr	Gln	His	Ala	Trp	Gln	Asn	Pro		
65					70					75					80		
gtt	ttc	gag	tcg	att	atc	tcc	acc	gat	cac	att	gat	ttc	cct	ggt	tgg	288	
Val	Phe	Glu	Ser	Ile	Ile	Ser	Thr	Asp	His	Ile	Asp	Phe	Pro	Gly	Trp		
				85					90					95			
ggc	gac	aac	gag	ggt	ttc	caa	gtc	tgg	aac	gat	aac	gcc	ttg	ttc	atg	336	
Gly	Asp	Asn	Glu	Gly	Phe	Gln	Val	Trp	Asn	Asp	Asn	Ala	Leu	Phe	Met		
		100						105					110				
aac	gat	cct	gat	ggc	atc	ggc	ggc	aag	acc	ggc	tac	acc	gac	gac	gcg	384	
Asn	Asp	Pro	Asp	Gly	Ile	Gly	Gly	Lys	Thr	Gly	Tyr	Thr	Asp	Asp	Ala		
		115					120						125				
aac	cac	acc	ttt	gtc	ggc	ggt	ctc	gat	cgg	ggt	ggt	cgc	cgc	ctc	gcc	432	
Asn	His	Thr	Phe	Val	Gly	Gly	Leu	Asp	Arg	Gly	Gly	Arg	Arg	Leu	Ala		
	130					135					140						
gcc	gta	ctc	ttg	gat	tcc	acc	gtc	agc	gac	att	cgt	ccg	tgg	gaa	caa	480	
Ala	Val	Leu	Leu	Asp	Ser	Thr	Val	Ser	Asp	Ile	Arg	Pro	Trp	Glu	Gln		
145					150					155					160		
gca	cga	ttg	ctt	atc	gac	gcc	tcc	ctc	ccc	atc	acg	ccg	ggg	tcc	ggc	528	
Ala	Arg	Leu	Leu	Ile	Asp	Ala	Ser	Leu	Pro	Ile	Thr	Pro	Gly	Ser	Gly		
				165					170					175			
gtg	ggc	cag	ctg	ggc	tcc	ggc	agc	gcg	aac	gat	gtg	gca	ccg	gcg	acc	576	
Val	Gly	Gln	Leu	Gly	Ser	Gly	Ser	Ala	Asn	Asp	Val	Ala	Pro	Ala	Thr		
			180					185					190				
cca	gaa	tta	cca	gaa	ccc	acc	gac	aac	ctg	act	tca	ggt	gag	ggt	ggg	624	
Pro	Glu	Leu	Pro	Glu	Pro	Thr	Asp	Asn	Leu	Thr	Ser	Gly	Glu	Gly	Gly		
		195					200					205					
tcg	cag	aac	acg	ctg	ctt	aag	ctc	gtg	gtg	ccc	atc	gga	atc	atc	gtg	672	
Ser	Gln	Asn	Thr	Leu	Leu	Lys	Leu	Val	Val	Pro	Ile	Gly	Ile	Ile	Val		
	210					215					220						
ctg	ttg	cta	atc	gcc	gca	cta	gcg	tgg	aca	ttc	aga	tct	ccc	aag	aaa	720	
Leu	Leu	Leu	Ile	Ala	Ala	Leu	Ala	Trp	Thr	Phe	Arg	Ser	Pro	Lys	Lys		
225					230					235					240		
aag	aac	taggtgttct	tcttcacgac	ctc												749	
Lys	Asn																

<210> 74

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 74

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Asn Asp Ala Ala Tyr Leu Leu Ala Gln Glu Leu Gly Gly Asp Gln Ala
 20 25 30

Thr Leu Glu Lys Val Asn Ala Leu Ala Lys Glu Leu Gly Thr Gln Asp
 35 40 45

Thr Phe Val Ala Thr Tyr Ser Gly Leu Asp Ala Pro Gly Met Ser Thr
 50 55 60

Ser Ala Tyr Asp Met Ser Leu Ile Tyr Gln His Ala Trp Gln Asn Pro
 65 70 75 80

Val Phe Glu Ser Ile Ile Ser Thr Asp His Ile Asp Phe Pro Gly Trp
 85 90 95

Gly Asp Asn Glu Gly Phe Gln Val Trp Asn Asp Asn Ala Leu Phe Met
 100 105 110

Asn Asp Pro Asp Gly Ile Gly Gly Lys Thr Gly Tyr Thr Asp Asp Ala
 115 120 125

Asn His Thr Phe Val Gly Gly Leu Asp Arg Gly Gly Arg Arg Leu Ala
 130 135 140

Ala Val Leu Leu Asp Ser Thr Val Ser Asp Ile Arg Pro Trp Glu Gln
 145 150 155 160

Ala Arg Leu Leu Ile Asp Ala Ser Leu Pro Ile Thr Pro Gly Ser Gly
 165 170 175

Val Gly Gln Leu Gly Ser Gly Ser Ala Asn Asp Val Ala Pro Ala Thr
 180 185 190

Pro Glu Leu Pro Glu Pro Thr Asp Asn Leu Thr Ser Gly Glu Gly Gly
 195 200 205

Ser Gln Asn Thr Leu Leu Lys Leu Val Val Pro Ile Gly Ile Ile Val
 210 215 220

Leu Leu Leu Ile Ala Ala Leu Ala Trp Thr Phe Arg Ser Pro Lys Lys
 225 230 235 240

Lys Asn

<210> 75

<211> 1437

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1414)

<223> RXN01267

<400> 75

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aat ggc ggt ttt att cca gag ggc acc gtg cgg gta agc ggc gca aaa 163 Asn Gly Gly Phe Ile Pro Glu Gly Thr Val Arg Val Ser Gly Ala Lys 10 15 20						
aac tct gct act aga ctt ctc gcg gcg gca ctg cta acc gat gag gtg 211 Asn Ser Ala Thr Arg Leu Leu Ala Ala Leu Leu Thr Asp Glu Val 25 30 35						
gtg cat ctt ggt aat ttc cca acc aag ctt gtg gat gtt gaa cat aaa 259 Val His Leu Gly Asn Phe Pro Thr Lys Leu Val Asp Val Glu His Lys 40 45 50						
att cgc ttt att gaa gag ctt ggc gga aaa gtg cat gtc gac cat gat 307 Ile Arg Phe Ile Glu Glu Leu Gly Gly Lys Val His Val Asp His Asp 55 60 65						
gag caa att tta gta gtt gat gct aag gat ctt gca gcg cga gaa atg 355 Glu Gln Ile Leu Val Val Asp Ala Lys Asp Leu Ala Ala Arg Glu Met 70 75 80 85						
act act gat gaa ctg aat att ccg att cga act act tat ctc cta gca 403 Thr Thr Asp Glu Leu Asn Ile Pro Ile Arg Thr Thr Tyr Leu Leu Ala 90 95 100						
gca gcg cag att ggg cgt ggg gaa att gct cga gtt cct ttt cct ggg 451 Ala Ala Gln Ile Gly Arg Gly Glu Ile Ala Arg Val Pro Phe Pro Gly 105 110 115						
ggg tgt gct att gga gga ggt cct gct ggc gga cga gga tat gat ctt 499 Gly Cys Ala Ile Gly Gly Gly Pro Ala Gly Gly Arg Gly Tyr Asp Leu 120 125 130						
cat ctt atg gtc tgg gaa cag cta ggt tgt aaa att ctt gaa aaa gat 547 His Leu Met Val Trp Glu Gln Leu Gly Cys Lys Ile Leu Glu Lys Asp 135 140 145						
gat cac att gaa gta act gca ccc cag ggc ttt atc ggg gga gtt att 595 Asp His Ile Glu Val Thr Ala Pro Gln Gly Phe Ile Gly Gly Val Ile 150 155 160 165						
gac ttt cct att tct act gtg gga ggc act gaa aac gcg tta cta tgc 643 Asp Phe Pro Ile Ser Thr Val Gly Gly Thr Glu Asn Ala Leu Leu Cys 170 175 180						
gca agt att gct tca ggg gat act aaa att gcc aat gct tat att acc 691 Ala Ser Ile Ala Ser Gly Asp Thr Lys Ile Ala Asn Ala Tyr Ile Thr 185 190 195						
cct gag ata act gat ctt att gaa ctt ctg cga cgt atg ggt gcg gag 739 Pro Glu Ile Thr Asp Leu Ile Glu Leu Leu Arg Arg Met Gly Ala Glu 200 205 210						
atc act gtc tac ggt acc agc cgt att cat gta aag ggt cga gca ggt 787 Ile Thr Val Tyr Gly Thr Ser Arg Ile His Val Lys Gly Arg Ala Gly 215 220 225						

ctt ttg cag ggc gca tat atg gac gta atg ccg gat cgt att gag gca	835
Leu Leu Gln Gly Ala Tyr Met Asp Val Met Pro Asp Arg Ile Glu Ala	
230 235 240 245	
ttg acg tgg atc gtg tat gga att att tca ggc gga agg att acc gtc	883
Leu Thr Trp Ile Val Tyr Gly Ile Ile Ser Gly Gly Arg Ile Thr Val	
250 255 260	
gaa ggt gtt cca ttt agc tcg atg gaa gtt cct ttt atc cac ctt gag	931
Glu Gly Val Pro Phe Ser Ser Met Glu Val Pro Phe Ile His Leu Glu	
265 270 275	
aag gct gga gtg gat ctt ttc cgt aat tca agt tcc gta tat att aca	979
Lys Ala Gly Val Asp Leu Phe Arg Asn Ser Ser Ser Val Tyr Ile Thr	
280 285 290	
cca gaa tgc ttg cct tca ggc tca gtt cag cca ttt gag cta gcg tgt	1027
Pro Glu Cys Leu Pro Ser Gly Ser Val Gln Pro Phe Glu Leu Ala Cys	
295 300 305	
gga act cac ccc gga gta att tcg gac atg cag gca ctt ttt gtt ctt	1075
Gly Thr His Pro Gly Val Ile Ser Asp Met Gln Ala Leu Phe Val Leu	
310 315 320 325	
tta gga tta aaa ggt gca gga act tca cgc gtc tat gac tat cga tac	1123
Leu Gly Leu Lys Gly Ala Gly Thr Ser Arg Val Tyr Asp Tyr Arg Tyr	
330 335 340	
cca gaa aga att gca ttt gtt gag gaa ttg aca aat cta gtt tcg ggc	1171
Pro Glu Arg Ile Ala Phe Val Glu Glu Leu Thr Asn Leu Val Ser Gly	
345 350 355	
gac aaa tta agt gca gag gct ggc aag atc act atc cag gga gat gct	1219
Asp Lys Leu Ser Ala Glu Ala Gly Lys Ile Thr Ile Gln Gly Asp Ala	
360 365 370	
act ttc cgg cca gga tat gcg aac tca act gat cta cgt ggt tct atg	1267
Thr Phe Arg Pro Gly Tyr Ala Asn Ser Thr Asp Leu Arg Gly Ser Met	
375 380 385	
gct gtt gtt tta gcg gcg ctt tgc gct gat gga aag tcc acg att aat	1315
Ala Val Val Leu Ala Ala Leu Cys Ala Asp Gly Lys Ser Thr Ile Asn	
390 395 400 405	
aac gtc cat atg gcg tta cgt ggg tac aac gag ttg gat aaa aaa ctt	1363
Asn Val His Met Ala Leu Arg Gly Tyr Asn Glu Leu Asp Lys Lys Leu	
410 415 420	
cgt tta ctt ggt gcg gat tta act atc aga gaa ggc gaa gtt cct tca	1411
Arg Leu Leu Gly Ala Asp Leu Thr Ile Arg Glu Gly Glu Val Pro Ser	
425 430 435	
cct taagaacgaa agttttacat tga	1437
Pro	

<210> 76

<211> 438

<212> PRT

<213> Corynebacterium glutamicum

<400> 76

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 20 25 30
 Leu Thr Asp Glu Val Val His Leu Gly Asn Phe Pro Thr Lys Leu Val
 35 40 45
 Asp Val Glu His Lys Ile Arg Phe Ile Glu Glu Leu Gly Gly Lys Val
 50 55 60
 His Val Asp His Asp Glu Gln Ile Leu Val Val Asp Ala Lys Asp Leu
 65 70 75 80
 Ala Ala Arg Glu Met Thr Thr Asp Glu Leu Asn Ile Pro Ile Arg Thr
 85 90 95
 Thr Tyr Leu Leu Ala Ala Ala Gln Ile Gly Arg Gly Glu Ile Ala Arg
 100 105 110
 Val Pro Phe Pro Gly Gly Cys Ala Ile Gly Gly Gly Pro Ala Gly Gly
 115 120 125
 Arg Gly Tyr Asp Leu His Leu Met Val Trp Glu Gln Leu Gly Cys Lys
 130 135 140
 Ile Leu Glu Lys Asp Asp His Ile Glu Val Thr Ala Pro Gln Gly Phe
 145 150 155 160
 Ile Gly Gly Val Ile Asp Phe Pro Ile Ser Thr Val Gly Gly Thr Glu
 165 170 175
 Asn Ala Leu Leu Cys Ala Ser Ile Ala Ser Gly Asp Thr Lys Ile Ala
 180 185 190
 Asn Ala Tyr Ile Thr Pro Glu Ile Thr Asp Leu Ile Glu Leu Leu Arg
 195 200 205
 Arg Met Gly Ala Glu Ile Thr Val Tyr Gly Thr Ser Arg Ile His Val
 210 215 220
 Lys Gly Arg Ala Gly Leu Leu Gln Gly Ala Tyr Met Asp Val Met Pro
 225 230 235 240
 Asp Arg Ile Glu Ala Leu Thr Trp Ile Val Tyr Gly Ile Ile Ser Gly
 245 250 255
 Gly Arg Ile Thr Val Glu Gly Val Pro Phe Ser Ser Met Glu Val Pro
 260 265 270
 Phe Ile His Leu Glu Lys Ala Gly Val Asp Leu Phe Arg Asn Ser Ser
 275 280 285
 Ser Val Tyr Ile Thr Pro Glu Cys Leu Pro Ser Gly Ser Val Gln Pro
 290 295 300
 Phe Glu Leu Ala Cys Gly Thr His Pro Gly Val Ile Ser Asp Met Gln

305 310 315 320
 Ala Leu Phe Val Leu Leu Gly Leu Lys Gly Ala Gly Thr Ser Arg Val
 325 330 335
 Tyr Asp Tyr Arg Tyr Pro Glu Arg Ile Ala Phe Val Glu Glu Leu Thr
 340 345 350
 Asn Leu Val Ser Gly Asp Lys Leu Ser Ala Glu Ala Gly Lys Ile Thr
 355 360 365
 Ile Gln Gly Asp Ala Thr Phe Arg Pro Gly Tyr Ala Asn Ser Thr Asp
 370 375 380
 Leu Arg Gly Ser Met Ala Val Val Leu Ala Ala Leu Cys Ala Asp Gly
 385 390 395 400
 Lys Ser Thr Ile Asn Asn Val His Met Ala Leu Arg Gly Tyr Asn Glu
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 Gly Glu Val Pro Ser Pro
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1009)
 <223> RXN00045

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 Met Thr Asp Pro Thr
 1 5
 tgc acc ctt gcc ctt gat att ggt gcc aca aag att gcc tac gca cta 163
 Cys Thr Leu Ala Leu Asp Ile Gly Ala Thr Lys Ile Ala Tyr Ala Leu
 10 15 20
 gtc ccc gat aac acc ccg acg aca aca ttg tcc acg gga cgc ttg gga 211
 Val Pro Asp Asn Thr Pro Thr Thr Thr Leu Ser Thr Gly Arg Leu Gly
 25 30 35
 aca aaa gaa ggc gac agc cct atc gag cag atc cgg ctg gtt ctt ctg 259
 Thr Lys Glu Gly Asp Ser Pro Ile Glu Gln Ile Arg Leu Val Leu Leu
 40 45 50
 gca ggc tta aaa gct gcc gag gaa cac ggt ctc agt gtc gcc cgc atc 307
 Ala Gly Leu Lys Ala Ala Glu Glu His Gly Leu Ser Val Ala Arg Ile
 55 60 65
 ggc atg ggc gct cct ggt gta att ctg gga cca gag gga acc atc gtg 355

[illegible]

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<211> 303

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 78

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Ile Ala Tyr Ala Leu Val Pro Asp Asn Thr Pro Thr Thr Thr Leu Ser
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Thr Gly Arg Leu Gly Thr Lys Glu Gly Asp Ser Pro Ile Glu Gln Ile
          35              40              45

Arg Leu Val Leu Leu Ala Gly Leu Lys Ala Ala Glu Glu His Gly Leu
          50              55              60

Ser Val Ala Arg Ile Gly Met Gly Ala Pro Gly Val Ile Leu Gly Pro
          65              70              75              80

Glu Gly Thr Ile Val Tyr Asn Gly Glu Thr Leu Thr Glu Trp Ala Gly
          85              90              95

Thr Asp Leu Arg Gly Leu Ser Arg Glu Val Leu Asn Val Pro Phe Ala
          100              105              110

Ala His Asn Asp Val Arg Val Trp Ala Tyr Gly Glu His His Leu Gly
          115              120              125

Thr Gly Lys Asp Leu Thr Gly Arg Val Leu Tyr Val Ser Leu Gly Thr
          130              135              140

Gly Val Gly Gly Ala Ile Ile Glu Asp Gly Ile Met Met Ser Ser Pro
          145              150              155              160

Thr Gly Thr Ala Gly Glu Phe Ala Glu Val Val Cys Ser Asp His Ala
          165              170              175

Gly Leu Ala Val Arg Cys Glu Asn Val Ala Ser Gly Thr Gly Leu Thr
          180              185              190

Arg Tyr Tyr Asn Glu Ala Ala Ala Thr Gln Leu Asp Leu Pro Ala Ile
          195              200              205

Met Glu Arg Phe His Gln Gly Asp Gly Leu Ala Gln Gln Ile Ile Thr
          210              215              220

Gly Asn Leu Arg Gly Phe Gly Gln Ala Leu Gly Ala Leu Val Thr Val
          225              230              235              240

Leu Asp Leu Ser Ala Val Val Val Gly Gly Gly Val Ala Gly Ile Gly
          245              250              255

Ala Pro Val Met Asp Pro Ile Thr Ala Gly Ile Phe Asp Arg Val Leu
          260              265              270

Thr Pro Asn Lys Ser Val Gln Val Leu Ser Thr Ser Leu Gly Ala Gln
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 <223> RXN02704

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 Met Thr Thr Gly Ala
 1 5
 tca aaa aaa ccc gca cgt ccg aac act ggc gct aaa acc aga acg ggg 163
 Ser Lys Lys Pro Ala Arg Pro Asn Thr Gly Ala Lys Thr Arg Thr Gly
 10 15 20
 ctg gga att agg gag cgt att tcc ggt gca tgg aat gat ctt ctc gcg 211
 Leu Gly Ile Arg Glu Arg Ile Ser Gly Ala Trp Asn Asp Leu Leu Ala
 25 30 35
 cgc cct tta act gac tac atc atg atc ttg tgc atc gtg gtc att ttg 259
 Arg Pro Leu Thr Asp Tyr Ile Met Ile Leu Cys Ile Val Val Ile Leu
 40 45 50
 tcg tgc ctc ggt gta gtc atg gtg tat tcc tcc tca atg aca tgg tcg 307
 Ser Cys Leu Gly Val Val Met Val Tyr Ser Ser Ser Met Thr Trp Ser
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 Leu Arg Glu Gly Gly Ser Val Trp Gly Thr Ala Val Arg Gln Gly Ile
 70 75 80 85
 atg atc gtg ttg ggt ttc ttt gcc atg tgg gtg gcg ttg atg acg cgc 403
 Met Ile Val Leu Gly Phe Phe Ala Met Trp Val Ala Leu Met Thr Arg
 90 95 100
 ccg caa acc att aga aac cta tcc aac ctg ata ttg att gtg tct att 451
 Pro Gln Thr Ile Arg Asn Leu Ser Asn Leu Ile Leu Ile Val Ser Ile
 105 110 115
 gtc ttg ctg ctt gcc gtg cag att cct ggc att ggt aca ggt aaa gaa 499
 Val Leu Leu Leu Ala Val Gln Ile Pro Gly Ile Gly Thr Gly Lys Glu
 120 125 130
 gag gtc ggg tcg cag tcg tgg att gct ctt gga cct att cag ttt cag 547
 Glu Val Gly Ser Gln Ser Trp Ile Ala Leu Gly Pro Ile Gln Phe Gln
 135 140 145
 cct tcg gag atc gcc aaa gtg gcc att gcc gtg tgg gga gcg cac tac 595
 Pro Ser Glu Ile Ala Lys Val Ala Ile Ala Val Trp Gly Ala His Tyr
 150 155 160 165

ctc gca ggc aag ggc cct gtg cag cac tgg ttc aat aat cac ttg atg Leu Ala Gly Lys Gly Pro Val Gln His Trp Phe Asn Asn His Leu Met 170 175 180	643
cgt ttt ggt ggc gtc ggt gca ttc atg gcg ttt ttg atc ttc atg gaa Arg Phe Gly Gly Val Gly Ala Phe Met Ala Phe Leu Ile Phe Met Glu 185 190 195	691
ggc gac gcc ggc atg gcg atg tct ttc gtg ctg gtt gta ttg ttc atg Gly Asp Ala Gly Met Ala Met Ser Phe Val Leu Val Val Leu Phe Met 200 205 210	739
ctg ttt ttt gcg ggc atc gcc atg ggt tgg atc gcg att gcc ggc gta Leu Phe Phe Ala Gly Ile Ala Met Gly Trp Ile Ala Ile Ala Gly Val 215 220 225	787
ctg att atc gca gcc ctc gca gtc ctg gca ttg ggc gga ggc ttc cgt Leu Ile Ile Ala Ala Leu Ala Val Leu Ala Leu Gly Gly Gly Phe Arg 230 235 240 245	835
tca agc cga ttc gag gtg tat ttc gat gcg ctg ttt ggc aat ttc cac Ser Ser Arg Phe Glu Val Tyr Phe Asp Ala Leu Phe Gly Asn Phe His 250 255 260	883
gat gtg cga ggc att gcc ttc cag tcc tat cag ggc ttc ctc tct ctt Asp Val Arg Gly Ile Ala Phe Gln Ser Tyr Gln Gly Phe Leu Ser Leu 265 270 275	931
gca gat ggt tcc ggc ttg gga gtt ggt ttg ggc caa tca agg gcg aag Ala Asp Gly Ser Gly Leu Gly Val Gly Leu Gly Gln Ser Arg Ala Lys 280 285 290	979
tgg ttc tac ctg ccc gaa gct aaa aat gac ttc atc ttt gcc atc att Trp Phe Tyr Leu Pro Glu Ala Lys Asn Asp Phe Ile Phe Ala Ile Ile 295 300 305	1027
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gcg ggg ctg ctg tac ttc ggt ctg cgc aca gcc aag aag agc cac gat Ala Gly Leu Leu Tyr Phe Gly Leu Arg Thr Ala Lys Lys Ser His Asp 330 335 340	1123
cca ttc ttg ggc ttg atg gct gca acc ttg acg gca tcc gtg gtg tcg Pro Phe Leu Gly Leu Met Ala Ala Thr Leu Thr Ala Ser Val Val Ser 345 350 355	1171
cag gcg ttc atc aac att ggc tac gtg gtt ggt ctg ctg cca gtt acc Gln Ala Phe Ile Asn Ile Gly Tyr Val Val Gly Leu Leu Pro Val Thr 360 365 370	1219
ggt att cag ctg ccc atg att tcc gcc ggt ggt acc tcc gcg atc att Gly Ile Gln Leu Pro Met Ile Ser Ala Gly Gly Thr Ser Ala Ile Ile 375 380 385	1267
acc ttg gct tcc atg ggc ttg ctc att agc tgt gca cgc cac gaa cca Thr Leu Ala Ser Met Gly Leu Leu Ile Ser Cys Ala Arg His Glu Pro 390 395 400 405	1315
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<212> PRT
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35 40 45
Ile Val Val Ile Leu Ser Cys Leu Gly Val Val Met Val Tyr Ser Ser
50 55 60
Ser Met Thr Trp Ser Leu Arg Glu Gly Gly Ser Val Trp Gly Thr Ala

65	70	75	80
Val Arg Gln Gly Ile Met Ile Val Leu Gly Phe Phe Ala Met Trp Val	85	90	95
Ala Leu Met Thr Arg Pro Gln Thr Ile Arg Asn Leu Ser Asn Leu Ile	100	105	110
Leu Ile Val Ser Ile Val Leu Leu Leu Ala Val Gln Ile Pro Gly Ile	115	120	125
Gly Thr Gly Lys Glu Glu Val Gly Ser Gln Ser Trp Ile Ala Leu Gly	130	135	140
Pro Ile Gln Phe Gln Pro Ser Glu Ile Ala Lys Val Ala Ile Ala Val	145	150	155
Trp Gly Ala His Tyr Leu Ala Gly Lys Gly Pro Val Gln His Trp Phe	165	170	175
Asn Asn His Leu Met Arg Phe Gly Gly Val Gly Ala Phe Met Ala Phe	180	185	190
Leu Ile Phe Met Glu Gly Asp Ala Gly Met Ala Met Ser Phe Val Leu	195	200	205
Val Val Leu Phe Met Leu Phe Phe Ala Gly Ile Ala Met Gly Trp Ile	210	215	220
Ala Ile Ala Gly Val Leu Ile Ile Ala Ala Leu Ala Val Leu Ala Leu	225	230	235
Gly Gly Gly Phe Arg Ser Ser Arg Phe Glu Val Tyr Phe Asp Ala Leu	245	250	255
Phe Gly Asn Phe His Asp Val Arg Gly Ile Ala Phe Gln Ser Tyr Gln	260	265	270
Gly Phe Leu Ser Leu Ala Asp Gly Ser Gly Leu Gly Val Gly Leu Gly	275	280	285
Gln Ser Arg Ala Lys Trp Phe Tyr Leu Pro Glu Ala Lys Asn Asp Phe	290	295	300
Ile Phe Ala Ile Ile Gly Glu Glu Leu Gly Leu Trp Gly Gly Ala Leu	305	310	315
Val Ile Ala Leu Phe Ala Gly Leu Leu Tyr Phe Gly Leu Arg Thr Ala	325	330	335
Lys Lys Ser His Asp Pro Phe Leu Gly Leu Met Ala Ala Thr Leu Thr	340	345	350
Ala Ser Val Val Ser Gln Ala Phe Ile Asn Ile Gly Tyr Val Val Gly	355	360	365
Leu Leu Pro Val Thr Gly Ile Gln Leu Pro Met Ile Ser Ala Gly Gly	370	375	380
Thr Ser Ala Ile Ile Thr Leu Ala Ser Met Gly Leu Leu Ile Ser Cys	385	390	395
			400

Ala Arg His Glu Pro Glu Thr Val Ser Ala Met Ala Ser Tyr Gly Arg
 405 410 415

Pro Ala Ile Asp Arg Leu Leu Gly Leu Arg Glu Pro Ser Ser Thr Leu
 420 425 430

Thr Thr Ser Asn Ala Ser Leu Arg Ser Asn Lys Thr Lys Ala Ala Lys
 435 440 445

Gln Lys Pro Ser Pro Gln Lys Glu Ser Arg Asp Arg Phe Gly Glu Pro
 450 455 460

Val Thr Ala Arg Arg Ala Gln Ala Pro Arg Ser Gly Arg Ala Gly Val
 465 470 475 480

Gln Ser Glu Ala Pro Arg Arg Ser Thr Gly Ser Val Lys Gly Arg Ser
 485 490 495

Ser Gly Gln Asp Asn Gly Arg Ser Asn Glu Gly Thr Ala Arg Ser Gln
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Ser Thr Thr Gly Gly Arg Ala Ala Asp Arg Ser Val Asp Arg Ser Arg
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Gln Ser Arg Pro Thr Glu Arg Arg Ser Glu Ser Arg Ala Met Ile Gly
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Val Thr Thr Ala Thr Ala Asp Lys Cys Glu Ile Arg Arg Thr Thr Asn
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Lys Asp Gly

<210> 81
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> FRXA02704

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 Met Thr Thr Gly Ala
 1 5

tca aaa aaa ccc gca cgt ccg aac act ggc gct aaa acc aga acg ggg 163
 Ser Lys Lys Pro Ala Arg Pro Asn Thr Gly Ala Lys Thr Arg Thr Gly
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ctg gga att agg gag cgt att tcc ggt gca tgg aat gat ctt ctc gcg 211
 Leu Gly Ile Arg Glu Arg Ile Ser Gly Ala Trp Asn Asp Leu Leu Ala
 25 30 35

cgc cct tta act gac tac atc atg atc ttg tgc atc gtg gtc att ttg 259

Arg	Pro	Leu	Thr	Asp	Tyr	Ile	Met	Ile	Leu	Cys	Ile	Val	Val	Ile	Leu	
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tcg	tgc	ctc	ggg	gta	gtc	atg	gtg	tat	tcc	tcc	tca	atg	aca	tgg	tcg	307
Ser	Cys	Leu	Gly	Val	Val	Met	Val	Tyr	Ser	Ser	Ser	Met	Thr	Trp	Ser	
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ttg	agg	gaa	ggg	ggc	tcc	gtg	tgg	ggg	act	gcc	gtg	cgc	cag	ggc	atc	355
Leu	Arg	Glu	Gly	Gly	Ser	Val	Trp	Gly	Thr	Ala	Val	Arg	Gln	Gly	Ile	
		70			75					80					85	
atg	atc	gtg	ttg	ggg	ttc	ttt	gcc	atg	tgg	gtg	gcg	ttg	atg	acg	cgc	403
Met	Ile	Val	Leu	Gly	Phe	Phe	Ala	Met	Trp	Val	Ala	Leu	Met	Thr	Arg	
				90					95					100		
ccg	caa	acc	att	aga	aac	cta	tcc	aac	ctg	ata	ttg	att	gtg	tct	att	451
Pro	Gln	Thr	Ile	Arg	Asn	Leu	Ser	Asn	Leu	Ile	Leu	Ile	Val	Ser	Ile	
			105					110					115			
gtc	ttg	ctg	ctt	gcc	gtg	cag	att	cct	ggc	att	ggg	aca	ggg	aaa	gaa	499
Val	Leu	Leu	Leu	Ala	Val	Gln	Ile	Pro	Gly	Ile	Gly	Thr	Gly	Lys	Glu	
		120					125					130				
gag	gtc	ggg	tcg	cag	tcg	tgg	att	gct	ctt	gga	cct	att	cag	ttt	cag	547
Glu	Val	Gly	Ser	Gln	Ser	Trp	Ile	Ala	Leu	Gly	Pro	Ile	Gln	Phe	Gln	
		135				140					145					
cct	tcg	gag	atc	gcc	aaa	gtg	gcc	att	gcc	gtg	tgg	gga	gcg	cac	tac	595
Pro	Ser	Glu	Ile	Ala	Lys	Val	Ala	Ile	Ala	Val	Trp	Gly	Ala	His	Tyr	
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ctc	gca	ggc	aag	ggc	cct	gtg	cag	cac	tgg	ttc	aat	aat	cac	ttg	atg	643
Leu	Ala	Gly	Lys	Gly	Pro	Val	Gln	His	Trp	Phe	Asn	Asn	His	Leu	Met	
				170					175					180		
cgt	ttt	ggg	ggc	gtc	ggg	gca	ttc	atg	gcg	ttt	ttg	atc	ttc	atg	gaa	691
Arg	Phe	Gly	Gly	Val	Gly	Ala	Phe	Met	Ala	Phe	Leu	Ile	Phe	Met	Glu	
			185					190					195			
ggc	gac	gcc	ggc	atg	gcg	atg	tct	ttc	gtg	ctg	gtt	gta	ttg	ttc	atg	739
Gly	Asp	Ala	Gly	Met	Ala	Met	Ser	Phe	Val	Leu	Val	Val	Leu	Phe	Met	
		200					205					210				
ctg	ttt	ttt	gcg	ggc	atc	gcc	atg	ggg	tgg	atc	gcg	att	gcc	ggc	gta	787
Leu	Phe	Phe	Ala	Gly	Ile	Ala	Met	Gly	Trp	Ile	Ala	Ile	Ala	Gly	Val	
		215				220					225					
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Leu	Ile	Ile	Ala	Ala	Leu	Ala	Val	Leu	Ala	Leu	Gly	Gly	Gly	Phe	Arg	
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tca	agc	cga	ttc	gag	gtg	tat	ttc	gat	gcg	ctg	ttt	ggc	aat	ttc	cac	883
Ser	Ser	Arg	Phe	Glu	Val	Tyr	Phe	Asp	Ala	Leu	Phe	Gly	Asn	Phe	His	
				250					255					260		
gat	gtg	cga	ggc	att	gcc	ttc	cag	tcc	tat	cag	ggc	ttc	ctc	tct	ctt	931
Asp	Val	Arg	Gly	Ile	Ala	Phe	Gln	Ser	Tyr	Gln	Gly	Phe	Leu	Ser	Leu	
			265					270					275			
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Ala	Asp	Gly	Ser	Gly	Leu	Gly	Val	Gly	Leu	Gly	Gln	Ser	Arg	Ala	Lys	

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Trp	Phe	Tyr	Leu	Pro	Glu	Ala	Lys	Asn	Asp	Phe	Ile	Phe	Ala	Ile	Ile		
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Gly	Glu	Glu	Leu	Gly	Leu	Trp	Gly	Gly	Ala	Leu	Val	Ile	Ala	Leu	Phe		
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Pro	Phe	Leu	Gly	Leu	Met	Ala	Ala	Thr	Leu	Thr	Ala	Ser	Val	Val	Ser		
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cag	gcg	ttc	atc	aac	att	ggc	tac	gtg	ggt	ggt	ctg	ctg	cca	ggt	acc	1219	
Gln	Ala	Phe	Ile	Asn	Ile	Gly	Tyr	Val	Val	Gly	Leu	Leu	Pro	Val	Thr		
360					365					370							
ggt	att	cag	ctg	ccc	atg	att	tcc	gcc	ggt	ggt	acc	tcc	gcg	atc	att	1267	
Gly	Ile	Gln	Leu	Pro	Met	Ile	Ser	Ala	Gly	Gly	Thr	Ser	Ala	Ile	Ile		
375					380					385							
acc	ttg	gct	tcc	atg	ggc	ttg	ctc	att	agc	tgt	gca	cgc	cac	gaa	cca	1315	
Thr	Leu	Ala	Ser	Met	Gly	Leu	Leu	Ile	Ser	Cys	Ala	Arg	His	Glu	Pro		
390					395					400					405		
gag	aca	ggt	tct	gcg	atg	gct	tcc	tat	gga	cgc	ccc	gca	atc	gat	cga	1363	
Glu	Thr	Val	Ser	Ala	Met	Ala	Ser	Tyr	Gly	Arg	Pro	Ala	Ile	Asp	Arg		
410					415					420							
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Leu	Leu	Gly	Leu	Arg	Glu	Pro	Ser	Ser	Thr	Leu	Thr	Thr	Ser	Asn	Ala		
425					430					435							
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Ser	Leu	Arg	Ser	Asn	Lys	Thr	Lys	Ala	Ala	Lys	Gln	Lys	Pro	Ser	Pro		
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cag	aaa	gag	tct	cgg	gac	cgc	ttc	ggc	gag	cct	gtg	acc	gca	cgc	cga	1507	
Gln	Lys	Glu	Ser	Arg	Asp	Arg	Phe	Gly	Glu	Pro	Val	Thr	Ala	Arg	Arg		
455					460					465							
gcg	cag	gcg	cca	cga	agt	ggg	cga	gct	gga	gta	caa	tcg	gaa	gct	ccg	1555	
Ala	Gln	Ala	Pro	Arg	Ser	Gly	Arg	Ala	Gly	Val	Gln	Ser	Glu	Ala	Pro		
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cga	cgc	tcg	act	ggt	agc	gtc	aaa	ggt	cga	agc	agt	ggt	cag	gac	aac	1603	
Arg	Arg	Ser	Thr	Gly	Ser	Val	Lys	Gly	Arg	Ser	Ser	Gly	Gln	Asp	Asn		
490					495					500							
ggt	cga	agc	aac	gaa	ggt	acg	gcg	cgt	agc	caa	tca	act	act	ggt	ggg	1651	
Gly	Arg	Ser	Asn	Glu	Gly	Thr	Ala	Arg	Ser	Gln	Ser	Thr	Thr	Gly	Gly		
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cgc	gca	gcc	gat	cgc	agc	gtt	gat	cga	agt	cgt	caa	agc	agg	cct	acc	1699	
Arg	Ala	Ala	Asp	Arg	Ser	Val	Asp	Arg	Ser	Arg	Gln	Ser	Arg	Pro	Thr		
520					525					530							

gag cgc cgt tcc gag agt cgc gcg atg att ggc gtg aca acc gca acc 1747
 Glu Arg Arg Ser Glu Ser Arg Ala Met Ile Gly Val Thr Thr Ala Thr
 535 540 545

gca gat aaa tgt gaa atc agg aga act acg aat aaa gat ggc 1789
 Ala Asp Lys Cys Glu Ile Arg Arg Thr Thr Asn Lys Asp Gly
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taactcccca aaacccatgc ggg 1812

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<211> 563

<212> PRT

<213> Corynebacterium glutamicum

<400> 82

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 20 25 30

Asn Asp Leu Leu Ala Arg Pro Leu Thr Asp Tyr Ile Met Ile Leu Cys
 35 40 45

Ile Val Val Ile Leu Ser Cys Leu Gly Val Val Met Val Tyr Ser Ser
 50 55 60

Ser Met Thr Trp Ser Leu Arg Glu Gly Gly Ser Val Trp Gly Thr Ala
 65 70 75 80

Val Arg Gln Gly Ile Met Ile Val Leu Gly Phe Phe Ala Met Trp Val
 85 90 95

Ala Leu Met Thr Arg Pro Gln Thr Ile Arg Asn Leu Ser Asn Leu Ile
 100 105 110

Leu Ile Val Ser Ile Val Leu Leu Leu Ala Val Gln Ile Pro Gly Ile
 115 120 125

Gly Thr Gly Lys Glu Glu Val Gly Ser Gln Ser Trp Ile Ala Leu Gly
 130 135 140

Pro Ile Gln Phe Gln Pro Ser Glu Ile Ala Lys Val Ala Ile Ala Val
 145 150 155 160

Trp Gly Ala His Tyr Leu Ala Gly Lys Gly Pro Val Gln His Trp Phe
 165 170 175

Asn Asn His Leu Met Arg Phe Gly Gly Val Gly Ala Phe Met Ala Phe
 180 185 190

Leu Ile Phe Met Glu Gly Asp Ala Gly Met Ala Met Ser Phe Val Leu
 195 200 205

Val Val Leu Phe Met Leu Phe Phe Ala Gly Ile Ala Met Gly Trp Ile
 210 215 220

Ala Ile Ala Gly Val Leu Ile Ile Ala Ala Leu Ala Val Leu Ala Leu

225		230		235		240
Gly Gly Gly Phe Arg Ser Ser Arg Phe Glu Val Tyr Phe Asp Ala Leu						
		245		250		255
Phe Gly Asn Phe His Asp Val Arg Gly Ile Ala Phe Gln Ser Tyr Gln						
		260		265		270
Gly Phe Leu Ser Leu Ala Asp Gly Ser Gly Leu Gly Val Gly Leu Gly						
		275		280		285
Gln Ser Arg Ala Lys Trp Phe Tyr Leu Pro Glu Ala Lys Asn Asp Phe						
		290		295		300
Ile Phe Ala Ile Ile Gly Glu Glu Leu Gly Leu Trp Gly Gly Ala Leu						
305		310		315		320
Val Ile Ala Leu Phe Ala Gly Leu Leu Tyr Phe Gly Leu Arg Thr Ala						
		325		330		335
Lys Lys Ser His Asp Pro Phe Leu Gly Leu Met Ala Ala Thr Leu Thr						
		340		345		350
Ala Ser Val Val Ser Gln Ala Phe Ile Asn Ile Gly Tyr Val Val Gly						
		355		360		365
Leu Leu Pro Val Thr Gly Ile Gln Leu Pro Met Ile Ser Ala Gly Gly						
		370		375		380
Thr Ser Ala Ile Ile Thr Leu Ala Ser Met Gly Leu Leu Ile Ser Cys						
385		390		395		400
Ala Arg His Glu Pro Glu Thr Val Ser Ala Met Ala Ser Tyr Gly Arg						
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Pro Ala Ile Asp Arg Leu Leu Gly Leu Arg Glu Pro Ser Ser Thr Leu						
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Thr Thr Ser Asn Ala Ser Leu Arg Ser Asn Lys Thr Lys Ala Ala Lys						
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Gln Lys Pro Ser Pro Gln Lys Glu Ser Arg Asp Arg Phe Gly Glu Pro						
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Val Thr Ala Arg Arg Ala Gln Ala Pro Arg Ser Gly Arg Ala Gly Val						
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Gln Ser Glu Ala Pro Arg Arg Ser Thr Gly Ser Val Lys Gly Arg Ser						
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Ser Gly Gln Asp Asn Gly Arg Ser Asn Glu Gly Thr Ala Arg Ser Gln						
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Ser Thr Thr Gly Gly Arg Ala Ala Asp Arg Ser Val Asp Arg Ser Arg						
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Gln Ser Arg Pro Thr Glu Arg Arg Ser Glu Ser Arg Ala Met Ile Gly						
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Met Thr Ser Pro Asn																	
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Asn Tyr Leu Ala Lys Ile Lys Val Val Gly Val Gly Gly Gly Gly Val																	
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Asn Ala Val Asn Arg Met Ile Glu Glu Gly Leu Lys Gly Val Glu Phe																	
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Ile Ala Val Asn Thr Asp Ser Gln Ala Leu Met Phe Ser Asp Ala Asp																	
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Val Lys Leu Asp Ile Gly Arg Glu Ala Thr Arg Gly Leu Gly Ala Gly																	
55 60 65																	
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Ala Asn Pro Glu Val Gly Arg Ala Ser Ala Glu Asp His Lys Asn Glu																	
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Ile Glu Glu Thr Ile Lys Gly Ala Asp Met Val Phe Val Thr Ala Gly																	
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Glu Gly Gly Gly Thr Gly Thr Gly Ala Ala Pro Val Val Ala Gly Ile																	
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Ala Lys Lys Met Gly Ala Leu Thr Ile Gly Val Val Thr Lys Pro Phe																	
120 125 130																	
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Glu Phe Glu Gly Arg Arg Arg Thr Arg Gln Ala Glu Glu Gly Ile Ala																	
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Ala Leu Lys Glu Val Cys Asp Thr Leu Ile Val Ile Pro Asn Asp Arg																	
150 155 160 165																	

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<213> Corynebacterium glutamicum

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 35 40 45

Phe Ser Asp Ala Asp Val Lys Leu Asp Ile Gly Arg Glu Ala Thr Arg
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Gly Leu Gly Ala Gly Ala Asn Pro Glu Val Gly Arg Ala Ser Ala Glu
 65 70 75 80

Asp His Lys Asn Glu Ile Glu Glu Thr Ile Lys Gly Ala Asp Met Val
 85 90 95

Phe Val Thr Ala Gly Glu Gly Gly Gly Thr Gly Thr Gly Ala Ala Pro
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Val Val Ala Gly Ile Ala Lys Lys Met Gly Ala Leu Thr Ile Gly Val
 115 120 125

Val Thr Lys Pro Phe Glu Phe Glu Gly Arg Arg Arg Thr Arg Gln Ala
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Glu Glu Gly Ile Ala Ala Leu Lys Glu Val Cys Asp Thr Leu Ile Val
 145 150 155 160

Ile Pro Asn Asp Arg Leu Leu Glu Leu Gly Asp Ala Asn Leu Ser Ile
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Met Glu Ala Phe Arg Ala Ala Asp Glu Val Leu His Asn Gly Val Gln
 180 185 190

Gly Ile Thr Asn Leu Ile Thr Ile Pro Gly Val Ile Asn Val Asp Phe
 195 200 205

Ala Asp Val Arg Ser Val Met Ser Glu Ala Gly Ser Ala Leu Met Gly
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Val Gly Ser Ala Arg Gly Asp Asn Arg Val Val Ser Ala Thr Glu Gln
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 Ala Ile Asn Ser Pro Leu Leu Glu Ala Thr Met Asp Gly Ala Thr Gly
 245 250 255
 Val Leu Leu Ser Phe Ala Gly Gly Ser Asp Leu Gly Leu Met Glu Val
 260 265 270
 Asn Ala Ala Ala Ser Met Val Arg Glu Arg Ser Asp Glu Asp Val Asn
 275 280 285
 Leu Ile Phe Gly Thr Ile Ile Asp Asp Asn Leu Gly Asp Glu Val Arg
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 Val Thr Val Ile Ala Thr Gly Phe Asp Ala Ala Arg Ala Ser Ala Ala
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 Glu Asn Arg Arg Ala Gly Ile Ser Ala Ala Pro Ala Ala Glu Pro Val
 325 330 335
 Gln Gln Gln Val Pro Thr Thr Asn Ala Thr Leu Pro Pro Glu Lys Glu
 340 345 350
 Ser Ile Phe Gly Gly Ala Arg Glu Glu Asn Asp Pro Tyr Leu Ser Arg
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 Ser Ala Gly Ala Arg His Arg Ile Glu Glu Thr Arg Ser Gly Gly Gly
 370 375 380
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 385 390 395 400
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 Met Ala Phe Gly Tyr
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gta ctg cgt gaa gct gtt cgc ggc atg ggc cgc aac gtc acc atg acc 163

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Gly	Phe	Leu	Val	Thr	Asn	Met	Thr	Asp	Arg	Thr	Lys	Asp	Ile	Tyr	Leu	
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Asp	Arg	Val	Glu	Val	Met	Ile	Gln	Leu	Asp	Glu	Asp	Thr	Ser	Ala	Asn	
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Asp	Pro	Glu	Cys	Thr	Ala	Glu	Ser	Cys	Thr	Glu	Val	Arg	Asp	Val	Leu	
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Ser	Tyr	Glu	Arg	Phe	Val	Glu	Val	Phe	Lys	Asp	Thr	Asp	Pro	Val	Leu	
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Leu	Glu	Asp	Pro	Leu	Ala	Val	Glu	Ile	Leu	Asp	Pro	Val	Arg	Asp	Leu	
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cct	caa	gta	agc	aac	gtg	atc	gac	cag	gtg	gat	gat	ctg	cgc	gga	gca	595
Pro	Gln	Val	Ser	Asn	Val	Ile	Asp	Gln	Val	Asp	Asp	Leu	Arg	Gly	Ala	
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Thr	Glu	Asn	Leu	Asp	Ser	Ile	Arg	Asn	Ala	Thr	Phe	Leu	Ile	Ala	Ala	
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gtg	caa	gtt	ttg	gca	tcg	atc	ttc	ctg	att	gcc	aac	atg	gtg	caa	atc	691
Val	Gln	Val	Leu	Ala	Ser	Ile	Phe	Leu	Ile	Ala	Asn	Met	Val	Gln	Ile	
			185					190					195			
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Ala	Ala	Phe	Asn	Arg	Arg	Glu	Glu	Thr	Glu	Ile	Met	Arg	Ile	Val	Gly	
		200					205					210				
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tcc	acc	ctc	att	ggc	gcg	gtt	ttc	gcc	gtc	ggc	gcg	ctc	ttc	ttg	ggc	835
Ser	Thr	Leu	Ile	Gly	Ala	Val	Phe	Ala	Val	Gly	Ala	Leu	Phe	Leu	Gly	
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Lys	Glu	Leu	Val	Ile	Asp	Lys	Ala	Leu	Arg	Gly	Leu	Tyr	Asp	Ser	Gln	

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Leu Ile Ala Pro Val Thr Thr Thr Asp Ile Trp Leu Val Ala Pro Ile
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att tcc ggc att ggc gtg gtg atc gcc ggc att atc gca caa ctc acc 979
Ile Ser Gly Ile Gly Val Val Ile Ala Gly Ile Ile Ala Gln Leu Thr
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 <213> Corynebacterium glutamicum

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Ala Leu Leu Ala Thr Gly Phe Leu Val Thr Asn Met Thr Asp Arg Thr
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Lys Asp Ile Tyr Leu Asp Arg Val Glu Val Met Ile Gln Leu Asp Glu
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Asp Thr Ser Ala Asn Asp Pro Glu Cys Thr Ala Glu Ser Cys Thr Glu
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Val Arg Asp Val Leu Glu Gly Leu Asp Gly Ile Asp Ser Ile Thr Tyr
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Arg Ser Arg Glu Ala Ser Tyr Glu Arg Phe Val Glu Val Phe Lys Asp
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Thr Asp Pro Val Leu Val Ala Glu Thr Ser Pro Asp Ala Leu Pro Ala
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Ala Phe His Val Arg Leu Glu Asp Pro Leu Ala Val Glu Ile Leu Asp
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Pro Val Arg Asp Leu Pro Gln Val Ser Asn Val Ile Asp Gln Val Asp
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Asp Leu Arg Gly Ala Thr Glu Asn Leu Asp Ser Ile Arg Asn Ala Thr
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Phe Leu Ile Ala Ala Val Gln Val Leu Ala Ser Ile Phe Leu Ile Ala
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Asn Met Val Gln Ile Ala Ala Phe Asn Arg Arg Glu Glu Thr Glu Ile
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Met Arg Ile Val Gly Ala Ser Arg Phe Tyr Thr Gln Gly Pro Phe Val

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Leu Tyr Asp Ser Gln Leu Ile Ala Pro Val Thr Thr Thr Asp Ile Trp		
	260	265 270
Leu Val Ala Pro Ile Ile Ser Gly Ile Gly Val Val Ile Ala Gly Ile		
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 Val Ile Thr Phe Glu
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 Asn Val Thr Lys Asn Tyr Lys Thr Ser Thr Arg Pro Ala Leu Asp Asn
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 Val Ser Leu His Ile Glu Lys Gly Glu Phe Val Phe Leu Ile Gly Pro
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 Ser Gly Ser Gly Lys Ser Thr Phe Leu Arg Leu Met Thr Arg Glu Glu
 40 45 50

aac gtc agc tcc gga tcg ctg aca ctg gct gat ttt cag gtg aac aaa 307
 Asn Val Ser Ser Gly Ser Leu Thr Leu Ala Asp Phe Gln Val Asn Lys
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 Phe Gln Asp Phe Arg Leu Leu Lys Asn Lys Asn Val Tyr Asp Asn Val
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 Ala Phe Ala Leu Glu Val Ile Gly Lys Lys Lys Asp Lys Ile Gln Glu

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<211> 229

<212> PRT

<213> Corynebacterium glutamicum

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Met	Thr	Arg	Glu	Glu	Asn	Val	Ser	Ser	Gly	Ser	Leu	Thr	Leu	Ala	Asp
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Arg	Ile	Gly	Tyr	Val	Phe	Gln	Asp	Phe	Arg	Leu	Leu	Lys	Asn	Lys	Asn
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Asp	Lys	Ile	Gln	Glu	Leu	Val	Pro	Glu	Thr	Leu	Glu	Met	Val	Gly	Leu
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 Met Val Trp Asp Trp
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 cat acc cgc aag ggc gct gtc gca cgt ctg act ccc cca ttc atc cca 163
 His Thr Arg Lys Gly Ala Val Ala Arg Leu Thr Pro Pro Phe Ile Pro
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 Leu Asn Pro Ile Thr Gln Ala Glu Arg Leu Ala Asp Gly Thr Thr Ile
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 Phe Ser Leu Pro Ala Gly Leu Lys Trp Val Ala Arg His Asp Leu Ser
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 Val Lys Ala Leu Ala Asn Trp Arg His Val His Asn Phe Val Asp Gln
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Asp Gly Gly Thr Leu Ile Thr Asp Ser Val Ser Thr Arg Leu Pro Ala	
90 95 100	
tcc aca ctc acg ggc atg ttc gcc tat cgc caa act cag ctc atc gaa	451
Ser Thr Leu Thr Gly Met Phe Ala Tyr Arg Gln Thr Gln Leu Ile Glu	
105 110 115	
gac cta aaa ttc tta agt aga aca agc acg ctt ttc gac ggc tcc ccc	499
Asp Leu Lys Phe Leu Ser Arg Thr Ser Thr Leu Phe Asp Gly Ser Pro	
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ctc acc gta gcc atc acc ggc tcc agg ggg ctc gtc ggc cgc gcg ctg	547
Leu Thr Val Ala Ile Thr Gly Ser Arg Gly Leu Val Gly Arg Ala Leu	
135 140 145	
aca gcg cag ctg caa acc ggc ggc cac gaa gtc atc caa ctc gtg cgc	595
Thr Ala Gln Leu Gln Thr Gly Gly His Glu Val Ile Gln Leu Val Arg	
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aaa gaa ccc aaa cct ggc caa cgt ttc tgg gat cca ctc aac cca gca	643
Lys Glu Pro Lys Pro Gly Gln Arg Phe Trp Asp Pro Leu Asn Pro Ala	
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Ser Asp Leu Leu Asp Gly Ala Asp Val Leu Val His Leu Ala Gly Glu	
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ccg atc ttc ggg cga ttc aac gac tcc cac aaa gaa gcc atc cgc gag	739
Pro Ile Phe Gly Arg Phe Asn Asp Ser His Lys Glu Ala Ile Arg Glu	
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Ser Arg Val Leu Pro Thr Lys Phe Leu Ala Glu Leu Val Ala Glu Ser	
215 220 225	
acc cag tgc acc acc atg att tcc gcc tct gca gtt gga ttc tat ggt	835
Thr Gln Cys Thr Thr Met Ile Ser Ala Ser Ala Val Gly Phe Tyr Gly	
230 235 240 245	
cac gac cgc ggc gac gag atc ctg acc gaa gaa tcc gaa tcc ggc gat	883
His Asp Arg Gly Asp Glu Ile Leu Thr Glu Glu Ser Glu Ser Gly Asp	
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gat ttc ctc gcc gag gtc tgt agg gat tgg gaa cac gcc act gct cct	931
Asp Phe Leu Ala Glu Val Cys Arg Asp Trp Glu His Ala Thr Ala Pro	
265 270 275	
gcc tca gat gca gga aag cgc gta gcc ttc att cgc acc ggc gtg gcc	979
Ala Ser Asp Ala Gly Lys Arg Val Ala Phe Ile Arg Thr Gly Val Ala	
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Leu Ser Gly Arg Gly Gly Met Leu Pro Leu Leu Lys Thr Leu Phe Ser	
295 300 305	
acc gga cta ggc gga aaa ttc ggc gat ggc acc tcc tgg ttc agc tgg	1075
Thr Gly Leu Gly Gly Lys Phe Gly Asp Gly Thr Ser Trp Phe Ser Trp	
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Ile Ala Ile Asp Asp Leu Thr Asp Ile Tyr Tyr Arg Ala Ile Val Asp
                330                335                340

gcc cag atc tcc ggc ccc atc aac gcg gta gcc ccc aat cca gtc tcc 1171
Ala Gln Ile Ser Gly Pro Ile Asn Ala Val Ala Pro Asn Pro Val Ser
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aat gcg gac atg acc aag att ctg gcc acc agc atg cac cgt ccc gca 1219
Asn Ala Asp Met Thr Lys Ile Leu Ala Thr Ser Met His Arg Pro Ala
                360                365                370

ttc atc caa att cct tcc ctg ggc ccc aaa att ctg ctc gga agc caa 1267
Phe Ile Gln Ile Pro Ser Leu Gly Pro Lys Ile Leu Leu Gly Ser Gln
                375                380                385

ggc gct gaa gag cta gcc ctg gcg tcc caa cgc acc gcc cca gca gca 1315
Gly Ala Glu Glu Leu Ala Leu Ala Ser Gln Arg Thr Ala Pro Ala Ala
390                395                400                405

ctg gaa aac ctc agc cac acc ttc cgc tac acc gac atc ggg gcc gcc 1363
Leu Glu Asn Leu Ser His Thr Phe Arg Tyr Thr Asp Ile Gly Ala Ala
                410                415                420

atc gca cac gaa ctt ggc tac gaa caa ctc gca gat ttc gcc caa cag 1411
Ile Ala His Glu Leu Gly Tyr Glu Gln Leu Ala Asp Phe Ala Gln Gln
                425                430                435

caa gaa atc gaa gcc gaa cgc aaa cag gaa cga gcc gaa ctc aaa gcc 1459
Gln Glu Ile Glu Ala Glu Arg Lys Gln Glu Arg Ala Glu Leu Lys Ala
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gcc aag aag atc gcc aag aaa gcc cca gtc cta gag gaa tcc ccc acc 1507
Ala Lys Lys Ile Ala Lys Lys Ala Pro Val Leu Glu Glu Ser Pro Thr
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aac ctg gaa gat ccc gaa gaa gta gag caa agt atc ctt tca tca atc 1555
Asn Leu Glu Asp Pro Glu Glu Val Glu Gln Ser Ile Leu Ser Ser Ile
470                475                480                485

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<212> PRT

<213> Corynebacterium glutamicum

<400> 90

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Asp Gly Thr Thr Ile Phe Ser Leu Pro Ala Gly Leu Lys Trp Val Ala
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Arg His Asp Leu Ser Gly Phe Leu Asn Gly Ser Arg Phe Thr Asp Val
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Cys Leu Thr Ala Pro Val Lys Ala Leu Ala Asn Trp Arg His Val His
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 Thr Arg Leu Pro Ala Ser Thr Leu Thr Gly Met Phe Ala Tyr Arg Gln
 100 105 110
 Thr Gln Leu Ile Glu Asp Leu Lys Phe Leu Ser Arg Thr Ser Thr Leu
 115 120 125
 Phe Asp Gly Ser Pro Leu Thr Val Ala Ile Thr Gly Ser Arg Gly Leu
 130 135 140
 Val Gly Arg Ala Leu Thr Ala Gln Leu Gln Thr Gly Gly His Glu Val
 145 150 155 160
 Ile Gln Leu Val Arg Lys Glu Pro Lys Pro Gly Gln Arg Phe Trp Asp
 165 170 175
 Pro Leu Asn Pro Ala Ser Asp Leu Leu Asp Gly Ala Asp Val Leu Val
 180 185 190
 His Leu Ala Gly Glu Pro Ile Phe Gly Arg Phe Asn Asp Ser His Lys
 195 200 205
 Glu Ala Ile Arg Glu Ser Arg Val Leu Pro Thr Lys Phe Leu Ala Glu
 210 215 220
 Leu Val Ala Glu Ser Thr Gln Cys Thr Thr Met Ile Ser Ala Ser Ala
 225 230 235 240
 Val Gly Phe Tyr Gly His Asp Arg Gly Asp Glu Ile Leu Thr Glu Glu
 245 250 255
 Ser Glu Ser Gly Asp Asp Phe Leu Ala Glu Val Cys Arg Asp Trp Glu
 260 265 270
 His Ala Thr Ala Pro Ala Ser Asp Ala Gly Lys Arg Val Ala Phe Ile
 275 280 285
 Arg Thr Gly Val Ala Leu Ser Gly Arg Gly Gly Met Leu Pro Leu Leu
 290 295 300
 Lys Thr Leu Phe Ser Thr Gly Leu Gly Gly Lys Phe Gly Asp Gly Thr
 305 310 315 320
 Ser Trp Phe Ser Trp Ile Ala Ile Asp Asp Leu Thr Asp Ile Tyr Tyr
 325 330 335
 Arg Ala Ile Val Asp Ala Gln Ile Ser Gly Pro Ile Asn Ala Val Ala
 340 345 350
 Pro Asn Pro Val Ser Asn Ala Asp Met Thr Lys Ile Leu Ala Thr Ser
 355 360 365
 Met His Arg Pro Ala Phe Ile Gln Ile Pro Ser Leu Gly Pro Lys Ile
 370 375 380

Leu Leu Gly Ser Gln Gly Ala Glu Glu Leu Ala Leu Ala Ser Gln Arg
 385 390 395 400
 Thr Ala Pro Ala Ala Leu Glu Asn Leu Ser His Thr Phe Arg Tyr Thr
 405 410 415
 Asp Ile Gly Ala Ala Ile Ala His Glu Leu Gly Tyr Glu Gln Leu Ala
 420 425 430
 Asp Phe Ala Gln Gln Gln Glu Ile Glu Ala Glu Arg Lys Gln Glu Arg
 435 440 445
 Ala Glu Leu Lys Ala Ala Lys Lys Ile Ala Lys Lys Ala Pro Val Leu
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1684)
 <223> RXA00277

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 Met Lys Asp Asn Glu
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 gat ttc gat cca gat tca cca gca acc gaa gct gtt gcc ttc aac cct 163
 Asp Phe Asp Pro Asp Ser Pro Ala Thr Glu Ala Val Ala Phe Asn Pro
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 Phe Asp Asp Asp Asp Glu Asp Asp Ser Pro Ala Thr Ser Ala Val Ala
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 ttt aac cct ttt gaa gat gac gat gac gac gat gag ttc caa ggc gaa 259
 Phe Asn Pro Phe Glu Asp Asp Asp Asp Asp Asp Glu Phe Gln Gly Glu
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 ggc cta gaa ttc ctg ctg cgc gac ctc gac aat ctg cga gcc acc caa 307
 Gly Leu Glu Phe Leu Leu Arg Asp Leu Asp Asn Leu Arg Ala Thr Gln
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 Gly Gln Met Val Val Glu Gln Pro Ala Val Glu Asp Ser Leu Gly Ser
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 gca tct gcg cat acg gag aca act gcg gcc tca ctg cgt ccc cgc cca 403
 Ala Ser Ala His Thr Glu Thr Thr Ala Ala Ser Leu Arg Pro Arg Pro

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Glu	Val	Asp	Pro	Ser	Glu	Arg	Ser	Arg	Arg	Gln	Ala	Ile	Ser	Leu	Phe		
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cgc	gaa	cgg	cgc	cgc	gta	agg	cgc	caa	tcc	cgc	cca	gtt	gct	gat	ggc	499	
Arg	Glu	Arg	Arg	Arg	Val	Arg	Arg	Gln	Ser	Arg	Pro	Val	Ala	Asp	Gly		
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atg	gtg	gaa	ttg	ccg	ttc	atc	acc	ccc	aaa	ccg	gaa	gat	gag	ctg	ctc	547	
Met	Val	Glu	Leu	Pro	Phe	Ile	Thr	Pro	Lys	Pro	Glu	Asp	Glu	Leu	Leu		
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atc	gac	ccg	gaa	aag	aag	cgc	aaa	cct	ggt	gtg	gca	gcg	ccg	caa	ctt	595	
Ile	Asp	Pro	Glu	Lys	Lys	Arg	Lys	Pro	Gly	Val	Ala	Ala	Pro	Gln	Leu		
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Val	Ala	Gly	Asp	Ile	Val	Ala	Glu	Gln	Tyr	Glu	Val	Leu	Gly	Val	Ile		
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gcg	cac	ggc	ggc	atg	ggt	tgg	att	tac	ctc	gcc	aac	gac	cgc	aat	gtg	691	
Ala	His	Gly	Gly	Met	Gly	Trp	Ile	Tyr	Leu	Ala	Asn	Asp	Arg	Asn	Val		
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tcc	ggc	cgc	atc	gtg	gtg	ctc	aaa	ggc	atg	atg	gcg	caa	tct	tcc	gtt	739	
Ser	Gly	Arg	Ile	Val	Val	Leu	Lys	Gly	Met	Met	Ala	Gln	Ser	Ser	Val		
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caa	gac	caa	ggc	acc	gct	gaa	gcc	gaa	cgc	gaa	ttc	ctc	gcc	gac	atc	787	
Gln	Asp	Gln	Gly	Thr	Ala	Glu	Ala	Glu	Arg	Glu	Phe	Leu	Ala	Asp	Ile		
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Thr	His	Pro	Gly	Ile	Val	Lys	Ala	Tyr	Asn	Phe	Ile	Asp	Asp	Pro	Arg		
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gtc	ccc	ggc	gga	ttc	atc	gtc	atg	gaa	tac	gtc	aac	ggc	ccc	tcc	ctg	883	
Val	Pro	Gly	Gly	Phe	Ile	Val	Met	Glu	Tyr	Val	Asn	Gly	Pro	Ser	Leu		
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aaa	gac	cgc	tgc	aaa	gcc	caa	ccc	gac	ggc	gtg	ctc	cgc	gtc	gac	ctc	931	
Lys	Asp	Arg	Cys	Lys	Ala	Gln	Pro	Asp	Gly	Val	Leu	Arg	Val	Asp	Leu		
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gcc	atc	ggc	tac	atc	ctc	gaa	ctc	ctc	ccc	gcc	atg	gac	tac	ctg	cac	979	
Ala	Ile	Gly	Tyr	Ile	Leu	Glu	Leu	Leu	Pro	Ala	Met	Asp	Tyr	Leu	His		
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Gln	Arg	Gly	Val	Val	Tyr	Asn	Asp	Leu	Lys	Pro	Glu	Asn	Val	Ile	Ala		
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ggc	gca	ttc	ggc	tac	att	tac	ggc	acc	aaa	gga	ttc	caa	gca	ccc	gaa	1123	
Gly	Ala	Phe	Gly	Tyr	Ile	Tyr	Gly	Thr	Lys	Gly	Phe	Gln	Ala	Pro	Glu		
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gta gcc acc cat ggc ccc tca atc tcc tcc gat att ttc acc atc gga 1171
 Val Ala Thr His Gly Pro Ser Ile Ser Ser Asp Ile Phe Thr Ile Gly
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cgc acc ctc gca gca ctc acc atg ccc ctc ccc gtt gaa gac ggt gtc 1219
 Arg Thr Leu Ala Ala Leu Thr Met Pro Leu Pro Val Glu Asp Gly Val
 360 365 370

ctc gca ccg ggc atc ccc tcg ccc aaa aat tca cct ctt ctg cgc agg 1267
 Leu Ala Pro Gly Ile Pro Ser Pro Lys Asn Ser Pro Leu Leu Arg Arg
 375 380 385

cat ttg tcg ttc tac cgc ctc ctg caa cgc gcc acc gcc gac gac ccc 1315
 His Leu Ser Phe Tyr Arg Leu Leu Gln Arg Ala Thr Ala Asp Asp Pro
 390 395 400 405

caa cac cga ttc cgc aac gtc agc gaa cta cgc acc caa ctc tac ggc 1363
 Gln His Arg Phe Arg Asn Val Ser Glu Leu Arg Thr Gln Leu Tyr Gly
 410 415 420

gta ctg cgt gaa att ttg gca gtc cgc gac ggc aaa caa tac ccg cca 1411
 Val Leu Arg Glu Ile Leu Ala Val Arg Asp Gly Lys Gln Tyr Pro Pro
 425 430 435

cag cac tca cta ttc tcc cca cag cga agc acc ttt ggc acc aaa cac 1459
 Gln His Ser Leu Phe Ser Pro Gln Arg Ser Thr Phe Gly Thr Lys His
 440 445 450

ctc gtg ttc cgc acc gac cgc atc atc gac ggc atc gaa cga caa gca 1507
 Leu Val Phe Arg Thr Asp Arg Ile Ile Asp Gly Ile Glu Arg Gln Ala
 455 460 465

cgc atc aca gca cca gaa att gtc tcc gcg ctg cct gtc cca ctc atc 1555
 Arg Ile Thr Ala Pro Glu Ile Val Ser Ala Leu Pro Val Pro Leu Ile
 470 475 480 485

gac cgc acc gac ccc ggc gcc cgt atg ctc tcc gga tcc tcc tat gca 1603
 Asp Arg Thr Asp Pro Gly Ala Arg Met Leu Ser Gly Ser Ser Tyr Ala
 490 495 500

gaa ccc tcc gaa acc ctg gaa act ctg cgc aac tcc atg gaa gac gag 1651
 Glu Pro Ser Glu Thr Leu Glu Thr Leu Arg Asn Ser Met Glu Asp Glu
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<212> PRT

<213> Corynebacterium glutamicum

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Thr Ser Ala Val Ala Phe Asn Pro Phe Glu Asp Asp Asp Asp Asp Asp
 35 40 45
 Glu Phe Gln Gly Glu Gly Leu Glu Phe Leu Leu Arg Asp Leu Asp Asn
 50 55 60
 Leu Arg Ala Thr Gln Gly Gln Met Val Val Glu Gln Pro Ala Val Glu
 65 70 75 80
 Asp Ser Leu Gly Ser Ala Ser Ala His Thr Glu Thr Thr Ala Ala Ser
 85 90 95
 Leu Arg Pro Arg Pro Glu Val Asp Pro Ser Glu Arg Ser Arg Arg Gln
 100 105 110
 Ala Ile Ser Leu Phe Arg Glu Arg Arg Arg Val Arg Arg Gln Ser Arg
 115 120 125
 Pro Val Ala Asp Gly Met Val Glu Leu Pro Phe Ile Thr Pro Lys Pro
 130 135 140
 Glu Asp Glu Leu Leu Ile Asp Pro Glu Lys Lys Arg Lys Pro Gly Val
 145 150 155 160
 Ala Ala Pro Gln Leu Val Ala Gly Asp Ile Val Ala Glu Gln Tyr Glu
 165 170 175
 Val Leu Gly Val Ile Ala His Gly Gly Met Gly Trp Ile Tyr Leu Ala
 180 185 190
 Asn Asp Arg Asn Val Ser Gly Arg Ile Val Val Leu Lys Gly Met Met
 195 200 205
 Ala Gln Ser Ser Val Gln Asp Gln Gly Thr Ala Glu Ala Glu Arg Glu
 210 215 220
 Phe Leu Ala Asp Ile Thr His Pro Gly Ile Val Lys Ala Tyr Asn Phe
 225 230 235 240
 Ile Asp Asp Pro Arg Val Pro Gly Gly Phe Ile Val Met Glu Tyr Val
 245 250 255
 Asn Gly Pro Ser Leu Lys Asp Arg Cys Lys Ala Gln Pro Asp Gly Val
 260 265 270
 Leu Arg Val Asp Leu Ala Ile Gly Tyr Ile Leu Glu Leu Leu Pro Ala
 275 280 285
 Met Asp Tyr Leu His Gln Arg Gly Val Val Tyr Asn Asp Leu Lys Pro
 290 295 300
 Glu Asn Val Ile Ala Thr Glu Asp Gln Val Lys Leu Ile Asp Leu Gly
 305 310 315 320
 Ala Val Thr Gly Ile Gly Ala Phe Gly Tyr Ile Tyr Gly Thr Lys Gly
 325 330 335
 Phe Gln Ala Pro Glu Val Ala Thr His Gly Pro Ser Ile Ser Ser Asp
 340 345 350

Ile Phe Thr Ile Gly Arg Thr Leu Ala Ala Leu Thr Met Pro Leu Pro
 355 360 365
 Val Glu Asp Gly Val Leu Ala Pro Gly Ile Pro Ser Pro Lys Asn Ser
 370 375 380
 Pro Leu Leu Arg Arg His Leu Ser Phe Tyr Arg Leu Leu Gln Arg Ala
 385 390 395 400
 Thr Ala Asp Asp Pro Gln His Arg Phe Arg Asn Val Ser Glu Leu Arg
 405 410 415
 Thr Gln Leu Tyr Gly Val Leu Arg Glu Ile Leu Ala Val Arg Asp Gly
 420 425 430
 Lys Gln Tyr Pro Pro Gln His Ser Leu Phe Ser Pro Gln Arg Ser Thr
 435 440 445
 Phe Gly Thr Lys His Leu Val Phe Arg Thr Asp Arg Ile Ile Asp Gly
 450 455 460
 Ile Glu Arg Gln Ala Arg Ile Thr Ala Pro Glu Ile Val Ser Ala Leu
 465 470 475 480
 Pro Val Pro Leu Ile Asp Arg Thr Asp Pro Gly Ala Arg Met Leu Ser
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 <223> RXA00857

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 Gly Asp Val Leu Asn Ala Arg Ala Thr Val Glu Asn Lys Asp Ser Met
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 Leu Ile Gly Leu Gly Lys Asp Ile Glu Gly Asp Phe Val Ser Tyr Ser
 35 40 45
 gtg cag aaa atg cct cac ctt ctt gtg gct ggt tcc acc ggt tct ggt 192
 Val Gln Lys Met Pro His Leu Leu Val Ala Gly Ser Thr Gly Ser Gly
 50 55 60

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Lys	Pro	Glu	Glu	Val	Arg	Leu	Ile	Leu	Val	Asp	Pro	Lys	Met	Val	Glu	
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ctc	aca	cca	tac	gag	ggc	att	cca	cac	ctg	att	acg	ccg	atc	att	acc	336
Leu	Thr	Pro	Tyr	Glu	Gly	Ile	Pro	His	Leu	Ile	Thr	Pro	Ile	Ile	Thr	
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Gln	Pro	Lys	Lys	Ala	Ala	Ala	Ala	Leu	Gln	Trp	Leu	Val	Glu	Glu	Met	
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gaa	cag	cg	tac	atg	gac	atg	aaa	caa	acc	cgt	gtg	cg	cac	atc	aag	432
Glu	Gln	Arg	Tyr	Met	Asp	Met	Lys	Gln	Thr	Arg	Val	Arg	His	Ile	Lys	
	130					135					140					
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Asp	Phe	Asn	Arg	Lys	Ile	Lys	Ser	Gly	Glu	Ile	Glu	Thr	Pro	Pro	Gly	
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Ser	Lys	Arg	Glu	Tyr	Arg	Ala	Tyr	Pro	Tyr	Ile	Val	Cys	Val	Val	Asp	
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gag	ctc	gct	gac	ctg	atg	atg	acc	gca	ccg	aag	gaa	atc	gaa	gag	tcc	576
Glu	Leu	Ala	Asp	Leu	Met	Met	Thr	Ala	Pro	Lys	Glu	Ile	Glu	Glu	Ser	
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Ile	Val	Arg	Ile	Thr	Gln	Lys	Ala	Arg	Ala	Ala	Gly	Ile	His	Leu	Val	
		195					200					205				
ctg	gca	acg	cag	cg	cca	tcc	gtg	gac	gtt	gtg	acc	ggt	ctg	atc	aag	672
Leu	Ala	Thr	Gln	Arg	Pro	Ser	Val	Asp	Val	Val	Thr	Gly	Leu	Ile	Lys	
	210					215					220					
acc	aac	gtt	cct	tca	cgt	ttg	gct	ttc	gca	acc	tca	tcg	cta	act	gac	720
Thr	Asn	Val	Pro	Ser	Arg	Leu	Ala	Phe	Ala	Thr	Ser	Ser	Leu	Thr	Asp	
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tcc	cg	gtt	att	ttg	gac	cag	ggt	ggc	gct	gaa	aag	ctg	atc	ggc	atg	768
Ser	Arg	Val	Ile	Leu	Asp	Gln	Gly	Gly	Ala	Glu	Lys	Leu	Ile	Gly	Met	
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Gly	Asp	Ala	Leu	Phe	Ile	Pro	Gln	Gly	Ala	Gly	Lys	Pro	Gln	Arg	Ile	
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cag	ggt	gcc	ttt	gtc	acc	gat	gaa	gaa	atc	caa	gcg	gtc	gtg	gac	atg	864
Gln	Gly	Ala	Phe	Val	Thr	Asp	Glu	Glu	Ile	Gln	Ala	Val	Val	Asp	Met	
		275					280					285				
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Ala	Lys	Ala	Gln	Arg	Gln	Pro	Glu	Tyr	Thr	Asp	Gly	Val	Thr	Glu	Asp	
	290					295					300					
aag	gct	tcc	gaa	gct	aag	aag	atc	gat	gcc	gat	atc	gga	aac	gat	ctg	960

Lys Ala Ser Glu Ala Lys Lys Ile Asp Ala Asp Ile Gly Asn Asp Leu
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 Glu Asp Leu Leu Glu Ala Val Glu Leu Val Val Thr Ser Gln Met Gly
 325 330 335
 tcc acc tcc atg ctg cag cgc aaa ctg cgc atc ggt ttt gcc aag gcc 1056
 Ser Thr Ser Met Leu Gln Arg Lys Leu Arg Ile Gly Phe Ala Lys Ala
 340 345 350
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 Gly Arg Leu Met Asp Leu Met Glu Thr Arg Gly Val Val Gly Pro Ser
 355 360 365
 gaa ggc tct aag gct cgt gaa gtt ttg gtc aag cca gaa gag ctg gaa 1152
 Glu Gly Ser Lys Ala Arg Glu Val Leu Val Lys Pro Glu Glu Leu Glu
 370 375 380
 acc att ttg tgg atg ctt aaa ggt gca gac ccc gcc gac gca ccg aag 1200
 Thr Ile Leu Trp Met Leu Lys Gly Ala Asp Pro Ala Asp Ala Pro Lys
 385 390 395 400
 gaa gag acc tgg gat gac gag gtg gca gcg gaa gct gaa gaa gcg gct 1248
 Glu Glu Thr Trp Asp Asp Glu Val Ala Ala Glu Ala Glu Glu Ala Ala
 405 410 415
 aac acc acc gtc gtg cag gct gat cct tcc aag gga gtg tgt 1290
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<211> 430

<212> PRT

<213> Corynebacterium glutamicum

<400> 94

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 35 40 45
 Val Gln Lys Met Pro His Leu Leu Val Ala Gly Ser Thr Gly Ser Gly
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 Lys Ser Ala Phe Val Asn Ser Leu Leu Val Ser Leu Leu Thr Arg Ala
 65 70 75 80
 Lys Pro Glu Glu Val Arg Leu Ile Leu Val Asp Pro Lys Met Val Glu
 85 90 95
 Leu Thr Pro Tyr Glu Gly Ile Pro His Leu Ile Thr Pro Ile Ile Thr
 100 105 110

Gln Pro Lys Lys Ala Ala Ala Ala Leu Gln Trp Leu Val Glu Glu Met
 115 120 125
 Glu Gln Arg Tyr Met Asp Met Lys Gln Thr Arg Val Arg His Ile Lys
 130 135 140
 Asp Phe Asn Arg Lys Ile Lys Ser Gly Glu Ile Glu Thr Pro Pro Gly
 145 150 155 160
 Ser Lys Arg Glu Tyr Arg Ala Tyr Pro Tyr Ile Val Cys Val Val Asp
 165 170 175
 Glu Leu Ala Asp Leu Met Met Thr Ala Pro Lys Glu Ile Glu Glu Ser
 180 185 190
 Ile Val Arg Ile Thr Gln Lys Ala Arg Ala Ala Gly Ile His Leu Val
 195 200 205
 Leu Ala Thr Gln Arg Pro Ser Val Asp Val Val Thr Gly Leu Ile Lys
 210 215 220
 Thr Asn Val Pro Ser Arg Leu Ala Phe Ala Thr Ser Ser Leu Thr Asp
 225 230 235 240
 Ser Arg Val Ile Leu Asp Gln Gly Gly Ala Glu Lys Leu Ile Gly Met
 245 250 255
 Gly Asp Ala Leu Phe Ile Pro Gln Gly Ala Gly Lys Pro Gln Arg Ile
 260 265 270
 Gln Gly Ala Phe Val Thr Asp Glu Glu Ile Gln Ala Val Val Asp Met
 275 280 285
 Ala Lys Ala Gln Arg Gln Pro Glu Tyr Thr Asp Gly Val Thr Glu Asp
 290 295 300
 Lys Ala Ser Glu Ala Lys Lys Ile Asp Ala Asp Ile Gly Asn Asp Leu
 305 310 315 320
 Glu Asp Leu Leu Glu Ala Val Glu Leu Val Val Thr Ser Gln Met Gly
 325 330 335
 Ser Thr Ser Met Leu Gln Arg Lys Leu Arg Ile Gly Phe Ala Lys Ala
 340 345 350
 Gly Arg Leu Met Asp Leu Met Glu Thr Arg Gly Val Val Gly Pro Ser
 355 360 365
 Glu Gly Ser Lys Ala Arg Glu Val Leu Val Lys Pro Glu Glu Leu Glu
 370 375 380
 Thr Ile Leu Trp Met Leu Lys Gly Ala Asp Pro Ala Asp Ala Pro Lys
 385 390 395 400
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 <212> DNA
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 <222> (1)..(870)
 <223> RXA01435

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 cta gag gga cgc atc ggc gac gac tgg cga cac aaa tgg ttc tcc gga 96
 Leu Glu Gly Arg Ile Gly Asp Asp Trp Arg His Lys Trp Phe Ser Gly
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 atc acc tac ctc ctc ctc gac gac tac gcc acc gcc caa gta ttc ttc 144
 Ile Thr Tyr Leu Leu Leu Asp Asp Tyr Ala Thr Ala Gln Val Phe Phe
 35 40 45
 aac cac gtc ctg acc atc ctg ccc ggc gaa gcc gct cct aaa cta gcc 192
 Asn His Val Leu Thr Ile Leu Pro Gly Glu Ala Ala Pro Lys Leu Ala
 50 55 60
 ctc gca gct gtt gac gaa ctc atc ctc caa caa atc ggc gcc gaa tcc 240
 Leu Ala Ala Val Asp Glu Leu Ile Leu Gln Gln Ile Gly Ala Glu Ser
 65 70 75 80
 acc gcc tat ctc acc cca gac atc gtc tct gca acc gcg acc ctc agc 288
 Thr Ala Tyr Leu Thr Pro Asp Ile Val Ser Ala Thr Ala Thr Leu Ser
 85 90 95
 aaa gat ttc gaa gac ctc gac gcc tcc gcc ttc gaa tca ctc agc gac 336
 Lys Asp Phe Glu Asp Leu Asp Ala Ser Ala Phe Glu Ser Leu Ser Asp
 100 105 110
 acc tgg tcc cac atc tcc agc gac cca cac gta gtc cgc ttc cat tca 384
 Thr Trp Ser His Ile Ser Ser Asp Pro His Val Val Arg Phe His Ser
 115 120 125
 ctg cgc ctc tac gca ctt gtc tgg gca acc aac ccc acc acc gtg tcc 432
 Leu Arg Leu Tyr Ala Leu Val Trp Ala Thr Asn Pro Thr Thr Val Ser
 130 135 140
 tcc gcg ttc ggg ctc gcc cgc caa ctc atg gcc gaa aac caa atc gaa 480
 Ser Ala Phe Gly Leu Ala Arg Gln Leu Met Ala Glu Asn Gln Ile Glu
 145 150 155 160
 ctc gca gtc caa gcc cta gac aaa ctc ccc caa tca tcc acc cac tac 528
 Leu Ala Val Gln Ala Leu Asp Lys Leu Pro Gln Ser Ser Thr His Tyr
 165 170 175
 cga atg gcc acc ctc acc acc atc ttg ttg ctg gtc agc tcc aat ttg 576
 Arg Met Ala Thr Leu Thr Thr Ile Leu Leu Leu Val Ser Ser Asn Leu
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 agt gaa tcc cgc atc cga cgg gct gcc cgc cga ctc acc gaa atc ccc 624
 Ser Glu Ser Arg Ile Arg Arg Ala Ala Arg Arg Leu Thr Glu Ile Pro

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Thr Asn Glu Pro Arg Phe Asn Gln Ile Lys Ile Ala Ile Met Ser Ala			
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ggc ctc agc tgg ctt cga gag cga aaa ctc aaa gct tcc gcc tcc gcg			720
Gly Leu Ser Trp Leu Arg Glu Arg Lys Leu Lys Ala Ser Ala Ser Ala			
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aac cct ttg ttt gaa tac ccg ttc tcc caa aaa ggc ctg cgc acc ggc			768
Asn Pro Leu Phe Glu Tyr Pro Phe Ser Gln Lys Gly Leu Arg Thr Gly			
245	250	255	
atc tcc gag gca ctc cgc att cag gca cgt tct gca ccg ttc ccg cac			816
Ile Ser Glu Ala Leu Arg Ile Gln Ala Arg Ser Ala Pro Phe Pro His			
260	265	270	
cac cgt tac gca ctt gtg gat atg gcg aat gcc gtg cgg cca ctg agt			864
His Arg Tyr Ala Leu Val Asp Met Ala Asn Ala Val Arg Pro Leu Ser			
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Trp Phe			
290			

<210> 96

<211> 290

<212> PRT

<213> Corynebacterium glutamicum

<400> 96

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Leu	Glu	Gly	Arg	Ile	Gly	Asp	Asp	Trp	Arg	His	Lys	Trp	Phe	Ser	Gly
			20					25					30		

Ile	Thr	Tyr	Leu	Leu	Leu	Asp	Asp	Tyr	Ala	Thr	Ala	Gln	Val	Phe	Phe
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Asn	His	Val	Leu	Thr	Ile	Leu	Pro	Gly	Glu	Ala	Ala	Pro	Lys	Leu	Ala
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Leu	Ala	Ala	Val	Asp	Glu	Leu	Ile	Leu	Gln	Gln	Ile	Gly	Ala	Glu	Ser
65					70					75				80	

Thr	Ala	Tyr	Leu	Thr	Pro	Asp	Ile	Val	Ser	Ala	Thr	Ala	Thr	Leu	Ser
			85						90					95	

Lys	Asp	Phe	Glu	Asp	Leu	Asp	Ala	Ser	Ala	Phe	Glu	Ser	Leu	Ser	Asp
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Thr	Trp	Ser	His	Ile	Ser	Ser	Asp	Pro	His	Val	Val	Arg	Phe	His	Ser
		115					120					125			

Leu	Arg	Leu	Tyr	Ala	Leu	Val	Trp	Ala	Thr	Asn	Pro	Thr	Thr	Val	Ser
130						135					140				

Ser	Ala	Phe	Gly	Leu	Ala	Arg	Gln	Leu	Met	Ala	Glu	Asn	Gln	Ile	Glu
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<212> DNA
<213> Corynebacterium glutamicum
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											gtg	gca	tcc	ctc	atc	
											Val	Ala	Ser	Leu	Ile	
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ggg aat ctt gag ctg cct agg gta agc cct aat ttc ttg gaa tta cgc																163
Gly	Asn	Leu	Glu	Leu	Pro	Arg	Val	Ser	Pro	Asn	Phe	Leu	Glu	Leu	Arg	
				10					15					20		
aag gcg gtg cgc cct tac ctg aaa gag cat gtg cac att ggg ttg tcg																211
Lys	Ala	Val	Arg	Pro	Tyr	Leu	Lys	Glu	His	Val	His	Ile	gly	Leu	Ser	
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Gly	Gly	Pro	Asp	Ser	Leu	Ala	Leu	Val	Ala	Ala	Val	Leu	Ala	Glu	Lys	
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tcc cag gta acg gcg att tgt atc gat cat aat ctg cag acc ggt tct																307
Ser	Gln	Val	Thr	Ala	Ile	Cys	Ile	Asp	His	Asn	Leu	Gln	Thr	Gly	Ser	

55	60	65	
gct gaa gtc acg cac aac gct gct gcg atg gcg cgc cac atg ggc gca Ala Glu Val Thr His Asn Ala Ala Ala Met Ala Arg His Met Gly Ala 70 75 80 85			355
cag gcg atc gtg aag agc atc gag gtc gcg ccg ggg gag ggg atg gag Gln Ala Ile Val Lys Ser Ile Glu Val Ala Pro Gly Glu Gly Met Glu 90 95 100			403
gcc gcc gcc agg gag gct cgg tac gcg gct ttt gcg cag ctc acc gat Ala Ala Ala Arg Glu Ala Arg Tyr Ala Ala Phe Ala Gln Leu Thr Asp 105 110 115			451
gag att tgg gtg gcg cac acc atg gat gat caa gcc gag acc tat ctc Glu Ile Trp Val Ala His Thr Met Asp Asp Gln Ala Glu Thr Tyr Leu 120 125 130			499
ctt ggc ggt ttg cgg ggg aat ccc gcg ggc atg aaa gat gct tct cga Leu Gly Gly Leu Arg Gly Asn Pro Ala Gly Met Lys Asp Ala Ser Arg 135 140 145			547
cgc ccc gag cta tcc att att cga ccc ctt ctg ggg gct cgg cgt gcg Arg Pro Glu Leu Ser Ile Ile Arg Pro Leu Leu Gly Ala Arg Arg Ala 150 155 160 165			595
cac acg cac ggg gcg tgc gtg gag ttg ggg ttg aaa ccg tgg cac gat His Thr His Gly Ala Cys Val Glu Leu Gly Leu Lys Pro Trp His Asp 170 175 180			643
ccg caa aat ttt gac gat gcc ttt cgg cgg gta gcc atc cga aac cag Pro Gln Asn Phe Asp Asp Ala Phe Arg Arg Val Ala Ile Arg Asn Gln 185 190 195			691
gtg att cct ctt ctt gcg cag gtg cac ggg gga gac cct gta cct ggt Val Ile Pro Leu Leu Ala Gln Val His Gly Gly Asp Pro Val Pro Gly 200 205 210			739
ttg gca ctt gcg gcg cga cgc gct gtg gag gat gcc gaa gtg gtg gag Leu Ala Leu Ala Ala Arg Arg Ala Val Glu Asp Ala Glu Val Val Glu 215 220 225			787
ggc gac gtc gag aag cgg cgt tta gag tgg cag gac ggt ttt cct gtg Gly Asp Val Glu Lys Arg Arg Leu Glu Trp Gln Asp Gly Phe Pro Val 230 235 240 245			835
acg ttg gcc ggg gaa cct acg ggc ctt agg cga cgc atg ttg gcg gat Thr Leu Ala Gly Glu Pro Thr Gly Leu Arg Arg Arg Met Leu Ala Asp 250 255 260			883
ttt ttg cgt ggg gaa ggc atc gct gtg acc tcg agg aaa ctc gac gcc Phe Leu Arg Gly Glu Gly Ile Ala Val Thr Ser Arg Lys Leu Asp Ala 265 270 275			931
att gac cga ttg ctc acc gat tgg cgc gga cag ggt ggc gta gcc gtg Ile Asp Arg Leu Leu Thr Asp Trp Arg Gly Gln Gly Gly Val Ala Val 280 285 290			979
ggt aaa agc gat aat gga agg ttg gaa gtg gtg cgg caa agt ggc aag Gly Lys Ser Asp Asn Gly Arg Leu Glu Val Val Arg Gln Ser Gly Lys 295 300 305			1027

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 Leu Lys Ile Thr Asp
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1065

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 <213> *Corynebacterium glutamicum*

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 His Ile Gly Leu Ser Gly Gly Pro Asp Ser Leu Ala Leu Val Ala Ala
 35 40 45
 Val Leu Ala Glu Lys Ser Gln Val Thr Ala Ile Cys Ile Asp His Asn
 50 55 60
 Leu Gln Thr Gly Ser Ala Glu Val Thr His Asn Ala Ala Ala Met Ala
 65 70 75 80
 Arg His Met Gly Ala Gln Ala Ile Val Lys Ser Ile Glu Val Ala Pro
 85 90 95
 Gly Glu Gly Met Glu Ala Ala Ala Arg Glu Ala Arg Tyr Ala Ala Phe
 100 105 110
 Ala Gln Leu Thr Asp Glu Ile Trp Val Ala His Thr Met Asp Asp Gln
 115 120 125
 Ala Glu Thr Tyr Leu Leu Gly Gly Leu Arg Gly Asn Pro Ala Gly Met
 130 135 140
 Lys Asp Ala Ser Arg Arg Pro Glu Leu Ser Ile Ile Arg Pro Leu Leu
 145 150 155 160
 Gly Ala Arg Arg Ala His Thr His Gly Ala Cys Val Glu Leu Gly Leu
 165 170 175
 Lys Pro Trp His Asp Pro Gln Asn Phe Asp Asp Ala Phe Arg Arg Val
 180 185 190
 Ala Ile Arg Asn Gln Val Ile Pro Leu Leu Ala Gln Val His Gly Gly
 195 200 205
 Asp Pro Val Pro Gly Leu Ala Leu Ala Ala Arg Arg Ala Val Glu Asp
 210 215 220
 Ala Glu Val Val Glu Gly Asp Val Glu Lys Arg Arg Leu Glu Trp Gln
 225 230 235 240
 Asp Gly Phe Pro Val Thr Leu Ala Gly Glu Pro Thr Gly Leu Arg Arg
 245 250 255
 Arg Met Leu Ala Asp Phe Leu Arg Gly Glu Gly Ile Ala Val Thr Ser

	260		265		270
Arg Lys Leu Asp Ala Ile Asp Arg Leu Leu Thr Asp Trp Arg Gly Gln					
275		280		285	
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 <212> DNA
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 <223> RXA01513

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 Met Lys Asn Lys Lys
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tac ctg cag ttc ggc ggt atc gca gcc gta atc ctc atc gtt ctg ttc 163
 Tyr Leu Gln Phe Gly Gly Ile Ala Ala Val Ile Leu Ile Val Leu Phe
 10 15 20

ttg gtg tcc ctg ttt agc agt gac acc agg aac ttc cag gag gtc gat 211
 Leu Val Ser Leu Phe Ser Ser Asp Thr Arg Asn Phe Gln Glu Val Asp
 25 30 35

acc tct gtt gcg atg gca cag ctt gac gcc gga aac gtc gcc gaa gct 259
 Thr Ser Val Ala Met Ala Gln Leu Asp Ala Gly Asn Val Ala Glu Ala
 40 45 50

caa atc gat gac agg gaa cag cgc gtc cga ctg acc ttg cgt gaa ccc 307
 Gln Ile Asp Asp Arg Glu Gln Arg Val Arg Leu Thr Leu Arg Glu Pro
 55 60 65

atc acg gtg gat gaa cgc gaa ggc gtt gaa gag atc ctc gcg cag tac 355
 Ile Thr Val Asp Glu Arg Glu Gly Val Glu Glu Ile Leu Ala Gln Tyr
 70 75 80 85

cca gct cgt acc gcg cca gcg atc ttt gag aag gtg gaa gca tcc aac 403
 Pro Ala Arg Thr Ala Pro Ala Ile Phe Glu Lys Val Glu Ala Ser Asn
 90 95 100

act gat tcc tat acc acc aat gtg acg cag gag agc ttc ctg atg tcc 451
 Thr Asp Ser Tyr Thr Thr Asn Val Thr Gln Glu Ser Phe Leu Met Ser
 105 110 115

atg ctg agc ttc atc ctg ccg atg gtg atc atc ttc ggt ttg ctg atg 499
 Met Leu Ser Phe Ile Leu Pro Met Val Ile Ile Phe Gly Leu Leu Met
 120 125 130

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Phe Phe Leu Thr Arg Met Gln Gly Gly Gly Met Phe Gly Ile Gly Gly	
135 140 145	
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Ser Lys Ala Lys Gln Leu Thr Lys Asp Met Pro Thr Asn Thr Phe Ala	
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Asp Val Ala Gly Ala Glu Glu Ala Val Asp Glu Leu His Glu Ile Lys	
170 175 180	
gac ttc ctg gaa gac ccc acc cgc tac gaa gcc ctc gga gcg aaa atc	691
Asp Phe Leu Glu Asp Pro Thr Arg Tyr Glu Ala Leu Gly Ala Lys Ile	
185 190 195	
cct cgt ggt gtg ctg ctt tac ggc cct ccc ggt act ggt aaa acc ctg	739
Pro Arg Gly Val Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys Thr Leu	
200 205 210	
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Leu Ala Arg Ala Val Ala Gly Glu Ala Gly Val Pro Phe Tyr Ser Ile	
215 220 225	
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Ser Gly Ser Asp Phe Val Glu Met Phe Val Gly Val Gly Ala Ser Arg	
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Val Arg Asp Leu Phe Lys Gln Ala Lys Glu Asn Ser Pro Cys Ile Ile	
250 255 260	
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Phe Val Asp Glu Ile Asp Ala Val Gly Arg Ala Arg Gly Ser Gly Met	
265 270 275	
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Gly Gly Gln His Asp Glu Arg Glu Gln Thr Leu Asn Gln Leu Leu Val	
280 285 290	
gag atg gat ggc ttt ggt gat cgt caa ggc gtc att ctg atg gct gct	1027
Glu Met Asp Gly Phe Gly Asp Arg Gln Gly Val Ile Leu Met Ala Ala	
295 300 305	
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Thr Asn Arg Pro Asp Val Leu Asp Pro Ala Leu Leu Arg Pro Gly Arg	
310 315 320 325	
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Phe Asp Arg Gln Ile Pro Val Thr Asn Pro Asp Leu Arg Gly Arg Glu	
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Gln Ile Leu Glu Val His Ala Lys Gly Lys Pro Phe Ala Pro Asp Ala	
345 350 355	
gat atc aag gca ttg gca aag cgc acc gcc ggc atg tcc ggc gct gac	1219
Asp Ile Lys Ala Leu Ala Lys Arg Thr Ala Gly Met Ser Gly Ala Asp	
360 365 370	
ctg gca aac gtg ctt aac gaa gcc gcg ctg cta acc gcc cgc gtg ggt	1267

Leu	Ala	Asn	Val	Leu	Asn	Glu	Ala	Ala	Leu	Leu	Thr	Ala	Arg	Val	Gly		
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Gly	Asn	Val	Ile	Thr	Ala	Asp	Ala	Leu	Glu	Glu	Ala	Thr	Asp	Arg	Val		
390					395				400					405			
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Val	Gly	Gly	Pro	Arg	Arg	Ser	Gly	Lys	Val	Ile	Ser	Glu	Lys	Glu	Lys		
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Lys	Val	Thr	Ala	Tyr	His	Glu	Gly	Gly	His	Thr	Leu	Ser	Ala	Trp	Ala		
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Leu	Glu	Asp	Ile	Glu	Arg	Val	Tyr	Lys	Val	Thr	Ile	Leu	Ala	Arg	Gly		
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cgc	acc	ggc	ggc	cac	gcc	atg	act	gcc	caa	gaa	gat	gac	aag	ggc	atg	1507	
Arg	Thr	Gly	Gly	His	Ala	Met	Thr	Ala	Gln	Glu	Asp	Asp	Lys	Gly	Met		
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Tyr	Asn	Arg	Asn	Glu	Leu	Phe	Ala	Arg	Leu	Val	Phe	Ala	Met	Gly	Gly		
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cgc	tcc	gcg	gaa	gaa	cta	gtc	ttc	ggc	gaa	ccc	acc	acc	ggc	gcc	tcc	1603	
Arg	Ser	Ala	Glu	Glu	Leu	Val	Phe	Gly	Glu	Pro	Thr	Thr	Gly	Ala	Ser		
				490					495					500			
gcc	gat	att	gaa	atg	gcc	acc	aag	atc	gcc	cga	tcc	atg	gtg	acc	gaa	1651	
Ala	Asp	Ile	Glu	Met	Ala	Thr	Lys	Ile	Ala	Arg	Ser	Met	Val	Thr	Glu		
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tat	ggc	atg	tcc	cca	gct	gtc	ggc	atg	gtg	aaa	tac	ggc	caa	gaa	cag	1699	
Tyr	Gly	Met	Ser	Pro	Ala	Val	Gly	Met	Val	Lys	Tyr	Gly	Gln	Glu	Gln		
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ggc	gac	cca	ttc	tcc	gga	cgc	ggc	ggc	gga	aac	ttg	gac	cac	tcc		1747	
Gly	Asp	Pro	Phe	Ser	Gly	Arg	Gly	Gly	Gly	Asn	Leu	Asp	His	Ser			
	535					540				545							
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Gln	Glu	Val	Ala	Ala	Thr	Ile	Asp	Thr	Glu	Val	Gln	Phe	Leu	Leu	Asp		
	550				555					560				565			
aaa	gcc	cat	gaa	gtg	tcc	tac	tcc	atc	ctg	gct	gaa	tac	cgc	gac	cac	1843	
Lys	Ala	His	Glu	Val	Ser	Tyr	Ser	Ile	Leu	Ala	Glu	Tyr	Arg	Asp	His		
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ctg	gac	cgc	ctc	gcg	gaa	aaa	ctc	ctg	gaa	aag	gaa	acc	ctg	cga	cgc	1891	
Leu	Asp	Arg	Leu	Ala	Glu	Lys	Leu	Leu	Glu	Lys	Glu	Thr	Leu	Arg	Arg		
			585				590						595				
cca	gac	ctc	gaa	gcg	ctt	ttc	gac	gac	atc	gtc	cca	cgc	aag	gtc	gcc	1939	
Pro	Asp	Leu	Glu	Ala	Leu	Phe	Asp	Asp	Ile	Val	Pro	Arg	Lys	Val	Ala		
		600					605					610					
gaa	gtc	ttc	ccc	gac	gag	tcc	aca	cga	ttc	cct	cgc	caa	gaa	aac	cgc	1987	
Glu	Val	Phe	Pro	Asp	Glu	Ser	Thr	Arg	Phe	Pro	Arg	Gln	Glu	Asn	Arg		

615	620	625	
gaa cca gta aaa acc cca gtg gag ctc gca ctg gaa cgt ggc gaa gaa Glu Pro Val Lys Thr Pro Val Glu Leu Ala Leu Glu Arg Gly Glu Glu 630 635 640 645			2035
cca cca aag aag ttc tcc att ctt gag gcc tcc cgc gca acc cgc gaa Pro Pro Lys Lys Phe Ser Ile Leu Glu Ala Ser Arg Ala Thr Arg Glu 650 655 660			2083
cgc cgt cgc aag gaa ttg gaa gct cag ggt aag ttg ccg gtg cag cct Arg Arg Arg Lys Glu Leu Glu Ala Gln Gly Lys Leu Pro Val Gln Pro 665 670 675			2131
gcg tct tct gcc ggc gtg gca cct gcg gcc gga gca gct gcc gga tcc Ala Ser Ser Ala Gly Val Ala Pro Ala Ala Gly Ala Ala Gly Ser 680 685 690			2179
tat ggc acc cca cct cca gct gat tgg agc gtg ccc ggt tcc gct gga Tyr Gly Thr Pro Pro Pro Ala Asp Trp Ser Val Pro Gly Ser Ala Gly 695 700 705			2227
aag cac cgc tca cgt gca gaa gaa cag cca gct gag cag ggc ttc ccg Lys His Arg Ser Arg Ala Glu Glu Gln Pro Ala Glu Gln Gly Phe Pro 710 715 720 725			2275
gct cag acc ccg gca caa gct cct gag cag tcc cct gat tca agt ggc Ala Gln Thr Pro Ala Gln Ala Pro Glu Gln Ser Pro Asp Ser Ser Gly 730 735 740			2323
ggc cgc ccc aac cct tac gcg act cca acc gca tcc ggt gag cac cct Gly Arg Pro Asn Pro Tyr Ala Thr Pro Thr Ala Ser Gly Glu His Pro 745 750 755			2371
ggt atg aag gcc tat ggc ttc ggc gat tcc gaa ctc atg gac caa tca Gly Met Lys Ala Tyr Gly Phe Gly Asp Ser Glu Leu Met Asp Gln Ser 760 765 770			2419
aca ggt gcg gaa cat acc cca ggt aac gtt tca cag gaa tcc cca acc Thr Gly Ala Glu His Thr Pro Gly Asn Val Ser Gln Glu Ser Pro Thr 775 780 785			2467
gaa atg atc ggg ttc cgt ttg ccg gat cat gaa cgt tcg gac tac cca Glu Met Ile Gly Phe Arg Leu Pro Asp His Glu Arg Ser Asp Tyr Pro 790 795 800 805			2515
gaa aag gcg caa aaa gag tcg gtg ctg gat gct tct gaa acc aca gaa Glu Lys Ala Gln Lys Glu Ser Val Leu Asp Ala Ser Glu Thr Thr Glu 810 815 820			2563
atg cct gtc gtt cca gat cag ccc atc gat ggt gat tcc ggg aag tcc Met Pro Val Val Pro Asp Gln Pro Ile Asp Gly Asp Ser Gly Lys Ser 825 830 835			2611
gct gag ggc aca cag gag aat ccg gaa aat gaa gga gac aac cgt gga Ala Glu Gly Thr Gln Glu Asn Pro Glu Asn Glu Gly Asp Asn Arg Gly 840 845 850			2659
taaccacgct gcagttcgcg agt			2682

<210> 100

<211> 853

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 100

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Met Lys Asn Lys Lys Tyr Leu Gln Phe Gly Gly Ile Ala Ala Val Ile
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Leu Ile Val Leu Phe Leu Val Ser Leu Phe Ser Ser Asp Thr Arg Asn
      20              25              30

Phe Gln Glu Val Asp Thr Ser Val Ala Met Ala Gln Leu Asp Ala Gly
      35              40              45

Asn Val Ala Glu Ala Gln Ile Asp Asp Arg Glu Gln Arg Val Arg Leu
 50              55              60

Thr Leu Arg Glu Pro Ile Thr Val Asp Glu Arg Glu Gly Val Glu Glu
 65              70              75              80

Ile Leu Ala Gln Tyr Pro Ala Arg Thr Ala Pro Ala Ile Phe Glu Lys
      85              90              95

Val Glu Ala Ser Asn Thr Asp Ser Tyr Thr Thr Asn Val Thr Gln Glu
      100              105              110

Ser Phe Leu Met Ser Met Leu Ser Phe Ile Leu Pro Met Val Ile Ile
      115              120              125

Phe Gly Leu Leu Met Phe Phe Leu Thr Arg Met Gln Gly Gly Gly Met
      130              135              140

Phe Gly Ile Gly Gly Ser Lys Ala Lys Gln Leu Thr Lys Asp Met Pro
      145              150              155              160

Thr Asn Thr Phe Ala Asp Val Ala Gly Ala Glu Glu Ala Val Asp Glu
      165              170              175

Leu His Glu Ile Lys Asp Phe Leu Glu Asp Pro Thr Arg Tyr Glu Ala
      180              185              190

Leu Gly Ala Lys Ile Pro Arg Gly Val Leu Leu Tyr Gly Pro Pro Gly
      195              200              205

Thr Gly Lys Thr Leu Leu Ala Arg Ala Val Ala Gly Glu Ala Gly Val
      210              215              220

Pro Phe Tyr Ser Ile Ser Gly Ser Asp Phe Val Glu Met Phe Val Gly
      225              230              235              240

Val Gly Ala Ser Arg Val Arg Asp Leu Phe Lys Gln Ala Lys Glu Asn
      245              250              255

Ser Pro Cys Ile Ile Phe Val Asp Glu Ile Asp Ala Val Gly Arg Ala
      260              265              270

Arg Gly Ser Gly Met Gly Gly Gly His Asp Glu Arg Glu Gln Thr Leu
      275              280              285

Asn Gln Leu Leu Val Glu Met Asp Gly Phe Gly Asp Arg Gln Gly Val

```

290	295	300
Ile Leu Met Ala Ala Thr Asn Arg Pro Asp Val Leu Asp Pro Ala Leu 305 310 315 320		
Leu Arg Pro Gly Arg Phe Asp Arg Gln Ile Pro Val Thr Asn Pro Asp 325 330 335		
Leu Arg Gly Arg Glu Gln Ile Leu Glu Val His Ala Lys Gly Lys Pro 340 345 350		
Phe Ala Pro Asp Ala Asp Ile Lys Ala Leu Ala Lys Arg Thr Ala Gly 355 360 365		
Met Ser Gly Ala Asp Leu Ala Asn Val Leu Asn Glu Ala Ala Leu Leu 370 375 380		
Thr Ala Arg Val Gly Gly Asn Val Ile Thr Ala Asp Ala Leu Glu Glu 385 390 395 400		
Ala Thr Asp Arg Val Val Gly Gly Pro Arg Arg Ser Gly Lys Val Ile 405 410 415		
Ser Glu Lys Glu Lys Lys Val Thr Ala Tyr His Glu Gly Gly His Thr 420 425 430		
Leu Ser Ala Trp Ala Leu Glu Asp Ile Glu Arg Val Tyr Lys Val Thr 435 440 445		
Ile Leu Ala Arg Gly Arg Thr Gly Gly His Ala Met Thr Ala Gln Glu 450 455 460		
Asp Asp Lys Gly Met Tyr Asn Arg Asn Glu Leu Phe Ala Arg Leu Val 465 470 475 480		
Phe Ala Met Gly Gly Arg Ser Ala Glu Glu Leu Val Phe Gly Glu Pro 485 490 495		
Thr Thr Gly Ala Ser Ala Asp Ile Glu Met Ala Thr Lys Ile Ala Arg 500 505 510		
Ser Met Val Thr Glu Tyr Gly Met Ser Pro Ala Val Gly Met Val Lys 515 520 525		
Tyr Gly Gln Glu Gln Gly Asp Pro Phe Ser Gly Arg Gly Gly Gly Gly 530 535 540		
Asn Leu Asp His Ser Gln Glu Val Ala Ala Thr Ile Asp Thr Glu Val 545 550 555 560		
Gln Phe Leu Leu Asp Lys Ala His Glu Val Ser Tyr Ser Ile Leu Ala 565 570 575		
Glu Tyr Arg Asp His Leu Asp Arg Leu Ala Glu Lys Leu Leu Glu Lys 580 585 590		
Glu Thr Leu Arg Arg Pro Asp Leu Glu Ala Leu Phe Asp Asp Ile Val 595 600 605		
Pro Arg Lys Val Ala Glu Val Phe Pro Asp Glu Ser Thr Arg Phe Pro 610 615 620		

Arg Gln Glu Asn Arg Glu Pro Val Lys Thr Pro Val Glu Leu Ala Leu
 625 630 635 640
 Glu Arg Gly Glu Glu Pro Pro Lys Lys Phe Ser Ile Leu Glu Ala Ser
 645 650 655
 Arg Ala Thr Arg Glu Arg Arg Arg Lys Glu Leu Glu Ala Gln Gly Lys
 660 665 670
 Leu Pro Val Gln Pro Ala Ser Ser Ala Gly Val Ala Pro Ala Ala Gly
 675 680 685
 Ala Ala Ala Gly Ser Tyr Gly Thr Pro Pro Pro Ala Asp Trp Ser Val
 690 695 700
 Pro Gly Ser Ala Gly Lys His Arg Ser Arg Ala Glu Glu Gln Pro Ala
 705 710 715 720
 Glu Gln Gly Phe Pro Ala Gln Thr Pro Ala Gln Ala Pro Glu Gln Ser
 725 730 735
 Pro Asp Ser Ser Gly Gly Arg Pro Asn Pro Tyr Ala Thr Pro Thr Ala
 740 745 750
 Ser Gly Glu His Pro Gly Met Lys Ala Tyr Gly Phe Gly Asp Ser Glu
 755 760 765
 Leu Met Asp Gln Ser Thr Gly Ala Glu His Thr Pro Gly Asn Val Ser
 770 775 780
 Gln Glu Ser Pro Thr Glu Met Ile Gly Phe Arg Leu Pro Asp His Glu
 785 790 795 800
 Arg Ser Asp Tyr Pro Glu Lys Ala Gln Lys Glu Ser Val Leu Asp Ala
 805 810 815
 Ser Glu Thr Thr Glu Met Pro Val Val Pro Asp Gln Pro Ile Asp Gly
 820 825 830
 Asp Ser Gly Lys Ser Ala Glu Gly Thr Gln Glu Asn Pro Glu Asn Glu
 835 840 845
 Gly Asp Asn Arg Gly
 850

<210> 101

<211> 1869

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1846)

<223> RXA02098

<400> 101

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acctgtgtgc atcgggggtca aacctgccac tatagagggt atg gat gcg act ttt 115

											Met 1	Asp	Ala	Thr	Phe 5	
tgg Trp	atc Ile	att Ile	gga Gly	cta Leu 10	gta Val	gtc Val	ctc Leu	gtg Val	gtt Val 15	ctc Leu	gcg Ala	atc Ile	atc Ile	att Ile 20	gta Val	163
ttg Leu	atc Ile	gta Val	gga Gly 25	aat Asn	cag Gln	cga Arg	ggt Gly	aaa Lys 30	tca Ser	aag Lys	acc Thr	gtt Val	agt Ser 35	ttt Phe	gaa Glu	211
aaa Lys	cct Pro	gaa Glu 40	gag Glu	aat Asn	aaa Lys	aaa Lys	gaa Glu 45	cta Leu	acc Thr	cag Gln	caa Gln	gag Glu 50	aag Lys	tct Ser	gga Gly	259
aat Asn	tac Tyr 55	caa Gln	gcc Ala	caa Gln	ggt Gly	gga Gly 60	ttc Phe	aac Asn	ttc Phe	gcc Ala	cca Pro 65	gct Ala	aaa Lys	caa Gln	aca Thr	307
gaa Glu 70	gag Glu	cca Pro	gtg Val	ctg Leu	cgt Arg 75	gaa Glu	ggc Gly	caa Gln	gat Asp	ctt Leu 80	ggc Gly	gca Ala	cca Pro	aag Lys	gct Ala 85	355
gaa Glu	aca Thr	aca Thr	ccg Pro	att Ile 90	gtt Val	cca Pro	cca Pro	gta Val	gtt Val 95	att Ile	ccg Pro	ccg Pro	gca Ala	gct Ala 100	cct Pro	403
gaa Glu	gag Glu	gaa Glu 105	aag Lys	gcg Ala	ccg Pro	gag Glu	caa Gln	tcg Ser 110	act Thr	gaa Glu	act Thr	ttc Phe 115	gca Ala	gct Ala	caa Gln	451
aag Lys	cct Pro	gct Ala 120	gaa Glu	gaa Glu	gca Ala	cct Pro	gca Ala 125	act Thr	cct Pro	gaa Glu	cca Pro	gaa Glu 130	acc Thr	tct Ser	gat Asp	499
gat Asp	gtt Val 135	gtc Val	gag Glu	gaa Glu	cca Pro	gaa Glu 140	gtt Val	aag Lys	gag Glu	cct Pro	gag Glu 145	gtt Val	aaa Lys	gaa Glu	gtt Val	547
gtc Val 150	gct Ala	gtt Val	gag Glu	cca Pro	gag Glu 155	gtc Val	gaa Glu	act Thr	gaa Glu	gag Glu 160	cca Pro	gca Ala	gtt Val	gtt Val	gaa Glu 165	595
gaa Glu	cct Pro	gca Ala	gta Val	gca Ala 170	gag Glu	gaa Glu	cca Pro	gca Ala	att Ile 175	gtt Val	gag Glu	gaa Glu	cct Pro	gca Ala 180	gta Val	643
gca Ala	gag Glu	gaa Glu	cct Pro 185	gca Ala	gta Val	gca Ala	gag Glu 190	gaa Glu	cct Pro	gca Ala	gta Val	gca Ala 195	gag Glu 195	gaa Glu	cca Pro	691
gca Ala	att Ile 200	gtt Val	gag Glu	gaa Glu	cct Pro	gca Ala	gta Val 205	gca Ala	gag Glu	gaa Glu	cct Pro	gca Ala 210	gtt Val	gtt Val	gag Glu	739
gaa Glu	cct Pro 215	gca Ala	gta Val	gcg Ala	gaa Glu	gtt Val 220	ccc Pro	gaa Glu	aca Thr	atc Ile	gaa Glu 225	gaa Glu	cct Pro	gca Ala	gtt Val	787
gaa Glu	gaa Glu	ctt Leu	gcg Ala	gca Ala	gtt Val	gct Ala	gag Glu	gtc Val	acc Thr	gag Glu	gct Ala	gca Ala	gag Glu	gct Ala	gct Ala	835

230	235	240	245	
cag gtt gct gtg gaa tct gcg gaa gct gcg ctg gag gaa act cca gtt Gln Val Ala Val Glu Ser Ala Glu Ala Ala Leu Glu Glu Thr Pro Val	250	255	260	883
cca gat gtg gag ccg gag cca gct gcg gag cct att gat gag atc gtg Pro Asp Val Glu Pro Glu Pro Ala Ala Glu Pro Ile Asp Glu Ile Val	265	270	275	931
ccg gcg gcg ggt cgt atc ggt aag ctg cgt ggt cgt ctt tct cgg tca Pro Ala Ala Gly Arg Ile Gly Lys Leu Arg Gly Arg Leu Ser Arg Ser	280	285	290	979
cag agt gtt ttc ggt aag tca gtg ttg ggc att ttg tct gcg ggt gac Gln Ser Val Phe Gly Lys Ser Val Leu Gly Ile Leu Ser Ala Gly Asp	295	300	305	1027
ttg gat gaa gac gca tgg gaa gac atc gaa gcg atg ttg atc aag gcg Leu Asp Glu Asp Ala Trp Glu Asp Ile Glu Ala Met Leu Ile Lys Ala	310	315	320	1075
gat ttg ggc gcc aag atc act gcg cgt gtg gtg gat gag ctg cgt gac Asp Leu Gly Ala Lys Ile Thr Ala Arg Val Val Asp Glu Leu Arg Asp	330	335	340	1123
aag atc gca gag cat ggt gtt ggt agt gag gca gag gcg cgt gcg atg Lys Ile Ala Glu His Gly Val Gly Ser Glu Ala Glu Ala Arg Ala Met	345	350	355	1171
ctg cgt gct tcg ctg att gat gct tgc cgt cct gac ctt gat cgc tcc Leu Arg Ala Ser Leu Ile Asp Ala Cys Arg Pro Asp Leu Asp Arg Ser	360	365	370	1219
att aag gct atg ccg tat gag ggt aag cca ccg gtg gtg ttg gtt gtt Ile Lys Ala Met Pro Tyr Glu Gly Lys Pro Pro Val Val Leu Val Val	375	380	385	1267
ggt gtg aac ggt acc ggt aag acg acg act act ggc aag ctt gct cgt Gly Val Asn Gly Thr Gly Lys Thr Thr Thr Thr Gly Lys Leu Ala Arg	390	395	400	1315
gtg ttg gtg tcc atg ggt cat aag gtg att ctt ggt gct gcg gat acg Val Leu Val Ser Met Gly His Lys Val Ile Leu Gly Ala Ala Asp Thr	410	415	420	1363
ttc cgt gcg gcg gct gcg gat cag ttg gag acg tgg ggt cgc cgt gtg Phe Arg Ala Ala Ala Asp Gln Leu Glu Thr Trp Gly Arg Arg Val	425	430	435	1411
ggt gcg gag act gtt cgt ggc gct gag ggc gcg gat cct gca tct att Gly Ala Glu Thr Val Arg Gly Ala Glu Gly Ala Asp Pro Ala Ser Ile	440	445	450	1459
gcg ttt gat gct gtg gct aag ggt gtt gag cgt cag gcg gat gtc gtt Ala Phe Asp Ala Val Ala Lys Gly Val Glu Arg Gln Ala Asp Val Val	455	460	465	1507
ttg gtt gac act gcg ggt cgt ttg cac acg tcg act ggt ttg atg gat Leu Val Asp Thr Ala Gly Arg Leu His Thr Ser Thr Gly Leu Met Asp	470	475	480	1555

cag ttg ggc aag gtt aag cgc gtg gtg gag aag aag gca gtg gtg gat 1603
 Gln Leu Gly Lys Val Lys Arg Val Val Glu Lys Lys Ala Val Val Asp
 490 495 500

gaa gtg ctg ctg gtt ttg gat gcc acg gtt ggt cag aac ggt atg cag 1651
 Glu Val Leu Leu Val Leu Asp Ala Thr Val Gly Gln Asn Gly Met Gln
 505 510 515

cag gct cgt att ttc cgt gaa gtt gtg gat att acg ggt gtg gtg ttg 1699
 Gln Ala Arg Ile Phe Arg Glu Val Val Asp Ile Thr Gly Val Val Leu
 520 525 530

acc aag ctg gat ggt act gcg aag ggc gga atc gtg ttc cag gtg cag 1747
 Thr Lys Leu Asp Gly Thr Ala Lys Gly Gly Ile Val Phe Gln Val Gln
 535 540 545

gaa gag ttg ggt gtt cct gtg aag ctt gtt ggt ctt ggt gaa ggt gcg 1795
 Glu Glu Leu Gly Val Pro Val Lys Leu Val Gly Leu Gly Glu Gly Ala
 550 555 560 565

gat gat ttg gca ccg ttt gag gtt gag ggc ttc gtg gac gct ttg ctg 1843
 Asp Asp Leu Ala Pro Phe Glu Val Glu Gly Phe Val Asp Ala Leu Leu
 570 575 580

ggc tagaaacccg ataagcgaga acc 1869
 Gly

<210> 102
 <211> 582
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 102
 Met Asp Ala Thr Phe Trp Ile Ile Gly Leu Val Val Leu Val Val Leu
 1 5 10 15

Ala Ile Ile Ile Val Leu Ile Val Gly Asn Gln Arg Gly Lys Ser Lys
 20 25 30

Thr Val Ser Phe Glu Lys Pro Glu Glu Asn Lys Lys Glu Leu Thr Gln
 35 40 45

Gln Glu Lys Ser Gly Asn Tyr Gln Ala Gln Gly Gly Phe Asn Phe Ala
 50 55 60

Pro Ala Lys Gln Thr Glu Glu Pro Val Leu Arg Glu Gly Gln Asp Leu
 65 70 75 80

Gly Ala Pro Lys Ala Glu Thr Thr Pro Ile Val Pro Pro Val Val Ile
 85 90 95

Pro Pro Ala Ala Pro Glu Glu Glu Lys Ala Pro Glu Gln Ser Thr Glu
 100 105 110

Thr Phe Ala Ala Gln Lys Pro Ala Glu Glu Ala Pro Ala Thr Pro Glu
 115 120 125

Pro Glu Thr Ser Asp Asp Val Val Glu Glu Pro Glu Val Lys Glu Pro

130					135					140				
Glu Val Lys Glu Val Val	Ala Val Glu Pro Glu Val Glu Thr Glu Glu													
145		150				155							160	
Pro Ala Val Val Glu Glu Pro Ala Val Ala Glu Glu Pro Ala Ile Val														
		165				170							175	
Glu Glu Pro Ala Val Ala Glu Glu Pro Ala Val Ala Glu Glu Pro Ala														
		180				185							190	
Val Ala Glu Glu Pro Ala Ile Val Glu Glu Pro Ala Val Ala Glu Glu														
		195				200							205	
Pro Ala Val Val Glu Glu Pro Ala Val Ala Glu Val Pro Glu Thr Ile														
		210				215							220	
Glu Glu Pro Ala Val Glu Glu Leu Ala Ala Val Ala Glu Val Thr Glu														
		225				230							240	
Ala Ala Glu Ala Ala Gln Val Ala Val Glu Ser Ala Glu Ala Ala Leu														
		245				250							255	
Glu Glu Thr Pro Val Pro Asp Val Glu Pro Glu Pro Ala Ala Glu Pro														
		260				265							270	
Ile Asp Glu Ile Val Pro Ala Ala Gly Arg Ile Gly Lys Leu Arg Gly														
		275				280							285	
Arg Leu Ser Arg Ser Gln Ser Val Phe Gly Lys Ser Val Leu Gly Ile														
		290				295							300	
Leu Ser Ala Gly Asp Leu Asp Glu Asp Ala Trp Glu Asp Ile Glu Ala														
		305				310							320	
Met Leu Ile Lys Ala Asp Leu Gly Ala Lys Ile Thr Ala Arg Val Val														
		325				330							335	
Asp Glu Leu Arg Asp Lys Ile Ala Glu His Gly Val Gly Ser Glu Ala														
		340				345							350	
Glu Ala Arg Ala Met Leu Arg Ala Ser Leu Ile Asp Ala Cys Arg Pro														
		355				360							365	
Asp Leu Asp Arg Ser Ile Lys Ala Met Pro Tyr Glu Gly Lys Pro Pro														
		370				375							380	
Val Val Leu Val Val Gly Val Asn Gly Thr Gly Lys Thr Thr Thr Thr														
		385				390							400	
Gly Lys Leu Ala Arg Val Leu Val Ser Met Gly His Lys Val Ile Leu														
		405				410							415	
Gly Ala Ala Asp Thr Phe Arg Ala Ala Ala Ala Asp Gln Leu Glu Thr														
		420				425							430	
Trp Gly Arg Arg Val Gly Ala Glu Thr Val Arg Gly Ala Glu Gly Ala														
		435				440							445	
Asp Pro Ala Ser Ile Ala Phe Asp Ala Val Ala Lys Gly Val Glu Arg														
		450				455							460	

Gln Ala Asp Val Val Leu Val Asp Thr Ala Gly Arg Leu His Thr Ser
465 470 475 480

Thr Gly Leu Met Asp Gln Leu Gly Lys Val Lys Arg Val Val Glu Lys
485 490 495

Lys Ala Val Val Asp Glu Val Leu Leu Val Leu Asp Ala Thr Val Gly
500 505 510

Gln Asn Gly Met Gln Gln Ala Arg Ile Phe Arg Glu Val Val Asp Ile
515 520 525

Thr Gly Val Val Leu Thr Lys Leu Asp Gly Thr Ala Lys Gly Gly Ile
530 535 540

Val Phe Gln Val Gln Glu Glu Leu Gly Val Pro Val Lys Leu Val Gly
545 550 555 560

Leu Gly Glu Gly Ala Asp Asp Leu Ala Pro Phe Glu Val Glu Gly Phe
565 570 575

Val Asp Ala Leu Leu Gly
580

<210> 103

<211> 1134

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1111)

<223> RXA027i3

<400> 103

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ttggacatct aggccggcag gaaaaggggg gaacacgcac atg gaa gat ttt tcc 115
Met Glu Asp Phe Ser
1 5

ttg gat ggc aac cac gga cac gtt ccc gta atg cgt gat cgt atg gcg 163
Leu Asp Gly Asn His Gly His Val Pro Val Met Arg Asp Arg Met Ala
10 15 20

gct ttg atc gcc gaa cac gtg gaa gca ttg gga gaa aac gct gtc att 211
Ala Leu Ile Ala Glu His Val Glu Ala Leu Gly Glu Asn Ala Val Ile
25 30 35

gtt gac gca acc ctt ggc gca ggc ggg cat gcg gag ttc ttc ctg aac 259
Val Asp Ala Thr Leu Gly Ala Gly Gly His Ala Glu Phe Phe Leu Asn
40 45 50

acg ttc ccc aaa gcg cgc ctg att ggc ctt gat cgt gac caa aat gcg 307
Thr Phe Pro Lys Ala Arg Leu Ile Gly Leu Asp Arg Asp Gln Asn Ala
55 60 65

ttg cgg gat gct cgc gcg cga ctt gct cct ttc ggg gag cgg ttc att 355
Leu Arg Asp Ala Arg Ala Arg Leu Ala Pro Phe Gly Glu Arg Phe Ile

70	75	80	85	
ggc gtc cag acg cgt ttc gac gga ctc cgc gag gtg ttg gaa tct gtc				403
Gly Val Gln Thr Arg Phe Asp Gly Leu Arg Glu Val Leu Glu Ser Val				
	90	95	100	
gag ggc gac atc att gat tta gct cgc gag cac ggt atc gct ggc gct				451
Glu Gly Asp Ile Ile Asp Leu Ala Arg Glu His Gly Ile Ala Gly Ala				
	105	110	115	
ctg ttt gat ctg ggt gtc tcc tcg atg cag ctt gat cag gtg gag cgt				499
Leu Phe Asp Leu Gly Val Ser Ser Met Gln Leu Asp Gln Val Glu Arg				
	120	125	130	
ggc ttt gcc tac cgc acg gac gcg cct ctg gac atg cgc atg gat gca				547
Gly Phe Ala Tyr Arg Thr Asp Ala Pro Leu Asp Met Arg Met Asp Ala				
	135	140	145	
act cag ggt att acg gct gca gat atc ctc aac act tat tcg cat ggt				595
Thr Gln Gly Ile Thr Ala Ala Asp Ile Leu Asn Thr Tyr Ser His Gly				
150	155	160	165	
gac atc gct cga atc ttg aag act tac ggc gat gaa cgc ttc gcc ggc				643
Asp Ile Ala Arg Ile Leu Lys Thr Tyr Gly Asp Glu Arg Phe Ala Gly				
	170	175	180	
aag att gct tct gcg gtg ctg aaa gaa cgt gaa aaa gag ccg ttc act				691
Lys Ile Ala Ser Ala Val Leu Lys Glu Arg Glu Lys Glu Pro Phe Thr				
	185	190	195	
acc tct gct cgt ttg gtg gag ctt ctg tac gac gcc atc cct gca gcg				739
Thr Ser Ala Arg Leu Val Glu Leu Leu Tyr Asp Ala Ile Pro Ala Ala				
	200	205	210	
acc cgc cga acc ggt gga cac ccc gcg aaa cgt act ttc cag gcg ttg				787
Thr Arg Arg Thr Gly Gly His Pro Ala Lys Arg Thr Phe Gln Ala Leu				
	215	220	225	
cgc gtt gag gtg aac aac gag ctt gat tcc ctg aag aat gtg ctt cct				835
Arg Val Glu Val Asn Asn Glu Leu Asp Ser Leu Lys Asn Val Leu Pro				
230	235	240	245	
caa atc act gac gcc ctc aat gtt ggg gga cgt gca gtg ttt atg agc				883
Gln Ile Thr Asp Ala Leu Asn Val Gly Gly Arg Ala Val Phe Met Ser				
	250	255	260	
tac cag tct cat gag gac aag ctg gtg aag aag ttc ttc acg gat ctg				931
Tyr Gln Ser His Glu Asp Lys Leu Val Lys Lys Phe Phe Thr Asp Leu				
	265	270	275	
acc acc tct aag acc cct ccg ggc ttg cct gtt gat ctt cct gga act				979
Thr Thr Ser Lys Thr Pro Pro Gly Leu Pro Val Asp Leu Pro Gly Thr				
	280	285	290	
gca cca cag ttt aag cag gtt act cgc ggt gct gaa acg gct tcg gaa				1027
Ala Pro Gln Phe Lys Gln Val Thr Arg Gly Ala Thr Ala Ser Glu				
	295	300	305	
gct gaa att gaa gaa aac cca cgt gcc gca cct gtg aag gtg cgc gca				1075
Ala Glu Ile Glu Glu Asn Pro Arg Ala Ala Pro Val Lys Val Arg Ala				
310	315	320	325	

atc gaa aga atc ggc aac aac tca gga gac ctc tca tgaccatgac 1121
 Ile Glu Arg Ile Gly Asn Asn Ser Gly Asp Leu Ser
 330 335

aaatggctcc cgc 1134

<210> 104

<211> 337

<212> PRT

<213> Corynebacterium glutamicum

<400> 104

Met Glu Asp Phe Ser Leu Asp Gly Asn His Gly His Val Pro Val Met
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Arg Asp Arg Met Ala Ala Leu Ile Ala Glu His Val Glu Ala Leu Gly
 20 25 30

Glu Asn Ala Val Ile Val Asp Ala Thr Leu Gly Ala Gly Gly His Ala
 35 40 45

Glu Phe Phe Leu Asn Thr Phe Pro Lys Ala Arg Leu Ile Gly Leu Asp
 50 55 60

Arg Asp Gln Asn Ala Leu Arg Asp Ala Arg Ala Arg Leu Ala Pro Phe
 65 70 75 80

Gly Glu Arg Phe Ile Gly Val Gln Thr Arg Phe Asp Gly Leu Arg Glu
 85 90 95

Val Leu Glu Ser Val Glu Gly Asp Ile Ile Asp Leu Ala Arg Glu His
 100 105 110

Gly Ile Ala Gly Ala Leu Phe Asp Leu Gly Val Ser Ser Met Gln Leu
 115 120 125

Asp Gln Val Glu Arg Gly Phe Ala Tyr Arg Thr Asp Ala Pro Leu Asp
 130 135 140

Met Arg Met Asp Ala Thr Gln Gly Ile Thr Ala Ala Asp Ile Leu Asn
 145 150 155 160

Thr Tyr Ser His Gly Asp Ile Ala Arg Ile Leu Lys Thr Tyr Gly Asp
 165 170 175

Glu Arg Phe Ala Gly Lys Ile Ala Ser Ala Val Leu Lys Glu Arg Glu
 180 185 190

Lys Glu Pro Phe Thr Thr Ser Ala Arg Leu Val Glu Leu Leu Tyr Asp
 195 200 205

Ala Ile Pro Ala Ala Thr Arg Arg Thr Gly Gly His Pro Ala Lys Arg
 210 215 220

Thr Phe Gln Ala Leu Arg Val Glu Val Asn Asn Glu Leu Asp Ser Leu
 225 230 235 240

Lys Asn Val Leu Pro Gln Ile Thr Asp Ala Leu Asn Val Gly Gly Arg
 245 250 255

Ala Val Phe Met Ser Tyr Gln Ser His Glu Asp Lys Leu Val Lys Lys
 260 265 270

Phe Phe Thr Asp Leu Thr Thr Ser Lys Thr Pro Pro Gly Leu Pro Val
 275 280 285

Asp Leu Pro Gly Thr Ala Pro Gln Phe Lys Gln Val Thr Arg Gly Ala
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Glu Thr Ala Ser Glu Ala Glu Ile Glu Glu Asn Pro Arg Ala Ala Pro
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Val Lys Val Arg Ala Ile Glu Arg Ile Gly Asn Asn Ser Gly Asp Leu
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Ser

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 Val Asn Lys Lys Val
 1 5

atc gcc att gtt gtg ggt gtg gtt gtt gtc ctc gtg gca atc ctg ggc 163
 Ile Ala Ile Val Val Gly Val Val Val Val Leu Val Ala Ile Leu Gly
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gtt gtt gcc tgg ttc gtt ccc atc ctc aag gtg gga aac att gaa gta 211
 Val Val Ala Trp Phe Val Pro Ile Leu Lys Val Gly Asn Ile Glu Val
 25 30 35

acc ggt gca acg cgc aca tat ccg gat caa gta ctg gaa gtc tcc ggg 259
 Thr Gly Ala Thr Arg Thr Tyr Pro Asp Gln Val Leu Glu Val Ser Gly
 40 45 50

att gtt gag ggc aaa aac ctc ttc cgc gtc gat gcg act gca gca ggg 307
 Ile Val Glu Gly Lys Asn Leu Phe Arg Val Asp Ala Thr Ala Ala Gly
 55 60 65

caa aac att gtg gaa ttg ccc tgg gtg aaa tcg gtg acc gtt aac cgt 355
 Gln Asn Ile Val Glu Leu Pro Trp Val Lys Ser Val Thr Val Asn Arg
 70 75 80 85

gcc ctg cca agc acc atc acc gtg gag ctg aca gag cgt gag cct gca 403
 Ala Leu Pro Ser Thr Ile Thr Val Glu Leu Thr Glu Arg Glu Pro Ala
 90 95 100

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Val Phe Ile Lys Arg Ala Asp Gly Asp His Val Ile Asp Thr Glu Gly
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Lys Glu Ile Ile Ile Gly Thr Pro Pro Val Gly Thr Val Glu Val Ser
      120                      125                      130

ggc gcg gat gaa gga aac tca gaa gtg ctt cct gcg gtt att gct gta 547
Gly Ala Asp Glu Gly Asn Ser Glu Val Leu Pro Ala Val Ile Ala Val
      135                      140                      145

atc aac gca att aaa gcg caa gat gcg cag atg aca gaa agt atc cag 595
Ile Asn Ala Ile Lys Ala Gln Asp Ala Gln Met Thr Glu Ser Ile Gln
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gta gtg gaa gct ccg gat caa ttt gat atc ttg ctg aaa atg aat gat 643
Val Val Glu Ala Pro Asp Gln Phe Asp Ile Leu Leu Lys Met Asn Asp
      170                      175                      180

ggc cgg gaa atc tac tgg gga tcc tcg gaa aac aac cac gat aaa gcg 691
Gly Arg Glu Ile Tyr Trp Gly Ser Ser Glu Asn Asn His Asp Lys Ala
      185                      190                      195

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Val Ala Met Ser Thr Val Leu Lys Arg Glu Gly Gln Arg Trp Asn Ile
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<213> Corynebacterium glutamicum

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Gly Asn Ile Glu Val Thr Gly Ala Thr Arg Thr Tyr Pro Asp Gln Val
      35                      40                      45

Leu Glu Val Ser Gly Ile Val Glu Gly Lys Asn Leu Phe Arg Val Asp
      50                      55                      60

Ala Thr Ala Ala Gly Gln Asn Ile Val Glu Leu Pro Trp Val Lys Ser
      65                      70                      75                      80

Val Thr Val Asn Arg Ala Leu Pro Ser Thr Ile Thr Val Glu Leu Thr
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Glu Arg Glu Pro Ala Val Phe Ile Lys Arg Ala Asp Gly Asp His Val
      100                      105                      110

Ile Asp Thr Glu Gly Lys Glu Ile Ile Ile Gly Thr Pro Pro Val Gly

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Thr	Glu	Ser	Ile	Gln	Val	Val	Glu	Ala	Pro	Asp	Gln	Phe	Asp	Ile	Leu
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Leu	Lys	Met	Asn	Asp	Gly	Arg	Glu	Ile	Tyr	Trp	Gly	Ser	Ser	Glu	Asn
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Asn	His	Asp	Lys	Ala	Val	Ala	Met	Ser	Thr	Val	Leu	Lys	Arg	Glu	Gly
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<220>

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Thr	Glu	Arg	Glu	Pro	Ala	Val	Phe	Ile	Lys	Arg	Ala	Asp	Gly	Asp	His	
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Val	Ile	Asp	Thr	Glu	Gly	Lys	Glu	Ile	Ile	Ile	Gly	Thr	Pro	Pro	Val	
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Gly	Thr	Val	Glu	Val	Ser	Gly	Ala	Asp	Glu	Gly	Asn	Ser	Glu	Val	Leu	
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cct	gcg	gtt	att	gct	gta	atc	aac	gca	att	aaa	gcg	caa	gat	gcg	cag	288
Pro	Ala	Val	Ile	Ala	Val	Ile	Asn	Ala	Ile	Lys	Ala	Gln	Asp	Ala	Gln	
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atg	aca	gaa	agt	atc	cag	gta	gtg	gaa	gct	ccg	gat	caa	ttt	gat	atc	336
Met	Thr	Glu	Ser	Ile	Gln	Val	Val	Glu	Ala	Pro	Asp	Gln	Phe	Asp	Ile	
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Leu Leu Lys Met Asn Asp Gly Arg Glu Ile Tyr Trp Gly Ser Ser Glu
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 Asn Asn His Asp Lys Ala Val Ala Met Ser Thr Val Leu Lys Arg Glu
 130 135 140
 ggc caa cgt tgg aac att agc tca ccc tca atg gtg aca gtc cgc 477
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 <213> Corynebacterium glutamicum

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 35 40 45
 Val Ile Asp Thr Glu Gly Lys Glu Ile Ile Ile Gly Thr Pro Pro Val
 50 55 60
 Gly Thr Val Glu Val Ser Gly Ala Asp Glu Gly Asn Ser Glu Val Leu
 65 70 75 80
 Pro Ala Val Ile Ala Val Ile Asn Ala Ile Lys Ala Gln Asp Ala Gln
 85 90 95
 Met Thr Glu Ser Ile Gln Val Val Glu Ala Pro Asp Gln Phe Asp Ile
 100 105 110
 Leu Leu Lys Met Asn Asp Gly Arg Glu Ile Tyr Trp Gly Ser Ser Glu
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Met Thr Thr Pro Pro																5
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His Glu Ser Leu Ala Thr Asp Gly Ser Val Arg Gly Phe Ile Gly Pro																35
25 30																
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Arg Glu Val Pro Arg Leu Trp Asp Arg His Ile Leu Asn Cys Gly Val																50
40 45																
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Ile Gly Glu Ala Met Asp Glu Gly Ile Ser Val Ala Asp Ile Gly Ser																65
55 60																
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Gly Ala Gly Leu Pro Gly Ile Pro Leu Ala Ile Ala Arg Pro Asp Leu																85
70 75 80																
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Asn Ile Thr Leu Ile Glu Pro Leu Leu Lys Arg Ser Val Tyr Leu Asn																100
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Glu Val Lys Glu Ala Leu Asn Leu Asp Asn Val Thr Val Arg Gly																115
105 110 115																
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Arg Ala Glu Glu Lys Val Val Arg Lys Gln Val Gly Leu Val Asp Ile																130
120 125 130																
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Val Thr Ser Arg Ala Val Ala Pro Leu Gly Lys Leu Ala Thr Trp Ser																145
135 140 145																
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Leu Pro Leu Val Lys Ile Gly Gly Arg Met Val Ala Met Lys Gly Ser																165
150 155 160																
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Ser Val Glu Glu Glu Ile Glu Arg Asp Ala Lys Glu Ile Arg Lys Ala																180
170 175 180																
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Gly Gly Thr Asp Ile Lys Val Tyr Thr Val Gly Glu Ala Leu Leu Ser																195
185 190 195																
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Glu Pro Thr Thr Leu Ile Ser Ile Arg Arg Glu Lys																205
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 <213> Corynebacterium glutamicum

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 Gly Phe Ile Gly Pro Arg Glu Val Pro Arg Leu Trp Asp Arg His Ile
 35 40 45
 Leu Asn Cys Gly Val Ile Gly Glu Ala Met Asp Glu Gly Ile Ser Val
 50 55 60
 Ala Asp Ile Gly Ser Gly Ala Gly Leu Pro Gly Ile Pro Leu Ala Ile
 65 70 75 80
 Ala Arg Pro Asp Leu Asn Ile Thr Leu Ile Glu Pro Leu Leu Lys Arg
 85 90 95
 Ser Val Tyr Leu Asn Glu Val Lys Glu Ala Leu Asn Leu Asp Asn Val
 100 105 110
 Thr Val Val Arg Gly Arg Ala Glu Glu Lys Val Val Arg Lys Gln Val
 115 120 125
 Gly Leu Val Asp Ile Val Thr Ser Arg Ala Val Ala Pro Leu Gly Lys
 130 135 140
 Leu Ala Thr Trp Ser Leu Pro Leu Val Lys Ile Gly Gly Arg Met Val
 145 150 155 160
 Ala Met Lys Gly Ser Ser Val Glu Glu Glu Ile Glu Arg Asp Ala Lys
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 Glu Ile Arg Lys Ala Gly Gly Thr Asp Ile Lys Val Tyr Thr Val Gly
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 Glu Ala Leu Leu Ser Glu Pro Thr Thr Leu Ile Ser Ile Arg Arg Glu
 195 200 205
 Lys

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 <223> RXA01428

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Met Ala Gln Asn Lys
1 5

ggt tcc gac aag tcc cag acg gaa aag cgt aag ggc ggt ctg ggg cgc 163
Gly Ser Asp Lys Ser Gln Thr Glu Lys Arg Lys Gly Gly Leu Gly Arg
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ggt ctg gcc gca ctt att ccc tca gga cca agt aat tcc cca ggt ctt 211
Gly Leu Ala Ala Leu Ile Pro Ser Gly Pro Ser Asn Ser Pro Gly Leu
25 30 35

ggt ggc ggt gcg gct gac atc att ttg ggc ggt acc gtg ggt gcg cgt 259
Gly Gly Gly Ala Ala Asp Ile Ile Leu Gly Gly Thr Val Gly Ala Arg
40 45 50

act gct gca gct ccc aag cgt gag tcc aca cca gca gct cct gca cct 307
Thr Ala Ala Ala Pro Lys Arg Glu Ser Thr Pro Ala Ala Pro Ala Pro
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gag gct cct gcg cag gcc gct cca caa cac act gag gcc aca aag cca 355
Glu Ala Pro Ala Gln Ala Ala Pro Gln His Thr Glu Ala Thr Lys Pro
70 75 80 85

gag gta gtt cca gag cca gca gct cct gct cca acg cag tca gca cag 403
Glu Val Val Pro Glu Pro Ala Ala Pro Ala Pro Thr Gln Ser Ala Gln
90 95 100

cag gaa gcg ccg cag gca cag cca gca cag cag tct gag ttc ggc gca 451
Gln Glu Ala Pro Gln Ala Gln Pro Ala Gln Gln Ser Glu Phe Gly Ala
105 110 115

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Ser Tyr Leu Glu Ile Pro Ile Glu Gln Ile Arg Pro Asn Pro Gln Gln
120 125 130

cct cgc cat gag ttt gat ccg cag gca ctt gac gag ttg gtg cat tcg 547
Pro Arg His Glu Phe Asp Pro Gln Ala Leu Asp Glu Leu Val His Ser
135 140 145

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Ile Ser Glu Phe Gly Leu Met Gln Pro Ile Val Val Arg Arg Ser Glu
150 155 160 165

gat ggc tat gag ctc atc atg ggt gag cgt cgt tgg cgt gca tcc aag 643
Asp Gly Tyr Glu Leu Ile Met Gly Glu Arg Arg Trp Arg Ala Ser Lys
170 175 180

cga gct ggc ctt gag gtt atc ccg gcg att gtc cgt gaa act gaa gac 691
Arg Ala Gly Leu Glu Val Ile Pro Ala Ile Val Arg Glu Thr Glu Asp
185 190 195

agc gcg atg ctg cgc gac gcc ctt ttg gaa aat atc cac agg gtg cag 739
Ser Ala Met Leu Arg Asp Ala Leu Leu Glu Asn Ile His Arg Val Gln
200 205 210

ctg aat cct ttg gaa gag gca gcc gcc tac cag cag ttg ctg gag gag 787
Leu Asn Pro Leu Glu Glu Ala Ala Ala Tyr Gln Gln Leu Leu Glu Glu
215 220 225

ttc ggt gtc acc cag gca gag ctg gcc gat aag ctg ggc cgt tcc cgt 835
 Phe Gly Val Thr Gln Ala Glu Leu Ala Asp Lys Leu Gly Arg Ser Arg
 230 235 240 245

 ccg gta atc acc aat atg att cgt ctg ctg ggc ctt cca gtc aac gtg 883
 Pro Val Ile Thr Asn Met Ile Arg Leu Leu Gly Leu Pro Val Asn Val
 250 255 260

 cag acc aag gtg gca gcc ggt gtg ctg tct gca ggc cat gca cgc gca 931
 Gln Thr Lys Val Ala Ala Gly Val Leu Ser Ala Gly His Ala Arg Ala
 265 270 275

 ttg ctg ggg ctc aag gcc ggc gag gat gct cag gac acc ctg gcg acc 979
 Leu Leu Gly Leu Lys Ala Gly Glu Asp Ala Gln Asp Thr Leu Ala Thr
 280 285 290

 cga atc atc gct gag ggc ctg tct gtg cgt gct act gag gaa ttg gtg 1027
 Arg Ile Ile Ala Glu Gly Leu Ser Val Arg Ala Thr Glu Glu Leu Val
 295 300 305

 ctg ctg cac aac cgt ggt gat cag gat gag gag aag aag cca cgc gaa 1075
 Leu Leu His Asn Arg Gly Asp Gln Asp Glu Glu Lys Lys Pro Arg Glu
 310 315 320 325

 aag gct gca act cct gag gtc ttt acc cgt gcg gct gag tcc ttg gcg 1123
 Lys Ala Ala Thr Pro Glu Val Phe Thr Arg Ala Ala Glu Ser Leu Ala
 330 335 340

 gat aat ttg gat acc aag gtc tcg gtg atg atg ggt aag aag aag ggc 1171
 Asp Asn Leu Asp Thr Lys Val Ser Val Met Met Gly Lys Lys Lys Gly
 345 350 355

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 Lys Leu Val Val Glu Phe Gly Asp Lys Asp Asp Phe Glu Arg Ile Met
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<210> 112

<211> 379

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 112

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 35 40 45

Thr Val Gly Ala Arg Thr Ala Ala Ala Pro Lys Arg Glu Ser Thr Pro
 50 55 60

Ala Ala Pro Ala Pro Glu Ala Pro Ala Gln Ala Ala Pro Gln His Thr

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Ser	Glu	Phe	Gly	Ala	Ser	Tyr	Leu	Glu	Ile	Pro	Ile	Glu	Gln	Ile	Arg
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Pro	Asn	Pro	Gln	Gln	Pro	Arg	His	Glu	Phe	Asp	Pro	Gln	Ala	Leu	Asp
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Val	Arg	Arg	Ser	Glu	Asp	Gly	Tyr	Glu	Leu	Ile	Met	Gly	Glu	Arg	Arg
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Arg	Glu	Thr	Glu	Asp	Ser	Ala	Met	Leu	Arg	Asp	Ala	Leu	Leu	Glu	Asn
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Ile	His	Arg	Val	Gln	Leu	Asn	Pro	Leu	Glu	Glu	Ala	Ala	Ala	Tyr	Gln
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Gln	Leu	Leu	Glu	Glu	Phe	Gly	Val	Thr	Gln	Ala	Glu	Leu	Ala	Asp	Lys
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Gly	His	Ala	Arg	Ala	Leu	Leu	Gly	Leu	Lys	Ala	Gly	Glu	Asp	Ala	Gln
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Asp	Thr	Leu	Ala	Thr	Arg	Ile	Ile	Ala	Glu	Gly	Leu	Ser	Val	Arg	Ala
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Thr	Glu	Glu	Leu	Val	Leu	Leu	His	Asn	Arg	Gly	Asp	Gln	Asp	Glu	Glu
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Lys	Lys	Pro	Arg	Glu	Lys	Ala	Ala	Thr	Pro	Glu	Val	Phe	Thr	Arg	Ala
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Ala	Glu	Ser	Leu	Ala	Asp	Asn	Leu	Asp	Thr	Lys	Val	Ser	Val	Met	Met
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Gly	Lys	Lys	Lys	Gly	Lys	Leu	Val	Val	Glu	Phe	Gly	Asp	Lys	Asp	Asp
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Met Phe Ala Pro Pro 5															
gaa ggt gac gat act gat gag gtt cgg cgc acc tat tta cgt cac ctg 163															
Glu Gly Asp Asp Thr Asp Glu Val Arg Arg Thr Tyr Leu Arg His Leu 20															
ggt gca ttg cgg gcg aaa gcg aca gat cac gcg gcg atg cag cgc agg 211															
Gly Ala Leu Arg Ala Lys Ala Thr Asp His Ala Ala Met Gln Arg Arg 35															
cat gaa tgg cac agg cat cct gat cca gca acc ttg tgg tcc acg ttg 259															
His Glu Trp His Arg His Pro Asp Pro Ala Thr Leu Trp Ser Thr Leu 50															
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Gly Thr Arg Arg Met Trp Glu Arg Thr Gln Asp Asp Gln Asp Cys Leu 65															
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Glu Ile Arg Phe Gly Leu Gly Val Thr Arg Leu Asp Pro Ala Ile Asn 85															
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Val Ser Asp Ser Gly Ala Pro Glu Asp Leu Asp Pro Val Cys Ala Val 100															
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Ser Leu Arg His Thr Ile Arg Asp Val Gly Ser Val Gln Ser Met Pro 115															
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Val Ser Val Gln Leu Gln Ala Phe Arg Phe Ile Gly Leu Asn Gly Ala 130															
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Gly Ala His Asp Leu Ala Arg Ala Leu Val Val Gln Leu Leu Tyr His 145															
cac gga ccg gag gtg gtg ggt atc aaa gcg atc ggg gag tcg ggt tgg 595															
His Gly Pro Glu Val Val Gly Ile Lys Ala Ile Gly Glu Ser Gly Trp 165															
gag tgg ctg aaa tgg gta ccg cac acc cgc gat ccg gag aag gca gcc 643															
Glu Trp Leu Lys Trp Val Pro His Thr Arg Asp Pro Glu Lys Ala Ala 180															
ttt cgg att ttg ctg gtg gat tcc gtg ttg acc aac ggc acc gaa agc 691															

Phe	Arg	Ile	Leu	Leu	Val	Asp	Ser	Val	Leu	Thr	Asn	Gly	Thr	Glu	Ser	
			185					190					195			
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Phe	Ile	Asp	Asp	Pro	Gln	Trp	Thr	Thr	Ile	Ile	Asn	Val	Gly	Ala	Gln	
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acc	agc	acc	gca	ttg	ggc	cag	ctg	gca	gag	gat	gaa	ggg	ctg	ctg	ttg	787
Thr	Ser	Thr	Ala	Leu	Gly	Gln	Leu	Ala	Glu	Asp	Glu	Gly	Leu	Leu	Leu	
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cac	gtc	gat	aag	cgt	ctg	cat	gtg	gct	acc	gcg	cac	ggc	gcg	gag	gag	835
His	Val	Asp	Lys	Arg	Leu	His	Val	Ala	Thr	Ala	His	Gly	Ala	Glu	Glu	
230				235						240					245	
ctg	ggc	acg	ccg	gat	gcg	gtt	agc	gct	gag	ctt	gcg	gag	gtt	ttt	ggc	883
Leu	Gly	Thr	Pro	Asp	Ala	Val	Ser	Ala	Glu	Leu	Ala	Glu	Val	Phe	Gly	
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Arg	Arg	Leu	Thr	Ala	Phe	Arg	Arg	Thr	Thr	Thr	Ala	His	Ala	Ala	Ser	
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Ser	Gly	Glu	Leu	Leu	Ser	Leu	Leu	Gly	Ile	Asp	Asp	Val	Glu	His	Leu	
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Thr	Pro	Glu	Thr	Leu	Trp	Met	Asn	Lys	Arg	Thr	Gln	Pro	Lys	Thr	Arg	
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Glu	Arg	Met	His	Asp	Ala	Ile	Ser	Gly	Glu	Met	Asn	Arg	Arg	Gln	Glu	
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Ser	Gln	Arg	Leu	Glu	Glu	Gly	Arg	Leu	Arg	Gly	Leu	Asp	Ser	His	Leu	
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Ser	Tyr	Arg	Ile	Gly	Leu	Lys	Thr	Phe	Ser	Ala	Ser	Glu	Ser	Arg	Gln	
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Gln	Arg	Gln	Asp	Pro	Leu	Leu	Ile	Asp	Phe	Ser	Leu	Thr	Gly	Gly	Ser	
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Lys Val Arg Arg Val Val Asp Glu Val Arg Gly Leu Ile Asn His Pro	
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 Lys Ser Ser Leu Ile Arg Thr Ile Val Thr Gly Leu Thr Ile Val Gly
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Pro	Val	Cys	Ala	Val	Ser	Leu	Arg	His	Thr	Ile	Arg	Asp	Val	Gly	Ser
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Ala	Glu	Val	Phe	Gly	Arg	Arg	Leu	Thr	Ala	Phe	Arg	Arg	Thr	Thr	Thr
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 Asp Glu Tyr Asn Gln Arg Asp Gly Val Lys Pro Met Pro Ala Leu Leu
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Ile Gln Pro Gly Glu Phe Ser Lys Ile Leu Leu Leu Leu Phe Phe Ala	
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Val Val Trp Ala Leu Ala Ile Leu Ile Met Ala Gly Ala Asn Asp Phe	
215 220 225	
ggg cct gca ctg ctg ctt ttc act acc gtt ttg gcc atg gtg tac ctg	835
Gly Pro Ala Leu Leu Phe Thr Thr Val Leu Ala Met Val Tyr Leu	
230 235 240 245	
gct acc ggc cgt ggt tcc tgg ctg ttg att ggt gct gtg ttg gtg gct	883
Ala Thr Gly Arg Gly Ser Trp Leu Leu Ile Gly Ala Val Leu Val Ala	
250 255 260	
gtc ggc gcg ttc acg gtg tac caa gtt tca agc aag att cag gaa cgc	931
Val Gly Ala Phe Thr Val Tyr Gln Val Ser Ser Lys Ile Gln Glu Arg	
265 270 275	
gtg caa aac ttc gtg gat cct gtg gcc cac tat gac acc acc ggt tac	979
Val Gln Asn Phe Val Asp Pro Val Ala His Tyr Asp Thr Thr Gly Tyr	
280 285 290	
cag ctg tcc cag tcc ttg ttt ggc atg agt tgg ggc gga atc acc ggc	1027
Gln Leu Ser Gln Ser Leu Phe Gly Met Ser Trp Gly Gly Ile Thr Gly	
295 300 305	
acc ggc att ggt cag ggt tac ccc aac atg atc cct gtc gtg cac tcg	1075
Thr Gly Ile Gly Gln Gly Tyr Pro Asn Met Ile Pro Val Val His Ser	
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Leu	Ala	Met	Gly	Asn	Glu	Leu	Gly	Thr	His	Ile	Leu	Met	Leu	Met	Gly
		35					40					45			
Gly	Tyr	Ile	Gly	Ile	Phe	Ile	Val	Ala	His	Leu	Ala	Met	Ala	Trp	Val
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Ala	Pro	Phe	Ala	Asp	Gln	Ile	Met	Leu	Pro	Val	Val	Ala	Val	Leu	Asn
65					70					75					80
Gly	Ile	Gly	Leu	Val	Met	Ile	Tyr	Arg	Leu	Asp	Glu	Ala	Thr	Gly	Tyr
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Ser	Thr	Val	Asn	Ser	Gln	Leu	Met	Trp	Thr	Val	Val	Gly	Val	Thr	Leu
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Met	Val	Ala	Val	Leu	Leu	Leu	Leu	Arg	Asp	Tyr	Lys	Ser	Leu	Ser	Arg
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Tyr Ser Tyr Leu Leu Gly Val Val Gly Ile Val Leu Leu Ala Leu Pro
 130 135 140
 Leu Val Trp Pro Gln Pro Gly Gly Val Glu Ala Arg Ile Trp Ile Trp
 145 150 155 160
 Leu Gly Pro Phe Ser Ile Gln Pro Gly Glu Phe Ser Lys Ile Leu Leu
 165 170 175
 Leu Leu Phe Phe Ala Gln Leu Leu Ala Thr Lys Arg Ala Leu Phe Thr
 180 185 190
 Val Ala Gly Tyr Arg Phe Leu Gly Met Asp Phe Pro Arg Leu Arg Asp
 195 200 205
 Leu Ala Pro Ile Leu Val Val Trp Ala Leu Ala Ile Leu Ile Met Ala
 210 215 220
 Gly Ala Asn Asp Phe Gly Pro Ala Leu Leu Leu Phe Thr Thr Val Leu
 225 230 235 240
 Ala Met Val Tyr Leu Ala Thr Gly Arg Gly Ser Trp Leu Leu Ile Gly
 245 250 255
 Ala Val Leu Val Ala Val Gly Ala Phe Thr Val Tyr Gln Val Ser Ser
 260 265 270
 Lys Ile Gln Glu Arg Val Gln Asn Phe Val Asp Pro Val Ala His Tyr
 275 280 285
 Asp Thr Thr Gly Tyr Gln Leu Ser Gln Ser Leu Phe Gly Met Ser Trp
 290 295 300
 Gly Gly Ile Thr Gly Thr Gly Ile Gly Gln Gly Tyr Pro Asn Met Ile
 305 310 315 320
 Pro Val Val His Ser Asp Phe Ile Leu Ala Ala Ile Gly Glu Glu Leu
 325 330 335
 Gly Leu Ile Gly Leu Ala Ala Ile Ile Val Leu Phe Gly Val Phe Val
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 Thr Arg Gly Met Arg Thr Ala Thr Leu Ala Arg Asp Ser Tyr Gly Lys
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 Leu Val Ala Ser Gly Leu Ser Met Thr Ile Met Ile Gln Ile Phe Val
 370 375 380
 Val Val Ala Gly Ile Ser Ser Leu Met Pro Met Thr Gly Leu Thr Thr
 385 390 395 400
 Pro Phe Met Ser Gln Gly Gly Ser Ser Leu Met Ala Asn Tyr Ile Leu
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 Ser Lys Gln Ala Ser Glu Val Ala Ala
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Trp	Glu	Asp	Thr	Pro	Ile	Ala	Ala	Ala	Ala	Arg	Arg	Ala	Ala	Gln	Val		
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Met	Thr	Pro	Asn	Ser	Leu	Thr	Leu	Pro	Lys	Pro	Lys	Glu	Pro	Arg	Leu		
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Ile	Thr	Ile	Ala	Asn	Gln	Lys	Gly	Gly	Val	Gly	Lys	Thr	Thr	Ser	Thr		
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gtg	aat	ttg	gct	gcg	tct	tta	gca	att	cat	ggg	ctt	aaa	ggt	ctc	gtc	307	
Val	Asn	Leu	Ala	Ala	Ser	Leu	Ala	Ile	His	Gly	Leu	Lys	Val	Leu	Val		
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Val	Asp	Leu	Asp	Pro	Gln	Gly	Asn	Ala	Ser	Thr	Ala	Leu	Gly	Val	Glu		
	70				75					80					85		
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His	Arg	Ser	Gly	Thr	Leu	Ser	Ser	Tyr	Glu	Leu	Leu	Ile	Gly	Glu	Cys		
				90					95					100			
act	gct	gat	gaa	gca	atg	cag	cca	tcc	aca	gct	aac	gaa	aac	ctc	ttc	451	
Thr	Ala	Asp	Glu	Ala	Met	Gln	Pro	Ser	Thr	Ala	Asn	Glu	Asn	Leu	Phe		
			105					110					115				
tgc	att	cca	gca	acc	ctg	gat	ctt	gct	ggc	gca	gaa	att	gaa	ttg	gtc	499	
Cys	Ile	Pro	Ala	Thr	Leu	Asp	Leu	Ala	Gly	Ala	Glu	Ile	Glu	Leu	Val		
		120					125					130					
agc	ttg	gtc	cg	cg	gaa	tac	cgt	ttg	gcg	gat	gcg	ttg	ggc	cgt	gag	547	
Ser	Leu	Val	Arg	Arg	Glu	Tyr	Arg	Leu	Ala	Asp	Ala	Leu	Gly	Arg	Glu		
	135					140					145						
ttc	att	gac	aag	cac	gat	ttt	gat	tac	atg	atc	att	gac	tgc	cca	ccg	595	
Phe	Ile	Asp	Lys	His	Asp	Phe	Asp	Tyr	Met	Ile	Ile	Asp	Cys	Pro	Pro		
	150				155				160						165		
tct	ttg	ggg	ctg	ctc	acc	att	aac	gcc	atg	acc	gcg	gtg	aat	gaa	gtg	643	
Ser	Leu	Gly	Leu	Leu	Thr	Ile	Asn	Ala	Met	Thr	Ala	Val	Asn	Glu	Val		
				170				175					180				

ctc att ccg atc cag tgt gag tac tac gct ctg gag ggc gtg ggc cag 691
 Leu Ile Pro Ile Gln Cys Glu Tyr Tyr Ala Leu Glu Gly Val Gly Gln
 185 190 195

cta ctg aac aac atc act atg ttg cgt cag cac ctg aac cgc cag ctg 739
 Leu Leu Asn Asn Ile Thr Met Leu Arg Gln His Leu Asn Arg Gln Leu
 200 205 210

cat att tcc gcg atc ttg ctg acc atg tat gac gcc cgc acc aac ctc 787
 His Ile Ser Ala Ile Leu Leu Thr Met Tyr Asp Ala Arg Thr Asn Leu
 215 220 225

gca gaa cag gtg gcc aca gag gtt aat gat cac ttc ggt gac gtg gtg 835
 Ala Glu Gln Val Ala Thr Glu Val Asn Asp His Phe Gly Asp Val Val
 230 235 240 245

ttg ggt aac aag att cca cgt tca gtg aag gtg tct gaa gct cct ggc 883
 Leu Gly Asn Lys Ile Pro Arg Ser Val Lys Val Ser Glu Ala Pro Gly
 250 255 260

tat ggg cag act gtc att gaa tat gat cca ggt tcc agg ggc gcc atg 931
 Tyr Gly Gln Thr Val Ile Glu Tyr Asp Pro Gly Ser Arg Gly Ala Met
 265 270 275

gcg tat ttg gat gct gct aaa gaa ttg gcc act cgt ggc gat tac ttg 979
 Ala Tyr Leu Asp Ala Ala Lys Glu Leu Ala Thr Arg Gly Asp Tyr Leu
 280 285 290

cct agc gat gaa tcc ggt ccg atc ggc cta aaa cct gcg aaa 1021
 Pro Ser Asp Glu Ser Gly Pro Ile Gly Leu Lys Pro Ala Lys
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tagcagtaaa cttctttgaa tac 1044

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<212> PRT

<213> Corynebacterium glutamicum

<400> 118

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Lys Glu Pro Arg Leu Ile Thr Ile Ala Asn Gln Lys Gly Gly Val Gly
 35 40 45

Lys Thr Thr Ser Thr Val Asn Leu Ala Ala Ser Leu Ala Ile His Gly
 50 55 60

Leu Lys Val Leu Val Val Asp Leu Asp Pro Gln Gly Asn Ala Ser Thr
 65 70 75 80

Ala Leu Gly Val Glu His Arg Ser Gly Thr Leu Ser Ser Tyr Glu Leu
 85 90 95

Leu Ile Gly Glu Cys Thr Ala Asp Glu Ala Met Gln Pro Ser Thr Ala

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Asn	Glu	Asn	Leu	Phe	Cys	Ile	Pro	Ala	Thr	Leu	Asp	Leu	Ala	Gly	Ala
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Glu	Ile	Glu	Leu	Val	Ser	Leu	Val	Arg	Arg	Glu	Tyr	Arg	Leu	Ala	Asp
	130					135					140				
Ala	Leu	Gly	Arg	Glu	Phe	Ile	Asp	Lys	His	Asp	Phe	Asp	Tyr	Met	Ile
145					150					155					160
Ile	Asp	Cys	Pro	Pro	Ser	Leu	Gly	Leu	Leu	Thr	Ile	Asn	Ala	Met	Thr
				165					170					175	
Ala	Val	Asn	Glu	Val	Leu	Ile	Pro	Ile	Gln	Cys	Glu	Tyr	Tyr	Ala	Leu
		180					185						190		
Glu	Gly	Val	Gly	Gln	Leu	Leu	Asn	Asn	Ile	Thr	Met	Leu	Arg	Gln	His
	195						200					205			
Leu	Asn	Arg	Gln	Leu	His	Ile	Ser	Ala	Ile	Leu	Leu	Thr	Met	Tyr	Asp
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Ala	Arg	Thr	Asn	Leu	Ala	Glu	Gln	Val	Ala	Thr	Glu	Val	Asn	Asp	His
225				230					235						240
Phe	Gly	Asp	Val	Val	Leu	Gly	Asn	Lys	Ile	Pro	Arg	Ser	Val	Lys	Val
			245						250					255	
Ser	Glu	Ala	Pro	Gly	Tyr	Gly	Gln	Thr	Val	Ile	Glu	Tyr	Asp	Pro	Gly
		260					265						270		
Ser	Arg	Gly	Ala	Met	Ala	Tyr	Leu	Asp	Ala	Ala	Lys	Glu	Leu	Ala	Thr
	275						280					285			
Arg	Gly	Asp	Tyr	Leu	Pro	Ser	Asp	Glu	Ser	Gly	Pro	Ile	Gly	Leu	Lys
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 <222> (101)..(754)
 <223> RXN02973

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 Val Ser Asp Ala Gly
 1 5
 aag aag gac tct tcc aag gtg gag atc gga ctg acc ggt cga ccc ctg 163
 Lys Lys Asp Ser Ser Lys Val Glu Ile Gly Leu Thr Gly Arg Pro Leu

Val Ser Asp Ala Gly Lys Lys Asp Ser Ser Lys Val Glu Ile Gly Leu
 1 5 10 15
 Thr Gly Arg Pro Leu Arg Glu Leu Pro Glu Pro Ser Pro Leu Glu Lys
 20 25 30
 His Gly Pro Ala Thr Ile Ile Ala Met Ala Asn Gln Lys Gly Gly Val
 35 40 45
 Gly Lys Thr Thr Ser Thr Ile Asn Leu Gly Ala Cys Leu Ala Glu Ala
 50 55 60
 Gly Arg Lys Val Leu Leu Val Asp Leu Asp Pro Gln Gly Ala Leu Thr
 65 70 75 80
 Ala Gly Leu Gly Ile His Tyr Asp Asp Val Asp Ile Thr Val Tyr Asp
 85 90 95
 Leu Met Val Asp Asn Asn Ser Thr Ile Asp Gln Ala Ile His His Thr
 100 105 110
 Gly Leu Pro Asp Leu Asp Val Val Pro Ala Asn Ile Asp Leu Ser Ala
 115 120 125
 Ala Glu Ile Gln Leu Val Asn Glu Val Gly Arg Glu Gln Thr Leu Ala
 130 135 140
 Arg Ala Leu Arg Pro Val Met Lys Asp Tyr Asp Phe Ile Ile Leu Asp
 145 150 155 160
 Cys Gln Pro Ser Leu Gly Leu Leu Thr Val Asn Ala Leu Ala Cys Ala
 165 170 175
 His Gly Val Ile Ile Pro Met Glu Cys Glu Asn Leu Ser Leu Arg Gly
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 Leu Ala Leu Leu Thr Asp Thr Val Glu Lys Val Ala Asp Arg Leu Asn
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 Phe Asp Leu Glu Ile Leu Gly Ile Leu Val
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<220>

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<223> FRXA01603

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 Val Ser Asp Ala Gly
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aag aag gac tct tcc aag gtg gag atc gga ctg acc ggt cga ccc ctg 163

Lys	Lys	Asp	Ser	Ser	Lys	Val	Glu	Ile	Gly	Leu	Thr	Gly	Arg	Pro	Leu		
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cgc	gag	ttg	cct	gag	cca	tct	cct	ttg	gaa	aaa	cat	ggc	cca	gca	acg	211	
Arg	Glu	Leu	Pro	Glu	Pro	Ser	Pro	Leu	Glu	Lys	His	Gly	Pro	Ala	Thr		
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Ile	Ile	Ala	Met	Ala	Asn	Gln	Lys	Gly	Gly	Val	Gly	Lys	Thr	Thr	Ser		
		40					45					50					
acc	atc	aac	ctc	gga	gca	tgc	ctt	gca	gag	gcg	gga	cgt	aaa	gtc	ctg	307	
Thr	Ile	Asn	Leu	Gly	Ala	Cys	Leu	Ala	Glu	Ala	Gly	Arg	Lys	Val	Leu		
		55				60					65						
ctc	gtt	gac	ttg	gat	ccg	caa	ggg	gcg	ttg	act	gct	ggg	ttg	gga	atc	355	
Leu	Val	Asp	Leu	Asp	Pro	Gln	Gly	Ala	Leu	Thr	Ala	Gly	Leu	Gly	Ile		
		70				75				80					85		
cac	tac	gac	gac	gtg	gat	atc	acc	gtg	tat	gac	ctc	atg	gtg	gac	aac	403	
His	Tyr	Asp	Asp	Val	Asp	Ile	Thr	Val	Tyr	Asp	Leu	Met	Val	Asp	Asn		
				90					95					100			
aat	tcc	acc	att	gat	cag	gcg	atc	cac	cac	act	ggg	ctt	cct	gat	ctg	451	
Asn	Ser	Thr	Ile	Asp	Gln	Ala	Ile	His	His	Thr	Gly	Leu	Pro	Asp	Leu		
			105					110					115				
gat	gtc	gtt	cct	gca	aat	att	gac	ttg	tcc	gct	gca	gaa	att	cag	ctg	499	
Asp	Val	Val	Pro	Ala	Asn	Ile	Asp	Leu	Ser	Ala	Ala	Glu	Ile	Gln	Leu		
			120				125						130				
gtc	aat	gaa	gtt	ggg	cgt	gaa	caa	aca	ctt	gcc	agg	gcg	ctg	cgt	cct	547	
Val	Asn	Glu	Val	Gly	Arg	Glu	Gln	Thr	Leu	Ala	Arg	Ala	Leu	Arg	Pro		
		135				140					145						
gtc	atg	aag	gac	tac	gac	ttc	atc	atc	ctt	gat	tgt	cag	cca	tca	ctt	595	
Val	Met	Lys	Asp	Tyr	Asp	Phe	Ile	Ile	Leu	Asp	Cys	Gln	Pro	Ser	Leu		
					155					160					165		
ggg	ctt	ttg	acg	gtg	aac	gct	ttg	gcg	tgc	gcg	cac	ggg	gtt	atc	atc	643	
Gly	Leu	Leu	Thr	Val	Asn	Ala	Leu	Ala	Cys	Ala	His	Gly	Val	Ile	Ile		
				170					175					180			
ccg	atg	gag	tgc	gag	tac	ttc	tca	ctg	cgt	ggc	ctc	gca	ttg	ctc	aca	691	
Pro	Met	Glu	Cys	Glu	Tyr	Phe	Ser	Leu	Arg	Gly	Leu	Ala	Leu	Leu	Thr		
			185					190					195				
gac	acc	gtg	gaa	aaa	gtt	gcc	gat	cgg	ttg							721	
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<213> Corynebacterium glutamicum

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							Val	Lys	His	Pro	Asp						
							1				5						
ccc	gcc	caa	aaa	gta	gag	ggc	acc	act	gcg	acc	acc	ccc	aca	aag	gtg	163	
Pro	Ala	Gln	Lys	Val	Glu	Gly	Thr	Thr	Ala	Thr	Thr	Pro	Thr	Lys	Val		
				10					15					20			
gct	gct	ttt	ttc	gat	ctg	gac	aag	acc	atc	atc	gcc	atg	agt	tcc	acc	211	
Ala	Ala	Phe	Phe	Asp	Leu	Asp	Lys	Thr	Ile	Ile	Ala	Met	Ser	Ser	Thr		
				25					30					35			

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Tyr Ala Tyr Gly Arg Glu Phe Met Asn Ser Gly Leu Ile Ser Pro Val	
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gaa gcc ctg caa tta agc ctc gcg caa gca acg tac atg ttc gcc ggc	307
Glu Ala Leu Gln Leu Ser Leu Ala Gln Ala Thr Tyr Met Phe Ala Gly	
55 60 65	
cac acc agt gaa caa atg gac aac acc cgc gac caa ctc acc gcc atg	355
His Thr Ser Glu Gln Met Asp Asn Thr Arg Asp Gln Leu Thr Ala Met	
70 75 80 85	
atc cgc ggc tgg gaa gtc caa cag gtg cgc tcg atc gcg gag gaa acc	403
Ile Arg Gly Trp Glu Val Gln Gln Val Arg Ser Ile Ala Glu Glu Thr	
90 95 100	
atg cat tcg gtg gtc act ccc acc atc tac gca gag gcc cgc gaa ctg	451
Met His Ser Val Val Thr Pro Thr Ile Tyr Ala Glu Ala Arg Glu Leu	
105 110 115	
atc gag cac cac cag gag ctc ggc cac gat gtc atc atc att tcc gcc	499
Ile Glu His His Gln Glu Leu Gly His Asp Val Ile Ile Ile Ser Ala	
120 125 130	
tct gtg aaa gaa ctg gtg gaa ccc atc gcc cgc gaa ctg ggt gta cat	547
Ser Val Lys Glu Leu Val Glu Pro Ile Ala Arg Glu Leu Gly Val His	
135 140 145	
aaa act gtc acc acc gtg ctt gaa gcc cac gac ggt atg tac acc ggt	595
Lys Thr Val Thr Thr Val Leu Glu Ala His Asp Gly Met Tyr Thr Gly	
150 155 160 165	
gaa gtg ctg ttt tac tgc aaa ggc gac gct aaa gcg cag tcc atc ctg	643
Glu Val Leu Phe Tyr Cys Lys Gly Asp Ala Lys Ala Gln Ser Ile Leu	
170 175 180	
gat ctc gcc gag gcg aac aat tac gac ctt tcc tta agc ttc gcc tac	691
Asp Leu Ala Glu Ala Asn Asn Tyr Asp Leu Ser Leu Ser Phe Ala Tyr	
185 190 195	
tcc gat tcc ttc acg gac ctg ccc atg ttg gaa gct gtc ggc aac ccg	739
Ser Asp Ser Phe Thr Asp Leu Pro Met Leu Glu Ala Val Gly Asn Pro	
200 205 210	
gcc gcc gtc aac ccc gac cgc gcg ctg aag aaa atc gcc ctt gaa cag	787
Ala Ala Val Asn Pro Asp Arg Ala Leu Lys Lys Ile Ala Leu Glu Gln	
215 220 225	
ggg tgg aaa atc tta agc ttc aaa aac cct gaa ccg ctg ttc caa atg	835
Gly Trp Lys Ile Leu Ser Phe Lys Asn Pro Glu Pro Leu Phe Gln Met	
230 235 240 245	
ccc agc acc cgc gac gtc ggc atc gga acc gga gtt gtt gcc ggc atc	883
Pro Ser Thr Arg Asp Val Gly Ile Gly Thr Gly Val Val Ala Gly Ile	
250 255 260	
gca gct gtt aca gca ggt agt atc tgg tgg atg aaa cgc gca cgg cgc	931
Ala Ala Val Thr Ala Gly Ser Ile Trp Trp Met Lys Arg Ala Arg Arg	
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 Gly Ser Ala
 280

963

<210> 124
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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Leu Ile Ser Pro Val Glu Ala Leu Gln Leu Ser Leu Ala Gln Ala Thr
 50 55 60
 Tyr Met Phe Ala Gly His Thr Ser Glu Gln Met Asp Asn Thr Arg Asp
 65 70 75 80
 Gln Leu Thr Ala Met Ile Arg Gly Trp Glu Val Gln Gln Val Arg Ser
 85 90 95
 Ile Ala Glu Glu Thr Met His Ser Val Val Thr Pro Thr Ile Tyr Ala
 100 105 110
 Glu Ala Arg Glu Leu Ile Glu His His Gln Glu Leu Gly His Asp Val
 115 120 125
 Ile Ile Ile Ser Ala Ser Val Lys Glu Leu Val Glu Pro Ile Ala Arg
 130 135 140
 Glu Leu Gly Val His Lys Thr Val Thr Thr Val Leu Glu Ala His Asp
 145 150 155 160
 Gly Met Tyr Thr Gly Glu Val Leu Phe Tyr Cys Lys Gly Asp Ala Lys
 165 170 175
 Ala Gln Ser Ile Leu Asp Leu Ala Glu Ala Asn Asn Tyr Asp Leu Ser
 180 185 190
 Leu Ser Phe Ala Tyr Ser Asp Ser Phe Thr Asp Leu Pro Met Leu Glu
 195 200 205
 Ala Val Gly Asn Pro Ala Ala Val Asn Pro Asp Arg Ala Leu Lys Lys
 210 215 220
 Ile Ala Leu Glu Gln Gly Trp Lys Ile Leu Ser Phe Lys Asn Pro Glu
 225 230 235 240
 Pro Leu Phe Gln Met Pro Ser Thr Arg Asp Val Gly Ile Gly Thr Gly
 245 250 255
 Val Val Ala Gly Ile Ala Ala Val Thr Ala Gly Ser Ile Trp Trp Met
 260 265 270

Lys Arg Ala Arg Arg Gly Ser Ala
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<210> 125

<211> 2898

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2875)

<223> RXN03028

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gtgaaagcga atttagaaat aaagaattaa ggggagagac atg ttc gag agg ttt 115
Met Phe Glu Arg Phe
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acc gat cgt gca cgc cgc gtg att gtg ctc gcg cag gaa gag gcg cgc 163
Thr Asp Arg Ala Arg Arg Val Ile Val Leu Ala Gln Glu Glu Ala Arg
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atg ctc aac cac aat tac atc ggc acg gag cac att ctc ctc ggc ctc 211
Met Leu Asn His Asn Tyr Ile Gly Thr Glu His Ile Leu Leu Gly Leu
25 30 35

att cac gag ggc gag ggc gtt gca gcc aag gct ttg gaa tcc atg gga 259
Ile His Glu Gly Glu Gly Val Ala Ala Lys Ala Leu Glu Ser Met Gly
40 45 50

att tcc ctg gac gcc gtc cgc cag gaa gtc gaa gag att atc ggc cag 307
Ile Ser Leu Asp Ala Val Arg Gln Glu Val Glu Glu Ile Ile Gly Gln
55 60 65

ggc tcc cag ccc acc acc ggc cac att cct ttt act cca cgt gcc aag 355
Gly Ser Gln Pro Thr Thr Gly His Ile Pro Phe Thr Pro Arg Ala Lys
70 75 80 85

aag gtc ctg gag ctc agc ctc cgc gaa ggc cta caa atg gga cac aag 403
Lys Val Leu Glu Leu Ser Leu Arg Glu Gly Leu Gln Met Gly His Lys
90 95 100

tac atc ggt act gag ttc ctg ctt ctc ggt ttg atc cgt gag ggc gag 451
Tyr Ile Gly Thr Glu Phe Leu Leu Leu Gly Leu Ile Arg Glu Gly Glu
105 110 115

ggc gtt gct gcc cag gtc ctg gtc aag ctt ggt gct gat ctg cca cgc 499
Gly Val Ala Ala Gln Val Leu Val Lys Leu Gly Ala Asp Leu Pro Arg
120 125 130

gtg cgt cag caa gtt att cag ctt ctc tcc ggc tac gaa ggt ggc cag 547
Val Arg Gln Gln Val Ile Gln Leu Leu Ser Gly Tyr Glu Gly Gly Gln
135 140 145

ggc gga tcc cca gag ggc ggc cag ggc gcc cct act ggc ggt gac gct 595
Gly Gly Ser Pro Glu Gly Gly Gln Gly Ala Pro Thr Gly Gly Asp Ala
150 155 160 165

gtt ggt gca gga gct gct cct ggc ggt cgt cca tct tcg ggc agc cca	643
Val Gly Ala Gly Ala Ala Pro Gly Gly Arg Pro Ser Ser Gly Ser Pro	
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ggc gag cgt tct acc tct ttg gtc ctt gac cag ttc ggc cgc aac ctc	691
Gly Glu Arg Ser Thr Ser Leu Val Leu Asp Gln Phe Gly Arg Asn Leu	
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Thr Gln Ala Ala Lys Asp Gly Lys Leu Asp Pro Val Val Gly Arg Asp	
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Lys Glu Ile Glu Arg Ile Met Gln Val Leu Ser Arg Arg Thr Lys Asn	
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aac cca gtt ctt att ggt gag cca ggt gtt ggt aag acc gca gtt gtt	835
Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly Lys Thr Ala Val Val	
230 235 240 245	
gaa ggt ctt gca cta gac att gtt aac ggc aag gtt cca gag acc ctc	883
Glu Gly Leu Ala Leu Asp Ile Val Asn Gly Lys Val Pro Glu Thr Leu	
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Lys Asp Lys Gln Val Tyr Ser Leu Asp Leu Gly Ser Leu Val Ala Gly	
265 270 275	
tcc cgt tac cgc ggt gac ttc gaa gag cga ctg aag aag gtc ctc aag	979
Ser Arg Tyr Arg Gly Asp Phe Glu Glu Arg Leu Lys Lys Val Leu Lys	
280 285 290	
gag att aac cag cgc ggc gac atc atc ctg ttt atc gat gag atc cac	1027
Glu Ile Asn Gln Arg Gly Asp Ile Ile Leu Phe Ile Asp Glu Ile His	
295 300 305	
acc ctc gtg ggt gca ggt gca gca gaa ggc gca atc gac gct gcc tcc	1075
Thr Leu Val Gly Ala Gly Ala Ala Glu Gly Ala Ile Asp Ala Ala Ser	
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Leu Leu Lys Pro Lys Leu Ala Arg Gly Glu Leu Gln Thr Ile Gly Ala	
330 335 340	
acc acc ctg gat gag tac cgt aag cac att gaa aag gac gca gct ctt	1171
Thr Thr Leu Asp Glu Tyr Arg Lys His Ile Glu Lys Asp Ala Ala Leu	
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Glu Arg Arg Phe Gln Pro Val Gln Val Pro Glu Pro Ser Val Asp Leu	
360 365 370	
acc gtt gag atc ttg aag ggt ctg cgc gac cgc tac gaa gct cac cac	1267
Thr Val Glu Ile Leu Lys Gly Leu Arg Asp Arg Tyr Glu Ala His His	
375 380 385	
cgc gta tcc atc acc gat ggt gct ctt act gca gca gct cag ctt gct	1315
Arg Val Ser Ile Thr Asp Gly Ala Leu Thr Ala Ala Ala Gln Leu Ala	
390 395 400 405	

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Asp	Arg	Tyr	Ile	Asn	Asp	Arg	Phe	Leu	Pro	Asp	Lys	Ala	Val	Asp	Leu	
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atc	gat	gag	gct	ggc	gcc	cgc	atg	cgc	atc	aag	cgc	atg	acc	gca	cct	1411
Ile	Asp	Glu	Ala	Gly	Ala	Arg	Met	Arg	Ile	Lys	Arg	Met	Thr	Ala	Pro	
			425					430					435			
tcc	tcc	ctc	cgc	gag	gtt	gat	gag	cgt	atc	gct	gat	gtt	cgc	cgt	gag	1459
Ser	Ser	Leu	Arg	Glu	Val	Asp	Glu	Arg	Ile	Ala	Asp	Val	Arg	Arg	Glu	
		440						445					450			
aag	gaa	gca	gcg	atc	gat	gct	cag	gac	ttt	gag	aag	gca	gca	ggc	ctt	1507
Lys	Glu	Ala	Ala	Ile	Asp	Ala	Gln	Asp	Phe	Glu	Lys	Ala	Ala	Gly	Leu	
	455					460					465					
cgc	gat	aag	gag	cgc	aag	ctc	ggc	gaa	gag	cgt	tca	gag	aag	gaa	aag	1555
Arg	Asp	Lys	Glu	Arg	Lys	Leu	Gly	Glu	Glu	Arg	Ser	Glu	Lys	Glu	Lys	
470					475					480					485	
cag	tgg	cgc	tcc	ggc	gac	ctc	gag	gac	atc	gct	gag	gtt	ggc	gaa	gag	1603
Gln	Trp	Arg	Ser	Gly	Asp	Leu	Glu	Asp	Ile	Ala	Glu	Val	Gly	Glu	Glu	
				490					495					500		
cag	atc	gca	gaa	gta	ctg	gcc	aac	tgg	act	ggc	att	cct	gtc	ttc	aag	1651
Gln	Ile	Ala	Glu	Val	Leu	Ala	Asn	Trp	Thr	Gly	Ile	Pro	Val	Phe	Lys	
			505					510					515			
ctc	acc	gaa	gct	gaa	tct	tca	cgc	ctg	ctc	aac	atg	gaa	gaa	gag	ttg	1699
Leu	Thr	Glu	Ala	Glu	Ser	Ser	Arg	Leu	Leu	Asn	Met	Glu	Glu	Glu	Leu	
		520					525						530			
cac	aag	cgc	atc	atc	gga	cag	gat	gaa	gct	gtc	aag	gct	gtc	tcc	cgt	1747
His	Lys	Arg	Ile	Ile	Gly	Gln	Asp	Glu	Ala	Val	Lys	Ala	Val	Ser	Arg	
	535					540					545					
gcg	atc	cgt	cgt	acc	cgt	gca	ggc	ctg	aag	gat	cct	aag	cgt	cct	tcc	1795
Ala	Ile	Arg	Arg	Thr	Arg	Ala	Gly	Leu	Lys	Asp	Pro	Lys	Arg	Pro	Ser	
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ggc	tcc	ttc	atc	ttc	gct	ggc	cca	tcc	ggc	gtt	ggc	aag	acc	gag	ctg	1843
Gly	Ser	Phe	Ile	Phe	Ala	Gly	Pro	Ser	Gly	Val	Gly	Lys	Thr	Glu	Leu	
				570					575					580		
tcc	aag	gct	ctc	gca	gga	ttc	ctc	ttc	ggc	gac	gat	gat	tcc	ctc	atc	1891
Ser	Lys	Ala	Leu	Ala	Gly	Phe	Leu	Phe	Gly	Asp	Asp	Asp	Ser	Leu	Ile	
			585					590					595			
caa	atc	gac	atg	ggc	gag	ttc	cac	gac	cgc	ttc	acc	gcg	tcc	cga	ctt	1939
Gln	Ile	Asp	Met	Gly	Glu	Phe	His	Asp	Arg	Phe	Thr	Ala	Ser	Arg	Leu	
		600					605					610				
ttc	ggc	gcc	cct	ccg	gga	tac	gtt	ggc	tac	gaa	gaa	ggc	ggc	cag	ctg	1987
Phe	Gly	Ala	Pro	Pro	Gly	Tyr	Val	Gly	Tyr	Glu	Glu	Gly	Gly	Gln	Leu	
	615					620					625					
acc	gag	aag	gtt	cgc	cgt	aag	cca	ttc	tcc	gtt	gtg	ctt	ttc	gac	gaa	2035
Thr	Glu	Lys	Val	Arg	Arg	Lys	Pro	Phe	Ser	Val	Val	Leu	Phe	Asp	Glu	
630					635					640					645	
atc	gag	aag	gcc	cac	aag	gag	atc	tac	aac	acc	ttg	ctg	cag	gtg	ttg	2083

Ile	Glu	Lys	Ala	His	Lys	Glu	Ile	Tyr	Asn	Thr	Leu	Leu	Gln	Val	Leu	
				650					655					660		
gaa	gat	ggt	cgc	ctt	acc	gat	ggt	cag	gga	cgc	atc	gtg	gac	ttc	aag	2131
Glu	Asp	Gly	Arg	Leu	Thr	Asp	Gly	Gln	Gly	Arg	Ile	Val	Asp	Phe	Lys	
			665					670					675			
aac	acc	gtc	ctg	atc	ttc	acc	tcc	aac	ctg	ggc	acc	gct	gac	atc	tcc	2179
Asn	Thr	Val	Leu	Ile	Phe	Thr	Ser	Asn	Leu	Gly	Thr	Ala	Asp	Ile	Ser	
		680					685					690				
aag	gct	gtt	ggc	ctg	ggc	ttc	tcc	gga	tcc	tcc	gag	act	gac	agc	gat	2227
Lys	Ala	Val	Gly	Leu	Gly	Phe	Ser	Gly	Ser	Ser	Glu	Thr	Asp	Ser	Asp	
	695					700					705					
gct	cag	tac	gac	cgc	atg	aag	aac	aag	gtc	cac	gac	gag	ctg	aag	aag	2275
Ala	Gln	Tyr	Asp	Arg	Met	Lys	Asn	Lys	Val	His	Asp	Glu	Leu	Lys	Lys	
710					715					720					725	
cac	ttc	cgc	cct	gag	ttc	ctg	aac	cgt	att	gat	gag	atc	gtg	gtc	ttc	2323
His	Phe	Arg	Pro	Glu	Phe	Leu	Asn	Arg	Ile	Asp	Glu	Ile	Val	Val	Phe	
				730					735					740		
cac	cag	ctc	acc	aag	gat	cag	atc	gtt	cag	atg	gtc	gac	ctt	ctt	atc	2371
His	Gln	Leu	Thr	Lys	Asp	Gln	Ile	Val	Gln	Met	Val	Asp	Leu	Leu	Ile	
			745					750					755			
ggt	cgc	gtt	tcc	aac	gca	ctg	gct	gag	aag	gac	atg	agc	atc	gaa	ctg	2419
Gly	Arg	Val	Ser	Asn	Ala	Leu	Ala	Glu	Lys	Asp	Met	Ser	Ile	Glu	Leu	
		760					765					770				
act	gag	aag	gcc	aag	gac	ctc	ctg	gct	aac	cga	ggc	ttc	gat	cca	gtt	2467
Thr	Glu	Lys	Ala	Lys	Asp	Leu	Leu	Ala	Asn	Arg	Gly	Phe	Asp	Pro	Val	
	775					780					785					
ctg	ggt	gca	cga	cca	ttg	cgt	cgc	acc	atc	cag	cgc	gaa	att	gaa	gac	2515
Leu	Gly	Ala	Arg	Pro	Leu	Arg	Arg	Thr	Ile	Gln	Arg	Glu	Ile	Glu	Asp	
790					795					800					805	
cag	atg	tcc	gag	aag	atc	ctc	ttc	ggt	gaa	atc	ggc	gca	ggc	gag	atc	2563
Gln	Met	Ser	Glu	Lys	Ile	Leu	Phe	Gly	Glu	Ile	Gly	Ala	Gly	Glu	Ile	
				810					815					820		
gtc	acc	gtt	gac	gtc	gaa	ggc	tgg	gac	ggc	gag	tcc	aag	gac	acc	gac	2611
Val	Thr	Val	Asp	Val	Glu	Gly	Trp	Asp	Gly	Glu	Ser	Lys	Asp	Thr	Asp	
			825					830					835			
cgt	gcg	aag	ttc	acc	ttc	aca	cca	cgt	cca	aag	cca	atg	cca	gaa	ggt	2659
Arg	Ala	Lys	Phe	Thr	Phe	Thr	Pro	Arg	Pro	Lys	Pro	Met	Pro	Glu	Gly	
		840					845					850				
aag	ttc	tct	gag	atc	tct	gtc	gag	gct	gcg	gaa	gca	att	caa	gat	gta	2707
Lys	Phe	Ser	Glu	Ile	Ser	Val	Glu	Ala	Ala	Glu	Ala	Ile	Gln	Asp	Val	
	855					860					865					
gat	tct	gca	gct	gac	ggc	gat	gtc	cca	gaa	acc	gat	tca	ctt	tcc	gac	2755
Asp	Ser	Ala	Ala	Asp	Gly	Asp	Val	Pro	Glu	Thr	Asp	Ser	Leu	Ser	Asp	
870					875					880					885	
att	gac	ctt	gaa	acc	ctt	gaa	aag	ttt	gag	gaa	gat	gta	gaa	aac	ggc	2803
Ile	Asp	Leu	Glu	Thr	Leu	Glu	Lys	Phe	Glu	Glu	Asp	Val	Glu	Asn	Gly	

	890	895	900	
acc gac att gat cag gtg tcc ggt gac tac tac ggc acc gat gat cag				2851
Thr Asp Ile Asp Gln Val Ser Gly Asp Tyr Tyr Gly Thr Asp Asp Gln				
	905	910	915	
gga ggc act gct cca agc aag gag tagcaacctt ttgaaaaagg gcc				2898
Gly Gly Thr Ala Pro Ser Lys Glu				
	920	925		

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<213> Corynebacterium glutamicum

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Ile Leu Leu Gly Leu Ile His Glu Gly Glu Gly Val Ala Ala Lys Ala				
35	40	45		

Leu Glu Ser Met Gly Ile Ser Leu Asp Ala Val Arg Gln Glu Val Glu				
50	55	60		

Glu Ile Ile Gly Gln Gly Ser Gln Pro Thr Thr Gly His Ile Pro Phe				
65	70	75	80	

Thr Pro Arg Ala Lys Lys Val Leu Glu Leu Ser Leu Arg Glu Gly Leu				
85	90	95		

Gln Met Gly His Lys Tyr Ile Gly Thr Glu Phe Leu Leu Leu Gly Leu				
100	105	110		

Ile Arg Glu Gly Glu Gly Val Ala Ala Gln Val Leu Val Lys Leu Gly				
115	120	125		

Ala Asp Leu Pro Arg Val Arg Gln Gln Val Ile Gln Leu Leu Ser Gly				
130	135	140		

Tyr Glu Gly Gly Gln Gly Gly Ser Pro Glu Gly Gly Gln Gly Ala Pro				
145	150	155	160	

Thr Gly Gly Asp Ala Val Gly Ala Gly Ala Ala Pro Gly Gly Arg Pro				
165	170	175		

Ser Ser Gly Ser Pro Gly Glu Arg Ser Thr Ser Leu Val Leu Asp Gln				
180	185	190		

Phe Gly Arg Asn Leu Thr Gln Ala Ala Lys Asp Gly Lys Leu Asp Pro				
195	200	205		

Val Val Gly Arg Asp Lys Glu Ile Glu Arg Ile Met Gln Val Leu Ser				
210	215	220		

Arg Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly				
225	230	235	240	

Lys Thr Ala Val Val Glu Gly Leu Ala Leu Asp Ile Val Asn Gly Lys
 245 250 255
 Val Pro Glu Thr Leu Lys Asp Lys Gln Val Tyr Ser Leu Asp Leu Gly
 260 265 270
 Ser Leu Val Ala Gly Ser Arg Tyr Arg Gly Asp Phe Glu Glu Arg Leu
 275 280 285
 Lys Lys Val Leu Lys Glu Ile Asn Gln Arg Gly Asp Ile Ile Leu Phe
 290 295 300
 Ile Asp Glu Ile His Thr Leu Val Gly Ala Gly Ala Ala Glu Gly Ala
 305 310 315 320
 Ile Asp Ala Ala Ser Leu Leu Lys Pro Lys Leu Ala Arg Gly Glu Leu
 325 330 335
 Gln Thr Ile Gly Ala Thr Thr Leu Asp Glu Tyr Arg Lys His Ile Glu
 340 345 350
 Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln Pro Val Gln Val Pro Glu
 355 360 365
 Pro Ser Val Asp Leu Thr Val Glu Ile Leu Lys Gly Leu Arg Asp Arg
 370 375 380
 Tyr Glu Ala His His Arg Val Ser Ile Thr Asp Gly Ala Leu Thr Ala
 385 390 395 400
 Ala Ala Gln Leu Ala Asp Arg Tyr Ile Asn Asp Arg Phe Leu Pro Asp
 405 410 415
 Lys Ala Val Asp Leu Ile Asp Glu Ala Gly Ala Arg Met Arg Ile Lys
 420 425 430
 Arg Met Thr Ala Pro Ser Ser Leu Arg Glu Val Asp Glu Arg Ile Ala
 435 440 445
 Asp Val Arg Arg Glu Lys Glu Ala Ala Ile Asp Ala Gln Asp Phe Glu
 450 455 460
 Lys Ala Ala Gly Leu Arg Asp Lys Glu Arg Lys Leu Gly Glu Glu Arg
 465 470 475 480
 Ser Glu Lys Glu Lys Gln Trp Arg Ser Gly Asp Leu Glu Asp Ile Ala
 485 490 495
 Glu Val Gly Glu Glu Gln Ile Ala Glu Val Leu Ala Asn Trp Thr Gly
 500 505 510
 Ile Pro Val Phe Lys Leu Thr Glu Ala Glu Ser Ser Arg Leu Leu Asn
 515 520 525
 Met Glu Glu Glu Leu His Lys Arg Ile Ile Gly Gln Asp Glu Ala Val
 530 535 540
 Lys Ala Val Ser Arg Ala Ile Arg Arg Thr Arg Ala Gly Leu Lys Asp
 545 550 555 560

Pro Lys Arg Pro Ser Gly Ser Phe Ile Phe Ala Gly Pro Ser Gly Val
 565 570 575
 Gly Lys Thr Glu Leu Ser Lys Ala Leu Ala Gly Phe Leu Phe Gly Asp
 580 585 590
 Asp Asp Ser Leu Ile Gln Ile Asp Met Gly Glu Phe His Asp Arg Phe
 595 600 605
 Thr Ala Ser Arg Leu Phe Gly Ala Pro Pro Gly Tyr Val Gly Tyr Glu
 610 615 620
 Glu Gly Gly Gln Leu Thr Glu Lys Val Arg Arg Lys Pro Phe Ser Val
 625 630 635 640
 Val Leu Phe Asp Glu Ile Glu Lys Ala His Lys Glu Ile Tyr Asn Thr
 645 650 655
 Leu Leu Gln Val Leu Glu Asp Gly Arg Leu Thr Asp Gly Gln Gly Arg
 660 665 670
 Ile Val Asp Phe Lys Asn Thr Val Leu Ile Phe Thr Ser Asn Leu Gly
 675 680 685
 Thr Ala Asp Ile Ser Lys Ala Val Gly Leu Gly Phe Ser Gly Ser Ser
 690 695 700
 Glu Thr Asp Ser Asp Ala Gln Tyr Asp Arg Met Lys Asn Lys Val His
 705 710 715 720
 Asp Glu Leu Lys Lys His Phe Arg Pro Glu Phe Leu Asn Arg Ile Asp
 725 730 735
 Glu Ile Val Val Phe His Gln Leu Thr Lys Asp Gln Ile Val Gln Met
 740 745 750
 Val Asp Leu Leu Ile Gly Arg Val Ser Asn Ala Leu Ala Glu Lys Asp
 755 760 765
 Met Ser Ile Glu Leu Thr Glu Lys Ala Lys Asp Leu Leu Ala Asn Arg
 770 775 780
 Gly Phe Asp Pro Val Leu Gly Ala Arg Pro Leu Arg Arg Thr Ile Gln
 785 790 795 800
 Arg Glu Ile Glu Asp Gln Met Ser Glu Lys Ile Leu Phe Gly Glu Ile
 805 810 815
 Gly Ala Gly Glu Ile Val Thr Val Asp Val Glu Gly Trp Asp Gly Glu
 820 825 830
 Ser Lys Asp Thr Asp Arg Ala Lys Phe Thr Phe Thr Pro Arg Pro Lys
 835 840 845
 Pro Met Pro Glu Gly Lys Phe Ser Glu Ile Ser Val Glu Ala Ala Glu
 850 855 860
 Ala Ile Gln Asp Val Asp Ser Ala Ala Asp Gly Asp Val Pro Glu Thr
 865 870 875 880
 Asp Ser Leu Ser Asp Ile Asp Leu Glu Thr Leu Glu Lys Phe Glu Glu

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 Met Phe Glu Arg Phe
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 Thr Asp Arg Ala Arg Arg Val Ile Val Leu Ala Gln Glu Glu Ala Arg
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 atg ctc aac cac aat tac atc ggc acg gag cac att ctc ctc ggc ctc 211
 Met Leu Asn His Asn Tyr Ile Gly Thr Glu His Ile Leu Leu Gly Leu
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 att cac gag ggc gag ggc gtt gca gcc aag gct ttg gaa tcc atg gga 259
 Ile His Glu Gly Glu Gly Val Ala Ala Lys Ala Leu Glu Ser Met Gly
 40 45 50
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 Ile Ser Leu Asp Ala Val Arg Gln Glu Val Glu Glu Ile Ile Gly Gln
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 ggc tcc cag ccc acc acc ggc cac att cct ttt act cca cgt gcc aag 355
 Gly Ser Gln Pro Thr Thr Gly His Ile Pro Phe Thr Pro Arg Ala Lys
 70 75 80 85
 aag gtc ctg gag ctc agc ctc cgc gaa ggc cta caa atg gga cac aag 403
 Lys Val Leu Glu Leu Ser Leu Arg Glu Gly Leu Gln Met Gly His Lys
 90 95 100
 tac atc ggt act gag ttc ctg ctt ctc ggt ttg atc cgt gag ggc gag 451
 Tyr Ile Gly Thr Glu Phe Leu Leu Leu Gly Leu Ile Arg Glu Gly Glu
 105 110 115
 ggc gtt gct gcc cag gtc ctg gtc aag ctt ggt gct gat ctg cca cgc 499
 Gly Val Ala Ala Gln Val Leu Val Lys Leu Gly Ala Asp Leu Pro Arg
 120 125 130
 gtg cgt cag caa gtt att cag ctt ctc tcc ggc tac gaa ggt ggc cag 547
 Val Arg Gln Gln Val Ile Gln Leu Leu Ser Gly Tyr Glu Gly Gly Gln
 135 140 145

ggc gga tcc cca gag ggc ggc cag ggc gcc cct act ggc ggt gac gct 595
 Gly Gly Ser Pro Glu Gly Gly Gln Gly Ala Pro Thr Gly Gly Asp Ala
 150 155 160 165

gtt ggt gca gga gct gct cct ggc ggt cgt cca tct tcg ggc agc cca 643
 Val Gly Ala Gly Ala Ala Pro Gly Gly Arg Pro Ser Ser Gly Ser Pro
 170 175 180

ggc gag cgt tct acc tct ttg gtc ctt gac cag ttc ggc cgc aac ctc 691
 Gly Glu Arg Ser Thr Ser Leu Val Leu Asp Gln Phe Gly Arg Asn Leu
 185 190 195

acc cag gct gca aag gac ggc aag ctg gat cca gtt gtt ggt cgc gat 739
 Thr Gln Ala Ala Lys Asp Gly Lys Leu Asp Pro Val Val Gly Arg Asp
 200 205 210

aag gaa atc gag cgc atc atg cag gtg ctc tcc cgt cgt acc aag aac 787
 Lys Glu Ile Glu Arg Ile Met Gln Val Leu Ser Arg Arg Thr Lys Asn
 215 220 225

aac cca gtt ctt att ggt gag cca ggt gtt ggt aag acc gca gtt gtt 835
 Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly Lys Thr Ala Val Val
 230 235 240 245

gaa ggt ctt gca cta gac att gtt aac ggc aag gtt cca gag acc ctc 883
 Glu Gly Leu Ala Leu Asp Ile Val Asn Gly Lys Val Pro Glu Thr Leu
 250 255 260

aag gac aag cag gtt tac tcc ctt gac tta ggt tcc ctg gtt gca ggt 931
 Lys Asp Lys Gln Val Tyr Ser Leu Asp Leu Gly Ser Leu Val Ala Gly
 265 270 275

tcc cgt tac cgc ggt gac ttc gaa gag cga ctg aag aag gtc ctc aag 979
 Ser Arg Tyr Arg Gly Asp Phe Glu Glu Arg Leu Lys Lys Val Leu Lys
 280 285 290

gag att aac cag cgc ggc gac atc atc ctg ttt atc gat gag atc cac 1027
 Glu Ile Asn Gln Arg Gly Asp Ile Ile Leu Phe Ile Asp Glu Ile His
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acc ctc gtg ggt gca ggt gca gca cga agg cgc aat cga cgc tgc ctc 1075
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cct gct taagccaaag cttgcccgcg gtg 1104
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<212> PRT

<213> Corynebacterium glutamicum

<400> 128

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Gln Glu Glu Ala Arg Met Leu Asn His Asn Tyr Ile Gly Thr Glu His
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Ile Leu Leu Gly Leu Ile His Glu Gly Glu Gly Val Ala Ala Lys Ala
 35 40 45
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 Glu Ile Ile Gly Gln Gly Ser Gln Pro Thr Thr Gly His Ile Pro Phe
 65 70 75 80
 Thr Pro Arg Ala Lys Lys Val Leu Glu Leu Ser Leu Arg Glu Gly Leu
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 Gln Met Gly His Lys Tyr Ile Gly Thr Glu Phe Leu Leu Leu Gly Leu
 100 105 110
 Ile Arg Glu Gly Glu Gly Val Ala Ala Gln Val Leu Val Lys Leu Gly
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 Ala Asp Leu Pro Arg Val Arg Gln Gln Val Ile Gln Leu Leu Ser Gly
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 Tyr Glu Gly Gly Gln Gly Gly Ser Pro Glu Gly Gly Gln Gly Ala Pro
 145 150 155 160
 Thr Gly Gly Asp Ala Val Gly Ala Gly Ala Ala Pro Gly Gly Arg Pro
 165 170 175
 Ser Ser Gly Ser Pro Gly Glu Arg Ser Thr Ser Leu Val Leu Asp Gln
 180 185 190
 Phe Gly Arg Asn Leu Thr Gln Ala Ala Lys Asp Gly Lys Leu Asp Pro
 195 200 205
 Val Val Gly Arg Asp Lys Glu Ile Glu Arg Ile Met Gln Val Leu Ser
 210 215 220
 Arg Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly
 225 230 235 240
 Lys Thr Ala Val Val Glu Gly Leu Ala Leu Asp Ile Val Asn Gly Lys
 245 250 255
 Val Pro Glu Thr Leu Lys Asp Lys Gln Val Tyr Ser Leu Asp Leu Gly
 260 265 270
 Ser Leu Val Ala Gly Ser Arg Tyr Arg Gly Asp Phe Glu Glu Arg Leu
 275 280 285
 Lys Lys Val Leu Lys Glu Ile Asn Gln Arg Gly Asp Ile Ile Leu Phe
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<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1933)

<223> FRXA02471

<400> 129

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 Val Gln His Glu Gly
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gca atc gac gct gcc tcc ctg ctt aag cca aag ctt gcc cgc ggt gaa 163
 Ala Ile Asp Ala Ala Ser Leu Leu Lys Pro Lys Leu Ala Arg Gly Glu
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ctg cag acc att ggt gca acc acc ctg gat gag tac cgt aag cac att 211
 Leu Gln Thr Ile Gly Ala Thr Thr Leu Asp Glu Tyr Arg Lys His Ile
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gaa aag gac gca gct ctt gag cgt cgt ttc cag cca gtg cag gtt cca 259
 Glu Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln Pro Val Gln Val Pro
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gag cct tcg gtt gat ctc acc gtt gag atc ttg aag ggt ctg cgc gac 307
 Glu Pro Ser Val Asp Leu Thr Val Glu Ile Leu Lys Gly Leu Arg Asp
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cgc tac gaa gct cac cac cgc gta tcc atc acc gat ggt gct ctt act 355
 Arg Tyr Glu Ala His His Arg Val Ser Ile Thr Asp Gly Ala Leu Thr
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gca gca gct cag ctt gct gat cgc tac atc aac gac cgc ttc ttg cca 403
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 90 95 100

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 Asp Lys Ala Val Asp Leu Ile Asp Glu Ala Gly Ala Arg Met Arg Ile
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aag cgc atg acc gca cct tcc tcc ctc cgc gag gtt gat gag cgt atc 499
 Lys Arg Met Thr Ala Pro Ser Ser Leu Arg Glu Val Asp Glu Arg Ile
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gct gat gtt cgc cgt gag aag gaa gca gcg atc gat gct cag gac ttt 547
 Ala Asp Val Arg Arg Glu Lys Glu Ala Ala Ile Asp Ala Gln Asp Phe
 135 140 145

gag aag gca gca ggt ctt cgc gat aag gag cgc aag ctc ggc gaa gag 595
 Glu Lys Ala Ala Gly Leu Arg Asp Lys Glu Arg Lys Leu Gly Glu Glu
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cgt tca gag aag gaa aag cag tgg cgc tcc ggc gac ctc gag gac atc 643
 Arg Ser Glu Lys Glu Lys Gln Trp Arg Ser Gly Asp Leu Glu Asp Ile
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gct gag gtt ggc gaa gag cag atc gca gaa gta ctg gcc aac tgg act 691
 Ala Glu Val Gly Glu Glu Gln Ile Ala Glu Val Leu Ala Asn Trp Thr

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Asn	Met	Glu	Glu	Glu	Leu	His	Lys	Arg	Ile	Ile	Gly	Gln	Asp	Glu	Ala		
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gtc	aag	gct	gtc	tcc	cgt	gcg	atc	cgt	cgt	acc	cgt	gca	ggt	ctg	aag	835	
Val	Lys	Ala	Val	Ser	Arg	Ala	Ile	Arg	Arg	Thr	Arg	Ala	Gly	Leu	Lys		
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Asp	Pro	Lys	Arg	Pro	Ser	Gly	Ser	Phe	Ile	Phe	Ala	Gly	Pro	Ser	Gly		
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gtt	ggt	aag	acc	gag	ctg	tcc	aag	gct	ctc	gca	gga	ttc	ctc	ttc	ggt	931	
Val	Gly	Lys	Thr	Glu	Leu	Ser	Lys	Ala	Leu	Ala	Gly	Phe	Leu	Phe	Gly		
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gac	gat	gat	tcc	ctc	atc	caa	atc	gac	atg	ggt	gag	ttc	cac	gac	cgc	979	
Asp	Asp	Asp	Ser	Leu	Ile	Gln	Ile	Asp	Met	Gly	Glu	Phe	His	Asp	Arg		
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Glu	Glu	Gly	Gly	Gln	Leu	Thr	Glu	Lys	Val	Arg	Arg	Lys	Pro	Phe	Ser		
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gtt	gtg	ctt	ttc	gac	gaa	atc	gag	aag	gcc	cac	aag	gag	atc	tac	aac	1123	
Val	Val	Leu	Phe	Asp	Glu	Ile	Glu	Lys	Ala	His	Lys	Glu	Ile	Tyr	Asn		
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acc	ttg	ctg	cag	gtg	ttg	gaa	gat	ggg	cgc	ctt	acc	gat	ggt	cag	gga	1171	
Thr	Leu	Leu	Gln	Val	Leu	Glu	Asp	Gly	Arg	Leu	Thr	Asp	Gly	Gln	Gly		
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cgc	atc	gtg	gac	ttc	aag	aac	acc	gtc	ctg	atc	ttc	acc	tcc	aac	ctg	1219	
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Gly	Thr	Ala	Asp	Ile	Ser	Lys	Ala	Val	Gly	Leu	Gly	Phe	Ser	Gly	Ser		
375							380					385					
tcc	gag	act	gac	agc	gat	gct	cag	tac	gac	cgc	atg	aag	aac	aag	gtc	1315	
Ser	Glu	Thr	Asp	Ser	Asp	Ala	Gln	Tyr	Asp	Arg	Met	Lys	Asn	Lys	Val		
390							395					400					
cac	gac	gag	ctg	aag	aag	cac	ttc	cgc	cct	gag	ttc	ctg	aac	cgt	att	1363	
His	Asp	Glu	Leu	Lys	Lys	His	Phe	Arg	Pro	Glu	Phe	Leu	Asn	Arg	Ile		
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 Met Val Asp Leu Leu Ile Gly Arg Val Ser Asn Ala Leu Ala Glu Lys
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gac atg agc atc gaa ctg act gag aag gcc aag gac ctc ctg gct aac 1507
 Asp Met Ser Ile Glu Leu Thr Glu Lys Ala Lys Asp Leu Leu Ala Asn
 455 460 465

cga ggc ttc gat cca gtt ctg ggt gca cga cca ttg cgt cgc acc atc 1555
 Arg Gly Phe Asp Pro Val Leu Gly Ala Arg Pro Leu Arg Arg Thr Ile
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cag cgc gaa att gaa gac cag atg tcc gag aag atc ctc ttc ggt gaa 1603
 Gln Arg Glu Ile Glu Asp Gln Met Ser Glu Lys Ile Leu Phe Gly Glu
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atc ggc gca ggc gag atc gtc acc gtt gac gtc gaa ggc tgg gac ggc 1651
 Ile Gly Ala Gly Glu Ile Val Thr Val Asp Val Glu Gly Trp Asp Gly
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 Glu Ser Lys Asp Thr Asp Arg Ala Lys Phe Thr Phe Thr Pro Arg Pro
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 Lys Pro Met Pro Glu Gly Lys Phe Ser Glu Ile Ser Val Glu Ala Ala
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 Glu Ala Ile Gln Asp Val Asp Ser Ala Ala Asp Gly Asp Val Pro Glu
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 Thr Asp Ser Leu Ser Asp Ile Asp Leu Glu Thr Leu Glu Lys Phe Glu
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<400> 130

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Tyr Arg Lys His Ile Glu Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln

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Asp	Arg	Phe	Leu	Pro	Asp	Lys	Ala	Val	Asp	Leu	Ile	Asp	Glu	Ala	Gly
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Ala	Arg	Met	Arg	Ile	Lys	Arg	Met	Thr	Ala	Pro	Ser	Ser	Leu	Arg	Glu
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Lys	Leu	Gly	Glu	Glu	Arg	Ser	Glu	Lys	Glu	Lys	Gln	Trp	Arg	Ser	Gly
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Asp	Leu	Glu	Asp	Ile	Ala	Glu	Val	Gly	Glu	Glu	Gln	Ile	Ala	Glu	Val
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Leu	Ala	Asn	Trp	Thr	Gly	Ile	Pro	Val	Phe	Lys	Leu	Thr	Glu	Ala	Glu
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Arg	Ala	Gly	Leu	Lys	Asp	Pro	Lys	Arg	Pro	Ser	Gly	Ser	Phe	Ile	Phe
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	275						280					285			
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Arg	Lys	Pro	Phe	Ser	Val	Val	Leu	Phe	Asp	Glu	Ile	Glu	Lys	Ala	His
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Lys	Glu	Ile	Tyr	Asn	Thr	Leu	Leu	Gln	Val	Leu	Glu	Asp	Gly	Arg	Leu
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Phe Thr Ser Asn Leu Gly Thr Ala Asp Ile Ser Lys Ala Val Gly Leu
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 Gly Phe Ser Gly Ser Ser Glu Thr Asp Ser Asp Ala Gln Tyr Asp Arg
 385 390 395 400
 Met Lys Asn Lys Val His Asp Glu Leu Lys Lys His Phe Arg Pro Glu
 405 410 415
 Phe Leu Asn Arg Ile Asp Glu Ile Val Val Phe His Gln Leu Thr Lys
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 Asp Gln Ile Val Gln Met Val Asp Leu Leu Ile Gly Arg Val Ser Asn
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 Ala Leu Ala Glu Lys Asp Met Ser Ile Glu Leu Thr Glu Lys Ala Lys
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 Asp Leu Leu Ala Asn Arg Gly Phe Asp Pro Val Leu Gly Ala Arg Pro
 465 470 475 480
 Leu Arg Arg Thr Ile Gln Arg Glu Ile Glu Asp Gln Met Ser Glu Lys
 485 490 495
 Ile Leu Phe Gly Glu Ile Gly Ala Gly Glu Ile Val Thr Val Asp Val
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 Glu Gly Trp Asp Gly Glu Ser Lys Asp Thr Asp Arg Ala Lys Phe Thr
 515 520 525
 Phe Thr Pro Arg Pro Lys Pro Met Pro Glu Gly Lys Phe Ser Glu Ile
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 Ser Val Glu Ala Ala Glu Ala Ile Gln Asp Val Asp Ser Ala Ala Asp
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 Gly Asp Val Pro Glu Thr Asp Ser Leu Ser Asp Ile Asp Leu Glu Thr
 565 570 575
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 Ser Lys Glu
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<210> 131

<211> 1875

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1852)

<223> RXN03094

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cca		act		acc		aaa		acc		aat		gaa		gcc		atg		cag		gct		gct		ctt		cag		cag		gca		163
Pro		Thr		Thr		Lys		Thr		Asn		Glu		Ala		Met		Gln		Ala		Ala		Leu		Gln		Gln		Ala		20
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Ile		Leu		Glu		Gln		Thr		Asp		Gly		Val		Ala		Ala		Pro		Val		Leu		Met		Ala		Thr		40
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Gly		Val		Asp		Pro		Lys		Glu		Ile		Leu		Ala		Glu		Ala		Lys		Lys		Leu		Val		Ala		55
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Ser		Tyr		Pro		Lys		Ala		Ser		Gly		Ala		Asn		Met		Ala		Asn		Pro		Asn		Phe		Asn		70
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Arg		Asp		Ala		Leu		Asn		Ala		Phe		Thr		Ala		Ala		Gln		Glu		Leu		Ala		Gly		Glu		90
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Leu		Gly		Asp		Glu		Tyr		Val		Ser		Thr		Glu		Val		Leu		Leu		Ala		Gly		Ile		Ala		105
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cca gaa tcc ctc aag ggc aaa act ctg atc agt ctt gat ctt ggt tcc	835
Pro Glu Ser Leu Lys Gly Lys Thr Leu Ile Ser Leu Asp Leu Gly Ser	
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Met Val Ala Gly Ala Lys Tyr Arg Gly Glu Phe Glu Glu Arg Leu Lys	
250 255 260	
gct gtt ctg gat gag atc aag gga gct aac ggc gaa gtc gtt acc ttc	931
Ala Val Leu Asp Glu Ile Lys Gly Ala Asn Gly Glu Val Val Thr Phe	
265 270 275	
atc gat gag ctg cac acc atc gtc ggc gct ggt gct tcg ggt gaa tcc	979
Ile Asp Glu Leu His Thr Ile Val Gly Ala Gly Ala Ser Gly Glu Ser	
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Glu Pro Thr Val Glu Asp Ala Ile Gly Ile Leu Arg Gly Leu Lys Glu	
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Arg Tyr Glu Val His His Gly Val Arg Ile Gln Asp Ser Ala Leu Val	
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gcc gca gct gaa ctc tca aac cgc tat atc acc agc cgt ttc ctt cct	1267
Ala Ala Ala Glu Leu Ser Asn Arg Tyr Ile Thr Ser Arg Phe Leu Pro	
375 380 385	
gat aag gct att gac tta gtt gat gag gca gca tca cgc ctg cgc atg	1315
Asp Lys Ala Ile Asp Leu Val Asp Glu Ala Ala Ser Arg Leu Arg Met	
390 395 400 405	
gag att gat tct tca cct cag gaa atc gat gag ctg gag cgt atc gtc	1363
Glu Ile Asp Ser Ser Pro Gln Glu Ile Asp Glu Leu Glu Arg Ile Val	
410 415 420	
cgc cgc ctc gag atc gaa gag atg gcg ctg tcc aag gaa tcc gat gca	1411
Arg Arg Leu Glu Ile Glu Glu Met Ala Leu Ser Lys Glu Ser Asp Ala	
425 430 435	
gct tcc aag gaa cgt cta gaa aag ctg cgc tcg gaa ctt gct gat gaa	1459
Ala Ser Lys Glu Arg Leu Glu Lys Leu Arg Ser Glu Leu Ala Asp Glu	
440 445 450	
cgc gaa aag ctc tct gag ttg aag gct cgt tgg cag aat gag aaa act	1507
Arg Glu Lys Leu Ser Glu Leu Lys Ala Arg Trp Gln Asn Glu Lys Thr	
455 460 465	

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 470 475 480 485

 tct gag tcg gat att gca aaa cgt gac ggc aat tat tgt cgt gtc gca 1603
 Ser Glu Ser Asp Ile Ala Lys Arg Asp Gly Asn Tyr Cys Arg Val Ala
 490 495 500

 aag ctt cgc tac ggc cga atc cct gag ctg gaa aag cag atc gag gat 1651
 Lys Leu Arg Tyr Gly Arg Ile Pro Glu Leu Glu Lys Gln Ile Glu Asp
 505 510 515

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 520 525 530

 gtc acg cca gac acg atc gcc gat gtg gtt tcc gca tgg acg ggc att 1747
 Val Thr Pro Asp Thr Ile Ala Asp Val Val Ser Ala Trp Thr Gly Ile
 535 540 545

 cct gca ggc aag atg atg cag ggt gag acc gag aag ctg ctc aac atg 1795
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 550 555 560 565

 gag cgc gtc ttg ggc aac cgt gtg gtc ggt cag cta gaa agc ggt aac 1843
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 Cys Ser Val

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<211> 584

<212> PRT

<213> Corynebacterium glutamicum

<400> 132

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 35 40 45

 Val Leu Met Ala Thr Gly Val Asp Pro Lys Glu Ile Leu Ala Glu Ala
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 Lys Lys Leu Val Ala Ser Tyr Pro Lys Ala Ser Gly Ala Asn Met Ala
 65 70 75 80

 Asn Pro Asn Phe Asn Arg Asp Ala Leu Asn Ala Phe Thr Ala Ala Gln
 85 90 95

 Glu Leu Ala Gly Glu Leu Gly Asp Glu Tyr Val Ser Thr Glu Val Leu
 100 105 110

 Leu Ala Gly Ile Ala Arg Gly Lys Ser Asp Ala Ala Asp Leu Leu Thr

115					120					125					
Asn	Lys	Gly	Ala	Thr	Tyr	Asp	Ala	Ile	Lys	Glu	Ala	Phe	Pro	Ser	Val
130						135					140				
Arg	Gly	Ser	Gln	Arg	Val	Thr	Thr	Gln	Asp	Pro	Glu	Gly	Gln	Phe	Gln
145					150					155					160
Ala	Leu	Glu	Lys	Tyr	Ser	Thr	Asp	Leu	Thr	Lys	Leu	Ala	Arg	Glu	Gly
				165					170					175	
Lys	Ile	Asp	Pro	Val	Ile	Gly	Arg	Asp	Gln	Glu	Ile	Arg	Arg	Val	Val
			180					185					190		
Gln	Val	Leu	Ser	Arg	Arg	Thr	Lys	Asn	Asn	Pro	Val	Leu	Ile	Gly	Glu
		195					200					205			
Pro	Gly	Val	Gly	Lys	Thr	Ala	Ile	Val	Glu	Gly	Leu	Ala	Arg	Arg	Ile
	210					215					220				
Val	Ala	Gly	Asp	Val	Pro	Glu	Ser	Leu	Lys	Gly	Lys	Thr	Leu	Ile	Ser
225					230					235					240
Leu	Asp	Leu	Gly	Ser	Met	Val	Ala	Gly	Ala	Lys	Tyr	Arg	Gly	Glu	Phe
				245					250					255	
Glu	Glu	Arg	Leu	Lys	Ala	Val	Leu	Asp	Glu	Ile	Lys	Gly	Ala	Asn	Gly
			260					265					270		
Glu	Val	Val	Thr	Phe	Ile	Asp	Glu	Leu	His	Thr	Ile	Val	Gly	Ala	Gly
		275					280					285			
Ala	Ser	Gly	Glu	Ser	Ala	Met	Asp	Ala	Gly	Asn	Met	Ile	Lys	Pro	Leu
	290					295					300				
Leu	Ala	Arg	Gly	Glu	Leu	Arg	Leu	Val	Gly	Ala	Thr	Thr	Leu	Asn	Glu
305					310					315					320
Tyr	Arg	Lys	Tyr	Ile	Glu	Lys	Asp	Ala	Ala	Leu	Glu	Arg	Arg	Phe	Gln
				325					330					335	
Gln	Val	Tyr	Val	Gly	Glu	Pro	Thr	Val	Glu	Asp	Ala	Ile	Gly	Ile	Leu
			340					345					350		
Arg	Gly	Leu	Lys	Glu	Arg	Tyr	Glu	Val	His	His	Gly	Val	Arg	Ile	Gln
		355					360					365			
Asp	Ser	Ala	Leu	Val	Ala	Ala	Ala	Glu	Leu	Ser	Asn	Arg	Tyr	Ile	Thr
	370					375					380				
Ser	Arg	Phe	Leu	Pro	Asp	Lys	Ala	Ile	Asp	Leu	Val	Asp	Glu	Ala	Ala
385					390					395					400
Ser	Arg	Leu	Arg	Met	Glu	Ile	Asp	Ser	Ser	Pro	Gln	Glu	Ile	Asp	Glu
				405					410					415	
Leu	Glu	Arg	Ile	Val	Arg	Arg	Leu	Glu	Ile	Glu	Glu	Met	Ala	Leu	Ser
			420					425					430		
Lys	Glu	Ser	Asp	Ala	Ala	Ser	Lys	Glu	Arg	Leu	Glu	Lys	Leu	Arg	Ser
		435					440					445			

Glu Leu Ala Asp Glu Arg Glu Lys Leu Ser Glu Leu Lys Ala Arg Trp
 450 455 460
 Gln Asn Glu Lys Thr Ala Ile Asp Asp Val Arg Glu Met Lys Glu Glu
 465 470 475 480
 Leu Glu Ala Leu Arg Ser Glu Ser Asp Ile Ala Lys Arg Asp Gly Asn
 485 490 495
 Tyr Cys Arg Val Ala Lys Leu Arg Tyr Gly Arg Ile Pro Glu Leu Glu
 500 505 510
 Lys Gln Ile Glu Asp Ala Glu Ser Lys Val Glu Val Asn Glu Asn Ala
 515 520 525
 Met Leu Thr Glu Glu Val Thr Pro Asp Thr Ile Ala Asp Val Val Ser
 530 535 540
 Ala Trp Thr Gly Ile Pro Ala Gly Lys Met Met Gln Gly Glu Thr Glu
 545 550 555 560
 Lys Leu Leu Asn Met Glu Arg Val Leu Gly Asn Arg Val Val Gly Gln
 565 570 575
 Leu Glu Ser Gly Asn Cys Ser Val
 580

<210> 133
 <211> 1816
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1816)
 <223> FRXA01668

<400> 133
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 ttgtgtaggt tggcgcccaa caaagaaagg gcgttgaaag atg agt tca ttc aat 115
 Met Ser Ser Phe Asn
 1 5
 cca act acc aaa acc aat gaa gcc atg cag gct gct ctt cag cag gca 163
 Pro Thr Thr Lys Thr Asn Glu Ala Met Gln Ala Ala Leu Gln Gln Ala
 10 15 20
 tcc tcg gct ggc aac cct gat att cgt cca gct cac ctg ttg gct gcc 211
 Ser Ser Ala Gly Asn Pro Asp Ile Arg Pro Ala His Leu Leu Ala Ala
 25 30 35
 atc ttg gag caa act gat ggc gta gca gcg cca gtc ctc atg gct act 259
 Ile Leu Glu Gln Thr Asp Gly Val Ala Ala Pro Val Leu Met Ala Thr
 40 45 50
 ggt gtg gat cct aag gag atc ctc gca gag gcc aag aag ttg gtt gct 307
 Gly Val Asp Pro Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu Val Ala
 55 60 65

tct tac ccc aag gct tct ggc gcc aat atg gct aat cca aac ttc aac	355
Ser Tyr Pro Lys Ala Ser Gly Ala Asn Met Ala Asn Pro Asn Phe Asn	
70 75 80 85	
cgg gat gcc ctc aat gcg ttc act gca gct cag gag ctt gcc ggt gag	403
Arg Asp Ala Leu Asn Ala Phe Thr Ala Ala Gln Glu Leu Ala Gly Glu	
90 95 100	
ttg ggc gat gag tac gtc tca acc gaa gta ctt ctt gcc ggt atc gct	451
Leu Gly Asp Glu Tyr Val Ser Thr Glu Val Leu Leu Ala Gly Ile Ala	
105 110 115	
cgc gga aag tct gat gct gcg gat ctg ttg acc aac aag ggt gca acc	499
Arg Gly Lys Ser Asp Ala Ala Asp Leu Leu Thr Asn Lys Gly Ala Thr	
120 125 130	
tat gac gcc atc aaa gag gct ttc cct tcg gtt cgt gga tct cag cgt	547
Tyr Asp Ala Ile Lys Glu Ala Phe Pro Ser Val Arg Gly Ser Gln Arg	
135 140 145	
gtc acc act cag gat cca gag gga cag ttc cag gct ttg gaa aag tac	595
Val Thr Thr Gln Asp Pro Glu Gly Gln Phe Gln Ala Leu Glu Lys Tyr	
150 155 160 165	
tcc act gac ctg acc aag ctt gct cgt gaa ggc aag att gat cct gtt	643
Ser Thr Asp Leu Thr Lys Leu Ala Arg Glu Gly Lys Ile Asp Pro Val	
170 175 180	
att ggc cgt gac cag gaa att cgt cgc gtc gtt cag gtg ctt agc cgt	691
Ile Gly Arg Asp Gln Glu Ile Arg Arg Val Val Gln Val Leu Ser Arg	
185 190 195	
cgt acc aag aac aac cct gtt ctg atc ggt gag cca ggt gtc ggt aaa	739
Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly Lys	
200 205 210	
acc gcc atc gtg gaa ggc ctt gca cgc cgc atc gtt gct ggt gac gtt	787
Thr Ala Ile Val Glu Gly Leu Ala Arg Arg Ile Val Ala Gly Asp Val	
215 220 225	
cca gaa tcc ctc aag ggc aaa act ctg atc agt ctt gat ctt ggt tcc	835
Pro Glu Ser Leu Lys Gly Lys Thr Leu Ile Ser Leu Asp Leu Gly Ser	
230 235 240 245	
atg gtt gcc ggc gct aag tat cgc ggt gaa ttc gag gag cga ctg aag	883
Met Val Ala Gly Ala Lys Tyr Arg Gly Glu Phe Glu Glu Arg Leu Lys	
250 255 260	
gct gtt ctg gat gag atc aag gga gct aac ggc gaa gtc gtt acc ttc	931
Ala Val Leu Asp Glu Ile Lys Gly Ala Asn Gly Glu Val Val Thr Phe	
265 270 275	
atc gat gag ctg cac acc atc gtc ggc gct ggt gct tcg ggt gaa tcc	979
Ile Asp Glu Leu His Thr Ile Val Gly Ala Gly Ala Ser Gly Glu Ser	
280 285 290	
gcc atg gat gcc gga aac atg att aag cca ctg ctt gcc cgc ggt gag	1027
Ala Met Asp Ala Gly Asn Met Ile Lys Pro Leu Leu Ala Arg Gly Glu	
295 300 305	

ctg cgc ttg gtt ggt gcc acc acg ctg aat gag tac cgc aag tac atc	1075
Leu Arg Leu Val Gly Ala Thr Thr Leu Asn Glu Tyr Arg Lys Tyr Ile	
310 315 320 325	
gaa aag gac gct gcc ctg gag cgt agg ttc cag cag gtt tat gtc ggt	1123
Glu Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln Gln Val Tyr Val Gly	
330 335 340	
gag cca acg gta gaa gat gcc atc ggt att ctt cgt gga ttg aag gaa	1171
Glu Pro Thr Val Glu Asp Ala Ile Gly Ile Leu Arg Gly Leu Lys Glu	
345 350 355	
cgc tac gag gtc cat cac ggt gtc cgc atc cag gac tcc gca ctg gtc	1219
Arg Tyr Glu Val His His Gly Val Arg Ile Gln Asp Ser Ala Leu Val	
360 365 370	
gcc gca gct gaa ctc tca aac cgc tat atc acc agc cgt ttc ctt cct	1267
Ala Ala Ala Glu Leu Ser Asn Arg Tyr Ile Thr Ser Arg Phe Leu Pro	
375 380 385	
gat aag gct att gac tta gtt gat gag gca gca tca cgc ctg cgc atg	1315
Asp Lys Ala Ile Asp Leu Val Asp Glu Ala Ala Ser Arg Leu Arg Met	
390 395 400 405	
gag att gat tct tca cct cag gaa atc gat gag ctg gag cgt atc gtc	1363
Glu Ile Asp Ser Ser Pro Gln Glu Ile Asp Glu Leu Glu Arg Ile Val	
410 415 420	
cgc cgc ctc gag atc gaa gag atg gcg ctg tcc aag gaa tcc gat gca	1411
Arg Arg Leu Glu Ile Glu Glu Met Ala Leu Ser Lys Glu Ser Asp Ala	
425 430 435	
gct tcc aag gaa cgt cta gaa aag ctg cgc tcg gaa ctt gct gat gaa	1459
Ala Ser Lys Glu Arg Leu Glu Lys Leu Arg Ser Glu Leu Ala Asp Glu	
440 445 450	
cgc gaa aag ctc tct gag ttg aag gct cgt tgg cag aat gag aaa act	1507
Arg Glu Lys Leu Ser Glu Leu Lys Ala Arg Trp Gln Asn Glu Lys Thr	
455 460 465	
gct att gac gat gtc cgg gag atg aaa gaa gag ctg gaa gcg ctg cgt	1555
Ala Ile Asp Asp Val Arg Glu Met Lys Glu Glu Leu Glu Ala Leu Arg	
470 475 480 485	
tct gag tcg gat att gca aaa cgt gac ggc aat tat tgt cgt gtc gca	1603
Ser Glu Ser Asp Ile Ala Lys Arg Asp Gly Asn Tyr Cys Arg Val Ala	
490 495 500	
aag ctt cgc tac ggc cga atc cct gag ctg gaa aag cag atc gag gat	1651
Lys Leu Arg Tyr Gly Arg Ile Pro Glu Leu Glu Lys Gln Ile Glu Asp	
505 510 515	
gca gaa tcc aag gtc gag gtc aat gaa aat gcc atg ctc act gag gag	1699
Ala Glu Ser Lys Val Glu Val Asn Glu Asn Ala Met Leu Thr Glu Glu	
520 525 530	
gtc acg cca gac acg atc gcc gat gtg gtt tcc gca tgg acg ggc att	1747
Val Thr Pro Asp Thr Ile Ala Asp Val Val Ser Ala Trp Thr Gly Ile	
535 540 545	
cct gca ggc aag atg atg cag ggt gag acc gag aag ctg ctc aac atg	1795

Pro Ala Gly Lys Met Met Gln Gly Glu Thr Glu Lys Leu Leu Asn Met
 550 555 560 565

gag cgc gtc ttg ggc aac ccg
 Glu Arg Val Leu Gly Asn Pro
 570

1816

<210> 134

<211> 572

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 134

Met Ser Ser Phe Asn Pro Thr Thr Lys Thr Asn Glu Ala Met Gln Ala
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Ala Leu Gln Gln Ala Ser Ser Ala Gly Asn Pro Asp Ile Arg Pro Ala
 20 25 30

His Leu Leu Ala Ala Ile Leu Glu Gln Thr Asp Gly Val Ala Ala Pro
 35 40 45

Val Leu Met Ala Thr Gly Val Asp Pro Lys Glu Ile Leu Ala Glu Ala
 50 55 60

Lys Lys Leu Val Ala Ser Tyr Pro Lys Ala Ser Gly Ala Asn Met Ala
 65 70 75 80

Asn Pro Asn Phe Asn Arg Asp Ala Leu Asn Ala Phe Thr Ala Ala Gln
 85 90 95

Glu Leu Ala Gly Glu Leu Gly Asp Glu Tyr Val Ser Thr Glu Val Leu
 100 105 110

Leu Ala Gly Ile Ala Arg Gly Lys Ser Asp Ala Ala Asp Leu Leu Thr
 115 120 125

Asn Lys Gly Ala Thr Tyr Asp Ala Ile Lys Glu Ala Phe Pro Ser Val
 130 135 140

Arg Gly Ser Gln Arg Val Thr Thr Gln Asp Pro Glu Gly Gln Phe Gln
 145 150 155 160

Ala Leu Glu Lys Tyr Ser Thr Asp Leu Thr Lys Leu Ala Arg Glu Gly
 165 170 175

Lys Ile Asp Pro Val Ile Gly Arg Asp Gln Glu Ile Arg Arg Val Val
 180 185 190

Gln Val Leu Ser Arg Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu
 195 200 205

Pro Gly Val Gly Lys Thr Ala Ile Val Glu Gly Leu Ala Arg Arg Ile
 210 215 220

Val Ala Gly Asp Val Pro Glu Ser Leu Lys Gly Lys Thr Leu Ile Ser
 225 230 235 240

Leu Asp Leu Gly Ser Met Val Ala Gly Ala Lys Tyr Arg Gly Glu Phe
 245 250 255

Glu Glu Arg Leu Lys Ala Val Leu Asp Glu Ile Lys Gly Ala Asn Gly
 260 265 270
 Glu Val Val Thr Phe Ile Asp Glu Leu His Thr Ile Val Gly Ala Gly
 275 280 285
 Ala Ser Gly Glu Ser Ala Met Asp Ala Gly Asn Met Ile Lys Pro Leu
 290 295 300
 Leu Ala Arg Gly Glu Leu Arg Leu Val Gly Ala Thr Thr Leu Asn Glu
 305 310 315 320
 Tyr Arg Lys Tyr Ile Glu Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln
 325 330 335
 Gln Val Tyr Val Gly Glu Pro Thr Val Glu Asp Ala Ile Gly Ile Leu
 340 345 350
 Arg Gly Leu Lys Glu Arg Tyr Glu Val His His Gly Val Arg Ile Gln
 355 360 365
 Asp Ser Ala Leu Val Ala Ala Ala Glu Leu Ser Asn Arg Tyr Ile Thr
 370 375 380
 Ser Arg Phe Leu Pro Asp Lys Ala Ile Asp Leu Val Asp Glu Ala Ala
 385 390 395 400
 Ser Arg Leu Arg Met Glu Ile Asp Ser Ser Pro Gln Glu Ile Asp Glu
 405 410 415
 Leu Glu Arg Ile Val Arg Arg Leu Glu Ile Glu Glu Met Ala Leu Ser
 420 425 430
 Lys Glu Ser Asp Ala Ala Ser Lys Glu Arg Leu Glu Lys Leu Arg Ser
 435 440 445
 Glu Leu Ala Asp Glu Arg Glu Lys Leu Ser Glu Leu Lys Ala Arg Trp
 450 455 460
 Gln Asn Glu Lys Thr Ala Ile Asp Asp Val Arg Glu Met Lys Glu Glu
 465 470 475 480
 Leu Glu Ala Leu Arg Ser Glu Ser Asp Ile Ala Lys Arg Asp Gly Asn
 485 490 495
 Tyr Cys Arg Val Ala Lys Leu Arg Tyr Gly Arg Ile Pro Glu Leu Glu
 500 505 510
 Lys Gln Ile Glu Asp Ala Glu Ser Lys Val Glu Val Asn Glu Asn Ala
 515 520 525
 Met Leu Thr Glu Glu Val Thr Pro Asp Thr Ile Ala Asp Val Val Ser
 530 535 540
 Ala Trp Thr Gly Ile Pro Ala Gly Lys Met Met Gln Gly Glu Thr Glu
 545 550 555 560
 Lys Leu Leu Asn Met Glu Arg Val Leu Gly Asn Pro
 565 570

<400> 136

Val Ile Ser Asn Gly Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile
 1 5 10 15
 Asp Ala Leu Pro Met Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr
 20 25 30
 Gly Val Thr Gln Val Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala
 35 40 45
 His Thr Cys Gly His Asp Val His Ile Ser Ser Leu Leu Gly Ala Val
 50 55 60
 Gln Ala Phe Asn Ser His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala
 65 70 75 80
 Val Phe Gln Pro Ala Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala
 85 90 95
 Asp Gln Asp Asn Ala Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp
 100 105 110
 Met Gln Pro Thr Leu Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala
 115 120 125
 Ser Ala Trp Leu Val Lys
 130

<210> 137
 <211> 1308
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1285)
 <223> RXN03077

<400> 137
 accccgatcc tttgttttcg tgggatcact attagactcg actctaccgc gctgcaggtt 60
 ttcttgatac gcctgcggac aaaacagaaa ggtatttcac gtg atg gaa att ggt 115
 Val Met Glu Ile Gly
 1 5
 gtg cag gtt gcc tca tgg atg gac cgc cac cat gac gag gtc ata aag 163
 Val Gln Val Ala Ser Trp Met Asp Arg His His Asp Glu Val Ile Lys
 10 15 20
 tgg cgc agg cat ttg cac agc cat cct gag ctc tcc cac atg gaa tac 211
 Trp Arg Arg His Leu His Ser His Pro Glu Leu Ser His Met Glu Tyr
 25 30 35
 cgc acg act gag tat ttg gcc tcg gtt ctg aaa gat cac ggc atg gaa 259
 Arg Thr Thr Glu Tyr Leu Ala Ser Val Leu Lys Asp His Gly Met Glu
 40 45 50
 cca cac ctg ttc cca gga acc ggt ttg atg gtg gat atc gga cca gaa 307
 Pro His Leu Phe Pro Gly Thr Gly Leu Met Val Asp Ile Gly Pro Glu
 55 60 65

ggg gac tcc cgc ctg gcg ttt cgc gct gat atc gat gcc ctt ccg ctg	355
Gly Asp Ser Arg Leu Ala Phe Arg Ala Asp Ile Asp Ala Leu Pro Leu	
70 75 80 85	
ctt gaa tca acc ggc tta gag ttc tct tcc aca gcc act ggc gtt gcg	403
Leu Glu Ser Thr Gly Leu Glu Phe Ser Ser Thr Ala Thr Gly Val Ala	
90 95 100	
cat gcc tgc gga cat gac gtg cac acg gtg atc gct ttg gca ctt gcc	451
His Ala Cys Gly His Asp Val His Thr Val Ile Ala Leu Ala Leu Ala	
105 110 115	
tgt gca ctg aac acc atc gaa ctg ccc atc ggc att cgg gtg att ttc	499
Cys Ala Leu Asn Thr Ile Glu Leu Pro Ile Gly Ile Arg Val Ile Phe	
120 125 130	
cag ccg gca gaa gaa gtc atg act ggt ggc gca acg gac gtc att gcc	547
Gln Pro Ala Glu Glu Val Met Thr Gly Gly Ala Thr Asp Val Ile Ala	
135 140 145	
cac ggt ggc ctt gat ggt gtg gat gcg att tac gcc atc cac gtt gaa	595
His Gly Gly Leu Asp Gly Val Asp Ala Ile Tyr Ala Ile His Val Glu	
150 155 160 165	
ccc aaa ttg aag gtc ggt cgc gtc ggt gta cgc gct ggc gcg att act	643
Pro Lys Leu Lys Val Gly Arg Val Gly Val Arg Ala Gly Ala Ile Thr	
170 175 180	
tct gcc tca gat gtg atc gaa atc aga gtc aag ggt gaa gga gga cat	691
Ser Ala Ser Asp Val Ile Glu Ile Arg Val Lys Gly Glu Gly His	
185 190 195	
agc gca cgt cca cac ctc tcc gct gat gtt gtt tac gcc ttg agc aaa	739
Ser Ala Arg Pro His Leu Ser Ala Asp Val Val Tyr Ala Leu Ser Lys	
200 205 210	
ttg gtc gtt gat ctt ccc ggt ttg ctg tcc agg cgc gtc gat cca cgc	787
Leu Val Val Asp Leu Pro Gly Leu Leu Ser Arg Arg Val Asp Pro Arg	
215 220 225	
acc ggc acc gtg ctt gtt ttc ggc acc atc aac gcc ggc tat gcg ccc	835
Thr Gly Thr Val Leu Val Phe Gly Thr Ile Asn Ala Gly Tyr Ala Pro	
230 235 240 245	
aac gcg atc cca gat tcc ggc atc gtg tca ggc acc ttg cgt aca gcc	883
Asn Ala Ile Pro Asp Ser Gly Ile Val Ser Gly Thr Leu Arg Thr Ala	
250 255 260	
gac atc tct acc tgg cgt gac atg cgt ccg ctt atc tct gag ctg gtg	931
Asp Ile Ser Thr Trp Arg Asp Met Arg Pro Leu Ile Ser Glu Leu Val	
265 270 275	
gaa cag gtg ctc gca ccc acc gga gtc acc cat gaa ctg atc tac aat	979
Glu Gln Val Leu Ala Pro Thr Gly Val Thr His Glu Leu Ile Tyr Asn	
280 285 290	
ccg ggt gtt cca cca gtg ctt aac gac gat gtc gcc acc gct ttg ttg	1027
Pro Gly Val Pro Pro Val Leu Asn Asp Asp Val Ala Thr Ala Leu Leu	
295 300 305	
gca agc gca gca cgc gac atg gac aca caa tct gtt gtc caa gcg ccg	1075

Ala Ser Ala Ala Arg Asp Met Asp Thr Gln Ser Val Val Gln Ala Pro
 310 315 320 325

cag tca tcc ggt gga gaa gac ttc tcg tgg tac ctt gaa cac gtc cca 1123
 Gln Ser Ser Gly Gly Glu Asp Phe Ser Trp Tyr Leu Glu His Val Pro
 330 335 340

gga tca atg gcc cgg ttg ggt tgc tgg ccg ggg cac gga ccc aag caa 1171
 Gly Ser Met Ala Arg Leu Gly Cys Trp Pro Gly His Gly Pro Lys Gln
 345 350 355

gac ctc cat caa agt gac ctg gtt gtg gat gag cga gcc atc gga gtt 1219
 Asp Leu His Gln Ser Asp Leu Val Val Asp Glu Arg Ala Ile Gly Val
 360 365 370

ggc gtc agg ctc ttt ggc tcc ctt gtg cag cag tac agt agc cga tct 1267
 Gly Val Arg Leu Phe Gly Ser Leu Val Gln Gln Tyr Ser Ser Arg Ser
 375 380 385

gaa gct ttc tta aat tcc taatgggggt agtgtgtagg gct 1308
 Glu Ala Phe Leu Asn Ser
 390 395

<210> 138

<211> 395

<212> PRT

<213> Corynebacterium glutamicum

<400> 138

Val Met Glu Ile Gly Val Gln Val Ala Ser Trp Met Asp Arg His His
 1 5 10 15

Asp Glu Val Ile Lys Trp Arg Arg His Leu His Ser His Pro Glu Leu
 20 25 30

Ser His Met Glu Tyr Arg Thr Thr Glu Tyr Leu Ala Ser Val Leu Lys
 35 40 45

Asp His Gly Met Glu Pro His Leu Phe Pro Gly Thr Gly Leu Met Val
 50 55 60

Asp Ile Gly Pro Glu Gly Asp Ser Arg Leu Ala Phe Arg Ala Asp Ile
 65 70 75 80

Asp Ala Leu Pro Leu Leu Glu Ser Thr Gly Leu Glu Phe Ser Ser Thr
 85 90 95

Ala Thr Gly Val Ala His Ala Cys Gly His Asp Val His Thr Val Ile
 100 105 110

Ala Leu Ala Leu Ala Cys Ala Leu Asn Thr Ile Glu Leu Pro Ile Gly
 115 120 125

Ile Arg Val Ile Phe Gln Pro Ala Glu Glu Val Met Thr Gly Gly Ala
 130 135 140

Thr Asp Val Ile Ala His Gly Gly Leu Asp Gly Val Asp Ala Ile Tyr
 145 150 155 160

Ala Ile His Val Glu Pro Lys Leu Lys Val Gly Arg Val Gly Val Arg

165										170					175				
Ala	Gly	Ala	Ile	Thr	Ser	Ala	Ser	Asp	Val	Ile	Glu	Ile	Arg	Val	Lys				
			180					185					190						
Gly	Glu	Gly	Gly	His	Ser	Ala	Arg	Pro	His	Leu	Ser	Ala	Asp	Val	Val				
		195					200					205							
Tyr	Ala	Leu	Ser	Lys	Leu	Val	Val	Asp	Leu	Pro	Gly	Leu	Leu	Ser	Arg				
	210					215					220								
Arg	Val	Asp	Pro	Arg	Thr	Gly	Thr	Val	Leu	Val	Phe	Gly	Thr	Ile	Asn				
225					230				235						240				
Ala	Gly	Tyr	Ala	Pro	Asn	Ala	Ile	Pro	Asp	Ser	Gly	Ile	Val	Ser	Gly				
				245					250					255					
Thr	Leu	Arg	Thr	Ala	Asp	Ile	Ser	Thr	Trp	Arg	Asp	Met	Arg	Pro	Leu				
			260					265					270						
Ile	Ser	Glu	Leu	Val	Glu	Gln	Val	Leu	Ala	Pro	Thr	Gly	Val	Thr	His				
		275					280					285							
Glu	Leu	Ile	Tyr	Asn	Pro	Gly	Val	Pro	Pro	Val	Leu	Asn	Asp	Asp	Val				
	290					295					300								
Ala	Thr	Ala	Leu	Leu	Ala	Ser	Ala	Ala	Arg	Asp	Met	Asp	Thr	Gln	Ser				
305					310				315						320				
Val	Val	Gln	Ala	Pro	Gln	Ser	Ser	Gly	Gly	Glu	Asp	Phe	Ser	Trp	Tyr				
				325					330					335					
Leu	Glu	His	Val	Pro	Gly	Ser	Met	Ala	Arg	Leu	Gly	Cys	Trp	Pro	Gly				
			340					345					350						
His	Gly	Pro	Lys	Gln	Asp	Leu	His	Gln	Ser	Asp	Leu	Val	Val	Asp	Glu				
		355					360					365							
Arg	Ala	Ile	Gly	Val	Gly	Val	Arg	Leu	Phe	Gly	Ser	Leu	Val	Gln	Gln				
	370					375					380								
Tyr	Ser	Ser	Arg	Ser	Glu	Ala	Phe	Leu	Asn	Ser									
385					390				395										

<210> 139

<211> 1308

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1285)

<223> FRXA02855

<400> 139

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 ttcttgatag gcctgcggac aaaacagaaa ggtatttcac gtg atg gaa att ggt 115
 Val Met Glu Ile Gly
 1 5

gtg	cag	gtt	gcc	tca	tgg	atg	gac	cgc	cac	cat	gac	gag	gtc	ata	aag	163
Val	Gln	Val	Ala	Ser	Trp	Met	Asp	Arg	His	His	Asp	Glu	Val	Ile	Lys	
			10					15					20			
tgg	cgc	agg	cat	ttg	cac	agc	cat	cct	gag	ctc	tcc	cac	atg	gaa	tac	211
Trp	Arg	Arg	His	Leu	His	Ser	His	Pro	Glu	Leu	Ser	His	Met	Glu	Tyr	
			25					30					35			
cgc	acg	act	gag	tat	ttg	gcc	tcg	gtt	ctg	aaa	gat	cac	ggc	atg	gaa	259
Arg	Thr		Glu	Tyr	Leu	Ala	Ser	Val	Leu	Lys	Asp	His	Gly	Met	Glu	
		40					45					50				
cca	cac	ctg	ttc	cca	gga	acc	ggg	ttg	atg	gtg	gat	atc	gga	cca	gaa	307
Pro	His	Leu	Phe	Pro	Gly	Thr	Gly	Leu	Met	Val	Asp	Ile	Gly	Pro	Glu	
	55					60					65					
ggg	gac	tcc	cgc	ctg	gcg	ttt	cgc	gct	gat	atc	gat	gcc	ctt	ccg	ctg	355
Gly	Asp	Ser	Arg	Leu	Ala	Phe	Arg	Ala	Asp	Ile	Asp	Ala	Leu	Pro	Leu	
70					75				80					85		
ctt	gaa	tca	acc	ggc	tta	gag	ttc	tct	tcc	aca	gcc	act	ggc	gtt	gcg	403
Leu	Glu	Ser	Thr	Gly	Leu	Glu	Phe	Ser	Ser	Thr	Ala	Thr	Gly	Val	Ala	
			90					95					100			
cat	gcc	tgc	gga	cat	gac	gtg	cac	acg	gtg	atc	gct	ttg	gca	ctt	gcc	451
His	Ala	Cys	Gly	His	Asp	Val	His	Thr	Val	Ile	Ala	Leu	Ala	Leu	Ala	
			105					110				115				
tgt	gca	ctg	aac	acc	atc	gaa	ctg	ccc	atc	ggc	att	cgg	gtg	att	ttc	499
Cys	Ala	Leu	Asn	Thr	Ile	Glu	Leu	Pro	Ile	Gly	Ile	Arg	Val	Ile	Phe	
		120					125					130				
cag	ccg	gca	gaa	gaa	gtc	atg	act	ggg	ggc	gca	acg	gac	gtc	att	gcc	547
Gln	Pro	Ala	Glu	Glu	Val	Met	Thr	Gly	Gly	Ala	Thr	Asp	Val	Ile	Ala	
	135					140					145					
cac	ggg	ggc	ctt	gat	ggg	gtg	gat	gcg	att	tac	gcc	atc	cac	gtt	gaa	595
His	Gly	Gly	Leu	Asp	Gly	Val	Asp	Ala	Ile	Tyr	Ala	Ile	His	Val	Glu	
150					155				160					165		
ccc	aaa	ttg	aag	gtc	ggg	cgc	gtc	ggg	gta	cgc	gct	ggc	gcg	att	act	643
Pro	Lys	Leu	Lys	Val	Gly	Arg	Val	Gly	Val	Arg	Ala	Gly	Ala	Ile	Thr	
				170				175						180		
tct	gcc	tca	gat	gtg	atc	gaa	atc	aga	gtc	aag	ggg	gaa	gga	gga	cat	691
Ser	Ala	Ser	Asp	Val	Ile	Glu	Ile	Arg	Val	Lys	Gly	Glu	Gly	Gly	His	
			185					190					195			
agc	gca	cgt	cca	cac	ctc	tcc	gct	gat	gtt	gtt	tac	gcc	ttg	agc	aaa	739
Ser	Ala	Arg	Pro	His	Leu	Ser	Ala	Asp	Val	Val	Tyr	Ala	Leu	Ser	Lys	
		200					205					210				
ttg	gtc	gtt	gat	ctt	ccc	ggg	ttg	ctg	tcc	agg	cgc	gtc	gat	cca	cgc	787
Leu	Val	Val	Asp	Leu	Pro	Gly	Leu	Leu	Ser	Arg	Arg	Val	Asp	Pro	Arg	
	215					220					225					
acc	ggc	acc	gtg	ctt	gtt	ttc	ggc	acc	atc	aac	gcc	ggc	tat	gcg	ccc	835
Thr	Gly	Thr	Val	Leu	Val	Phe	Gly	Thr	Ile	Asn	Ala	Gly	Tyr	Ala	Pro	
230					235					240					245	

aac gcg atc cca gat tcc ggc atc gtg tca ggc acc ttg cgt aca gcc 883
 Asn Ala Ile Pro Asp Ser Gly Ile Val Ser Gly Thr Leu Arg Thr Ala
 250 255 260

gac atc tct acc tgg cgt gac atg cgt ccg ctt atc tct gag ctg gtg 931
 Asp Ile Ser Thr Trp Arg Asp Met Arg Pro Leu Ile Ser Glu Leu Val
 265 270 275

gaa cag gtg ctc gca ccc acc gga gtc acc cat gaa ctg atc tac aat 979
 Glu Gln Val Leu Ala Pro Thr Gly Val Thr His Glu Leu Ile Tyr Asn
 280 285 290

ccg ggt gtt cca cca gtg ctt aac gac gat gtc gcc acc gct ttg ttg 1027
 Pro Gly Val Pro Pro Val Leu Asn Asp Asp Val Ala Thr Ala Leu Leu
 295 300 305

gca agc gca gca cgc gac atg gac aca caa tct gtt gtc caa gcg ccg 1075
 Ala Ser Ala Ala Arg Asp Met Asp Thr Gln Ser Val Val Gln Ala Pro
 310 315 320 325

cag tca tcc ggt gga gaa gac ttc tcg tgg tac ctt gaa cac gtc cca 1123
 Gln Ser Ser Gly Gly Glu Asp Phe Ser Trp Tyr Leu Glu His Val Pro
 330 335 340

gga tca atg gcc cgg ttg ggt tgc tgg ccg ggg cac gga ccc aag caa 1171
 Gly Ser Met Ala Arg Leu Gly Cys Trp Pro Gly His Gly Pro Lys Gln
 345 350 355

gac ctc cat caa agt gac ctg gtt gtg gat gag cga gcc atc gga gtt 1219
 Asp Leu His Gln Ser Asp Leu Val Val Asp Glu Arg Ala Ile Gly Val
 360 365 370

ggc gtc agg ctc ttt ggc tcc ctt gtg cag cag tac agt agc cga tct 1267
 Gly Val Arg Leu Phe Gly Ser Leu Val Gln Gln Tyr Ser Ser Arg Ser
 375 380 385

gaa gct ttc tta aat tcc taatgggggt agtgtgtagg gct 1308
 Glu Ala Phe Leu Asn Ser
 390 395

<210> 140

<211> 395

<212> PRT

<213> Corynebacterium glutamicum

<400> 140

Val Met Glu Ile Gly Val Gln Val Ala Ser Trp Met Asp Arg His His
 1 5 10 15

Asp Glu Val Ile Lys Trp Arg Arg His Leu His Ser His Pro Glu Leu
 20 25 30

Ser His Met Glu Tyr Arg Thr Thr Glu Tyr Leu Ala Ser Val Leu Lys
 35 40 45

Asp His Gly Met Glu Pro His Leu Phe Pro Gly Thr Gly Leu Met Val
 50 55 60

Asp Ile Gly Pro Glu Gly Asp Ser Arg Leu Ala Phe Arg Ala Asp Ile
 65 70 75 80

Asp Ala Leu Pro Leu Leu Glu Ser Thr Gly Leu Glu Phe Ser Ser Thr
 85 90 95
 Ala Thr Gly Val Ala His Ala Cys Gly His Asp Val His Thr Val Ile
 100 105 110
 Ala Leu Ala Leu Ala Cys Ala Leu Asn Thr Ile Glu Leu Pro Ile Gly
 115 120 125
 Ile Arg Val Ile Phe Gln Pro Ala Glu Glu Val Met Thr Gly Gly Ala
 130 135 140
 Thr Asp Val Ile Ala His Gly Gly Leu Asp Gly Val Asp Ala Ile Tyr
 145 150 155 160
 Ala Ile His Val Glu Pro Lys Leu Lys Val Gly Arg Val Gly Val Arg
 165 170 175
 Ala Gly Ala Ile Thr Ser Ala Ser Asp Val Ile Glu Ile Arg Val Lys
 180 185 190
 Gly Glu Gly Gly His Ser Ala Arg Pro His Leu Ser Ala Asp Val Val
 195 200 205
 Tyr Ala Leu Ser Lys Leu Val Val Asp Leu Pro Gly Leu Leu Ser Arg
 210 215 220
 Arg Val Asp Pro Arg Thr Gly Thr Val Leu Val Phe Gly Thr Ile Asn
 225 230 235 240
 Ala Gly Tyr Ala Pro Asn Ala Ile Pro Asp Ser Gly Ile Val Ser Gly
 245 250 255
 Thr Leu Arg Thr Ala Asp Ile Ser Thr Trp Arg Asp Met Arg Pro Leu
 260 265 270
 Ile Ser Glu Leu Val Glu Gln Val Leu Ala Pro Thr Gly Val Thr His
 275 280 285
 Glu Leu Ile Tyr Asn Pro Gly Val Pro Pro Val Leu Asn Asp Asp Val
 290 295 300
 Ala Thr Ala Leu Leu Ala Ser Ala Ala Arg Asp Met Asp Thr Gln Ser
 305 310 315 320
 Val Val Gln Ala Pro Gln Ser Ser Gly Gly Glu Asp Phe Ser Trp Tyr
 325 330 335
 Leu Glu His Val Pro Gly Ser Met Ala Arg Leu Gly Cys Trp Pro Gly
 340 345 350
 His Gly Pro Lys Gln Asp Leu His Gln Ser Asp Leu Val Val Asp Glu
 355 360 365
 Arg Ala Ile Gly Val Gly Val Arg Leu Phe Gly Ser Leu Val Gln Gln
 370 375 380
 Tyr Ser Ser Arg Ser Glu Ala Phe Leu Asn Ser
 385 390 395

<400> 141																
gaaaacaaac gtccttgaag ccgtaatgcc ccgttcgaca ataaaaaggg tagtagcagt 60																
tcttgccgcc tcgactgcgc ttagccccctt tttgggtatca atg ccc act gca gca 115																
Met Pro Thr Ala Ala 1 5																
gcg caa gaa aac atc cgc tgg gaa gaa tgc cca cct cag gta gat att 163																
Ala Gln Glu Asn Ile Arg Trp Glu Glu Cys Pro Pro Gln Val Asp Ile 10 15 20																
gcc tcc gct caa tgt ggc agc atc gac gtg ccc atg cac tat tct gat 211																
Ala Ser Ala Gln Cys Gly Ser Ile Asp Val Pro Met His Tyr Ser Asp 25 30 35																
ccc tca ctt ggc gat atc agc gtg ggc ttt gtc aag gtc cct gcc caa 259																
Pro Ser Leu Gly Asp Ile Ser Val Gly Phe Val Lys Val Pro Ala Gln 40 45 50																
ggc gaa aag cac ggc acc atc ttc ggt aac tcc ggt ggc cct ggt ggc 307																
Gly Glu Lys His Gly Thr Ile Phe Gly Asn Ser Gly Gly Pro Gly Gly 55 60 65																
gat gcc tat agc ttc ttc ggc agc caa tcc atg aac tgg cca gaa gcc 355																
Asp Ala Tyr Ser Phe Phe Gly Ser Gln Ser Met Asn Trp Pro Glu Ala 70 75 80 85																
atg tac caa aac tac gac ctc gtt gca gtg cag cct cgc gga atg gtc 403																
Met Tyr Gln Asn Tyr Asp Leu Val Ala Val Gln Pro Arg Gly Met Val 90 95 100																
ggc tcc aca ccg gtt aac tgc gac aac atc gca cca gga tac gat ttc 451																
Gly Ser Thr Pro Val Asn Cys Asp Asn Ile Ala Pro Gly Tyr Asp Phe 105 110 115																
ctc tcg ctg ctc acc cgc gaa ggc gct ttc gtt aaa gaa tcc tgc gag 499																
Leu Ser Leu Leu Thr Arg Glu Gly Ala Phe Val Lys Glu Ser Cys Glu 120 125 130																
atc ggc acc ccc ggc tac acc tcc agc ctg acc acc gac aac acc gcc 547																
Ile Gly Thr Pro Gly Tyr Thr Ser Ser Leu Thr Thr Asp Asn Thr Ala 135 140 145																
aac gac tgg gag cgc gtc cgc caa gca ctt ggc gat gac aag atc tcc 595																
Asn Asp Trp Glu Arg Val Arg Gln Ala Leu Gly Asp Asp Lys Ile Ser 150 155 160 165																
atc ttc gga ctg tcc tac gga acc tac ctc gga tcg gtc tac gcc acc 643																
Ile Phe Gly Leu Ser Tyr Gly Thr Tyr Leu Gly Ser Val Tyr Ala Thr 170 175 180																

cgc tac cca cag cac acc gac aag gtt gtc ctc gat tcc gca atg gcg Arg Tyr Pro Gln His Thr Asp Lys Val Val Leu Asp Ser Ala Met Ala	691
185 190 195	
ccc agc ctg gca tgg aac ggc atc atg gcc tcc caa gaa cag ggc tac Pro Ser Leu Ala Trp Asn Gly Ile Met Ala Ser Gln Glu Gln Gly Tyr	739
200 205 210	
aaa aac tcc ctc aac gac ttc ttc acc tgg gtt gca gaa aac aac gac Lys Asn Ser Leu Asn Asp Phe Phe Thr Trp Val Ala Glu Asn Asn Asp	787
215 220 225	
acg tat ggc ctc ggc act acc cca cta gcc gtg tac caa aac tgg tca Thr Tyr Gly Leu Gly Thr Thr Pro Leu Ala Val Tyr Gln Asn Trp Ser	835
230 235 240 245	
aac aag atc gtc gcc gaa acc gga acc aac cca acc gtt gct cca cca Asn Lys Ile Val Ala Glu Thr Gly Thr Asn Pro Thr Val Ala Pro Pro	883
250 255 260	
cca gca caa gtt ggc gat gtc cca cca gca ttc gca tgg gcc ggc caa Pro Ala Gln Val Gly Asp Val Pro Pro Ala Phe Ala Trp Ala Gly Gln	931
265 270 275	
gca ggc gca gac atg atg acc gcc acc aac cca acc tcc gtg caa ctc Ala Gly Ala Asp Met Met Thr Ala Thr Asn Pro Thr Ser Val Gln Leu	979
280 285 290	
cag ggc ctt gcc acc cag ctc cta aac cct gga tcc aac cag tca ctg Gln Gly Leu Ala Thr Gln Leu Leu Asn Pro Gly Ser Asn Gln Ser Leu	1027
295 300 305	
agc cct ctg ctc aac gtc acc cgc gcc tac att cca cag cca tca acc Ser Pro Leu Leu Asn Val Thr Arg Ala Tyr Ile Pro Gln Pro Ser Thr	1075
310 315 320 325	
tgg ccc atg ctc gca ggc gcc atc tca ggg caa aca ccc atc cct gac Trp Pro Met Leu Ala Gly Ala Ile Ser Gly Gln Thr Pro Ile Pro Asp	1123
330 335 340	
gta act gac acc ggc gac gac cca tac gtc atc gaa agc atc aac gcc Val Thr Asp Thr Gly Asp Asp Pro Tyr Val Ile Glu Ser Ile Asn Ala	1171
345 350 355	
agc gtc aac atg cag cgc atg gtc atg tgc aac gaa aac acc gtc gca Ser Val Asn Met Gln Arg Met Val Met Cys Asn Glu Asn Thr Val Ala	1219
360 365 370	
cca gac cca gta gca atg gca cgc atg gcc tgg aca agc atg gtc acc Pro Asp Pro Val Ala Met Ala Arg Met Ala Trp Thr Ser Met Val Thr	1267
375 380 385	
ggc gac gtc ttt gac att tac tcc gtt aaa ttc agc tcc gga caa gcc Gly Asp Val Phe Asp Ile Tyr Ser Val Lys Phe Ser Ser Gly Gln Ala	1315
390 395 400 405	
tgc tcc ggc atc acc cca aca agc ggc cgc cag cca acc gac gga tct Cys Ser Gly Ile Thr Pro Thr Ser Gly Arg Gln Pro Thr Asp Gly Ser	1363
410 415 420	

caa cta gca gtc caa cca cta ctc ctc cag gga acc agc gac cca caa 1411
 Gln Leu Ala Val Gln Pro Leu Leu Leu Gln Gly Thr Ser Asp Pro Gln
 425 430 435
 acc cca tac tgg acc cac aac gag ctt gcc gac gcc atg aac gcc cac 1459
 Thr Pro Tyr Trp Thr His Asn Glu Leu Ala Asp Ala Met Asn Ala His
 440 445 450
 gtg gtc acc gtc aac gga cca gga cac ggc caa tcc atc ggc ggc acc 1507
 Val Val Thr Val Asn Gly Pro Gly His Gly Gln Ser Ile Gly Gly Thr
 455 460 465
 aac caa gca atc aac gac att gtt gtg gac tac ctc cgc acc gga cac 1555
 Asn Gln Ala Ile Asn Asp Ile Val Val Asp Tyr Leu Arg Thr Gly His
 470 475 480 485
 acc gac gcc acc tgg gtc gaa ggc aac aca ccc acc cca att acg gct 1603
 Thr Asp Ala Thr Trp Val Glu Gly Asn Thr Pro Thr Pro Ile Thr Ala
 490 495 500
 ggc taattgcttt ccacttagta gat 1629
 Gly

<210> 142

<211> 502

<212> PRT

<213> Corynebacterium glutamicum

<400> 142

Met Pro Thr Ala Ala Ala Gln Glu Asn Ile Arg Trp Glu Glu Cys Pro
 1 5 10 15
 Pro Gln Val Asp Ile Ala Ser Ala Gln Cys Gly Ser Ile Asp Val Pro
 20 25 30
 Met His Tyr Ser Asp Pro Ser Leu Gly Asp Ile Ser Val Gly Phe Val
 35 40 45
 Lys Val Pro Ala Gln Gly Glu Lys His Gly Thr Ile Phe Gly Asn Ser
 50 55 60
 Gly Gly Pro Gly Gly Asp Ala Tyr Ser Phe Phe Gly Ser Gln Ser Met
 65 70 75 80
 Asn Trp Pro Glu Ala Met Tyr Gln Asn Tyr Asp Leu Val Ala Val Gln
 85 90 95
 Pro Arg Gly Met Val Gly Ser Thr Pro Val Asn Cys Asp Asn Ile Ala
 100 105 110
 Pro Gly Tyr Asp Phe Leu Ser Leu Leu Thr Arg Glu Gly Ala Phe Val
 115 120 125
 Lys Glu Ser Cys Glu Ile Gly Thr Pro Gly Tyr Thr Ser Ser Leu Thr
 130 135 140
 Thr Asp Asn Thr Ala Asn Asp Trp Glu Arg Val Arg Gln Ala Leu Gly
 145 150 155 160

Asp Asp Lys Ile Ser Ile Phe Gly Leu Ser Tyr Gly Thr Tyr Leu Gly
 165 170 175
 Ser Val Tyr Ala Thr Arg Tyr Pro Gln His Thr Asp Lys Val Val Leu
 180 185 190
 Asp Ser Ala Met Ala Pro Ser Leu Ala Trp Asn Gly Ile Met Ala Ser
 195 200 205
 Gln Glu Gln Gly Tyr Lys Asn Ser Leu Asn Asp Phe Phe Thr Trp Val
 210 215 220
 Ala Glu Asn Asn Asp Thr Tyr Gly Leu Gly Thr Thr Pro Leu Ala Val
 225 230 235 240
 Tyr Gln Asn Trp Ser Asn Lys Ile Val Ala Glu Thr Gly Thr Asn Pro
 245 250 255
 Thr Val Ala Pro Pro Pro Ala Gln Val Gly Asp Val Pro Pro Ala Phe
 260 265 270
 Ala Trp Ala Gly Gln Ala Gly Ala Asp Met Met Thr Ala Thr Asn Pro
 275 280 285
 Thr Ser Val Gln Leu Gln Gly Leu Ala Thr Gln Leu Leu Asn Pro Gly
 290 295 300
 Ser Asn Gln Ser Leu Ser Pro Leu Leu Asn Val Thr Arg Ala Tyr Ile
 305 310 315 320
 Pro Gln Pro Ser Thr Trp Pro Met Leu Ala Gly Ala Ile Ser Gly Gln
 325 330 335
 Thr Pro Ile Pro Asp Val Thr Asp Thr Gly Asp Asp Pro Tyr Val Ile
 340 345 350
 Glu Ser Ile Asn Ala Ser Val Asn Met Gln Arg Met Val Met Cys Asn
 355 360 365
 Glu Asn Thr Val Ala Pro Asp Pro Val Ala Met Ala Arg Met Ala Trp
 370 375 380
 Thr Ser Met Val Thr Gly Asp Val Phe Asp Ile Tyr Ser Val Lys Phe
 385 390 395 400
 Ser Ser Gly Gln Ala Cys Ser Gly Ile Thr Pro Thr Ser Gly Arg Gln
 405 410 415
 Pro Thr Asp Gly Ser Gln Leu Ala Val Gln Pro Leu Leu Leu Gln Gly
 420 425 430
 Thr Ser Asp Pro Gln Thr Pro Tyr Trp Thr His Asn Glu Leu Ala Asp
 435 440 445
 Ala Met Asn Ala His Val Val Thr Val Asn Gly Pro Gly His Gly Gln
 450 455 460
 Ser Ile Gly Gly Thr Asn Gln Ala Ile Asn Asp Ile Val Val Asp Tyr
 465 470 475 480
 Leu Arg Thr Gly His Thr Asp Ala Thr Trp Val Glu Gly Asn Thr Pro

485

490

495

Thr Pro Ile Thr Ala Gly
500

<210> 143

<211> 1114

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1114)

<223> FRXA00977

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tcttgccgcc tcgactgcgc ttagccctt tttggtatca atg ccc act gca gca 115
Met Pro Thr Ala Ala
1 5

gcg caa gaa aac atc cgc tgg gaa gaa tgc cca cct cag gta gat att 163
Ala Gln Glu Asn Ile Arg Trp Glu Glu Cys Pro Pro Gln Val Asp Ile
10 15 20

gcc tcc gct caa tgt ggc agc atc gac gtg ccc atg cac tat tct gat 211
Ala Ser Ala Gln Cys Gly Ser Ile Asp Val Pro Met His Tyr Ser Asp
25 30 35

ccc tca ctt ggc gat atc agc gtg ggc ttt gtc aag gtc cct gcc caa 259
Pro Ser Leu Gly Asp Ile Ser Val Gly Phe Val Lys Val Pro Ala Gln
40 45 50

ggc gaa aag cac ggc acc atc ttc ggt aac tcc ggt ggc cct ggt ggc 307
Gly Glu Lys His Gly Thr Ile Phe Gly Asn Ser Gly Gly Pro Gly Gly
55 60 65

gat gcc tat agc ttc ttc ggc agc caa tcc atg aac tgg cca gaa gcc 355
Asp Ala Tyr Ser Phe Phe Gly Ser Gln Ser Met Asn Trp Pro Glu Ala
70 75 80 85

atg tac caa aac tac gac ctc gtt gca gtg cag cct cgc gga atg gtc 403
Met Tyr Gln Asn Tyr Asp Leu Val Ala Val Gln Pro Arg Gly Met Val
90 95 100

ggc tcc aca ccg gtt aac tgc gac aac atc gca cca gga tac gat ttc 451
Gly Ser Thr Pro Val Asn Cys Asp Asn Ile Ala Pro Gly Tyr Asp Phe
105 110 115

ctc tcg ctg ctc acc cgc gaa ggc gct ttc gtt aaa gaa tcc tgc gag 499
Leu Ser Leu Leu Thr Arg Glu Gly Ala Phe Val Lys Glu Ser Cys Glu
120 125 130

atc ggc acc ccc ggc tac acc tcc agc ctg acc acc gac aac acc gcc 547
Ile Gly Thr Pro Gly Tyr Thr Ser Ser Leu Thr Thr Asp Asn Thr Ala
135 140 145

aac gac tgg gag cgc gtc cgc caa gca ctt ggc gat gac aag atc tcc 595
Asn Asp Trp Glu Arg Val Arg Gln Ala Leu Gly Asp Asp Lys Ile Ser

150	155	160	165	
atc ttc gga ctg tcc tac gga acc tac ctc gga tcg gtc tac gcc acc				643
Ile Phe Gly Leu Ser Tyr Gly Thr Tyr Leu Gly Ser Val Tyr Ala Thr	170	175	180	
cgc tac cca cag cac acc gac aag gtt gtc ctc gat tcc gca atg gcg				691
Arg Tyr Pro Gln His Thr Asp Lys Val Val Leu Asp Ser Ala Met Ala	185	190	195	
ccc agc ctg gca tgg aac ggc atc atg gcc tcc caa gaa cag ggc tac				739
Pro Ser Leu Ala Trp Asn Gly Ile Met Ala Ser Gln Glu Gln Gly Tyr	200	205	210	
aaa aac tcc ctc aac gac ttc ttc acc tgg gtt gca gaa aac aac gac				787
Lys Asn Ser Leu Asn Asp Phe Phe Thr Trp Val Ala Glu Asn Asn Asp	215	220	225	
acg tat ggc ctc ggc act acc cca cta gcc gtg tac caa aac tgg tca				835
Thr Tyr Gly Leu Gly Thr Thr Pro Leu Ala Val Tyr Gln Asn Trp Ser	230	235	240	245
aac aag atc gtc gcc gaa acc gga acc aac cca acc gtt gct cca cca				883
Asn Lys Ile Val Ala Glu Thr Gly Thr Asn Pro Thr Val Ala Pro Pro	250	255	260	
cca gca caa gtt ggc gat gtc cca cca gca ttc gca tgg gcc ggc caa				931
Pro Ala Gln Val Gly Asp Val Pro Pro Ala Phe Ala Trp Ala Gly Gln	265	270	275	
gca ggc gca gac atg atg acc gcc acc aac cca acc tcc gtg caa ctc				979
Ala Gly Ala Asp Met Met Thr Ala Thr Asn Pro Thr Ser Val Gln Leu	280	285	290	
cag ggc ctt gcc acc cag ctc cta aac cct gga tcc aac cag tca ctg				1027
Gln Gly Leu Ala Thr Gln Leu Leu Asn Pro Gly Ser Asn Gln Ser Leu	295	300	305	
agc cct ctg ctc aac gtc acc cgc gcc tac att cca cag cca tca acc				1075
Ser Pro Leu Leu Asn Val Thr Arg Ala Tyr Ile Pro Gln Pro Ser Thr	310	315	320	325
tgg ccc atg ctc gca ggc gcc atc tca ggg caa aca ccc				1114
Trp Pro Met Leu Ala Gly Ala Ile Ser Gly Gln Thr Pro	330	335		

<210> 144

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

Met Pro Thr Ala Ala Ala Gln Glu Asn Ile Arg Trp Glu Glu Cys Pro				
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Pro Gln Val Asp Ile Ala Ser Ala Gln Cys Gly Ser Ile Asp Val Pro				
20	25	30		

Met His Tyr Ser Asp Pro Ser Leu Gly Asp Ile Ser Val Gly Phe Val				
35	40	45		

Lys Val Pro Ala Gln Gly Glu Lys His Gly Thr Ile Phe Gly Asn Ser
 50 55 60
 Gly Gly Pro Gly Gly Asp Ala Tyr Ser Phe Phe Gly Ser Gln Ser Met
 65 70 75 80
 Asn Trp Pro Glu Ala Met Tyr Gln Asn Tyr Asp Leu Val Ala Val Gln
 85 90 95
 Pro Arg Gly Met Val Gly Ser Thr Pro Val Asn Cys Asp Asn Ile Ala
 100 105 110
 Pro Gly Tyr Asp Phe Leu Ser Leu Leu Thr Arg Glu Gly Ala Phe Val
 115 120 125
 Lys Glu Ser Cys Glu Ile Gly Thr Pro Gly Tyr Thr Ser Ser Leu Thr
 130 135 140
 Thr Asp Asn Thr Ala Asn Asp Trp Glu Arg Val Arg Gln Ala Leu Gly
 145 150 155 160
 Asp Asp Lys Ile Ser Ile Phe Gly Leu Ser Tyr Gly Thr Tyr Leu Gly
 165 170 175
 Ser Val Tyr Ala Thr Arg Tyr Pro Gln His Thr Asp Lys Val Val Leu
 180 185 190
 Asp Ser Ala Met Ala Pro Ser Leu Ala Trp Asn Gly Ile Met Ala Ser
 195 200 205
 Gln Glu Gln Gly Tyr Lys Asn Ser Leu Asn Asp Phe Phe Thr Trp Val
 210 215 220
 Ala Glu Asn Asn Asp Thr Tyr Gly Leu Gly Thr Thr Pro Leu Ala Val
 225 230 235 240
 Tyr Gln Asn Trp Ser Asn Lys Ile Val Ala Glu Thr Gly Thr Asn Pro
 245 250 255
 Thr Val Ala Pro Pro Pro Ala Gln Val Gly Asp Val Pro Pro Ala Phe
 260 265 270
 Ala Trp Ala Gly Gln Ala Gly Ala Asp Met Met Thr Ala Thr Asn Pro
 275 280 285
 Thr Ser Val Gln Leu Gln Gly Leu Ala Thr Gln Leu Leu Asn Pro Gly
 290 295 300
 Ser Asn Gln Ser Leu Ser Pro Leu Leu Asn Val Thr Arg Ala Tyr Ile
 305 310 315 320
 Pro Gln Pro Ser Thr Trp Pro Met Leu Ala Gly Ala Ile Ser Gly Gln
 325 330 335
 Thr Pro

<210> 145

<211> 269

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(246)

<223> FRXA00982

<400> 145

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Ser	Gln	Leu	Ala	Val	Gln	Pro	Leu	Leu	Leu	Gln	Gly	Thr	Ser	Asp	Pro	
1				5					10					15		

caa	acc	cca	tac	tgg	acc	cac	aac	gag	ctt	gcc	gac	gcc	atg	aac	gcc	96
Gln	Thr	Pro	Tyr	Trp	Thr	His	Asn	Glu	Leu	Ala	Asp	Ala	Met	Asn	Ala	
			20					25					30			

cac	gtg	gtc	acc	gtc	aac	gga	cca	gga	cac	ggc	caa	tcc	atc	ggc	ggc	144
His	Val	Val	Thr	Val	Asn	Gly	Pro	Gly	His	Gly	Gln	Ser	Ile	Gly	Gly	
			35				40					45				

acc	aac	caa	gca	atc	aac	gac	att	gtt	gtg	gac	tac	ctc	cgc	acc	gga	192
Thr	Asn	Gln	Ala	Ile	Asn	Asp	Ile	Val	Val	Asp	Tyr	Leu	Arg	Thr	Gly	
	50					55					60					

cac	acc	gac	gcc	acc	tgg	gtc	gaa	ggc	aac	aca	ccc	acc	cca	att	acg	240
His	Thr	Asp	Ala	Thr	Trp	Val	Glu	Gly	Asn	Thr	Pro	Thr	Pro	Ile	Thr	
	65				70				75						80	

gct	ggc	taattgcttt	ccacttagta	gat												269
Ala	Gly															

<210> 146

<211> 82

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 146

Ser	Gln	Leu	Ala	Val	Gln	Pro	Leu	Leu	Leu	Gln	Gly	Thr	Ser	Asp	Pro
1				5					10					15	

Gln	Thr	Pro	Tyr	Trp	Thr	His	Asn	Glu	Leu	Ala	Asp	Ala	Met	Asn	Ala
			20					25					30		

His	Val	Val	Thr	Val	Asn	Gly	Pro	Gly	His	Gly	Gln	Ser	Ile	Gly	Gly
			35				40					45			

Thr	Asn	Gln	Ala	Ile	Asn	Asp	Ile	Val	Val	Asp	Tyr	Leu	Arg	Thr	Gly
	50					55					60				

His	Thr	Asp	Ala	Thr	Trp	Val	Glu	Gly	Asn	Thr	Pro	Thr	Pro	Ile	Thr
	65				70				75						80

Ala Gly

<210> 147

<211> 980

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(957)

<223> RXN01181

<400> 147

tct gta ctg ctc gct cgc gac ttg gtg aac acc cct tca tca cac ctg	48
Ser Val Leu Leu Ala Arg Asp Leu Val Asn Thr Pro Ser Ser His Leu	
1 5 10 15	
tac cca gag tcc tac tca gta att gca tcc aac gaa gcg tcc aag cac	96
Tyr Pro Glu Ser Tyr Ser Val Ile Ala Ser Asn Glu Ala Ser Lys His	
20 25 30	
ggc ttg cag acc acc atc ctg gat gag aag cag ctt gct gat caa ggt	144
Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly	
35 40 45	
ttc ggc ggc atc ctc gca gtc ggt aac ggc tcc tcc cgc aag cct cgt	192
Phe Gly Gly Ile Leu Ala Val Gly Asn Gly Ser Ser Arg Lys Pro Arg	
50 55 60	
ctg ctg cgc atc gat tgg aag cca cgc aag gct aag aag tcg atc gct	240
Leu Leu Arg Ile Asp Trp Lys Pro Arg Lys Ala Lys Lys Ser Ile Ala	
65 70 75 80	
ttg gtt ggc aag ggc atc acc ttt gac acc ggc gga att tcc atc aag	288
Leu Val Gly Lys Gly Ile Thr Phe Asp Thr Gly Gly Ile Ser Ile Lys	
85 90 95	
cct ggc gca agc atg gag aac atg atc tcc gac atg ggt gga tcc gca	336
Pro Gly Ala Ser Met Glu Asn Met Ile Ser Asp Met Gly Gly Ser Ala	
100 105 110	
tcc gta ttg gcc acc att atc gct gca gct cgt ttg aac ctg tcg atc	384
Ser Val Leu Ala Thr Ile Ile Ala Ala Ala Arg Leu Asn Leu Ser Ile	
115 120 125	
aac gtc ttc gcg ttc cta cca atg gct gag aac atg cca tcc ggt gac	432
Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp	
130 135 140	
gct ttc cgc ccc ggc gat gtc atc act cat ttc ggt ggt atc acc tcc	480
Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser	
145 150 155 160	
gaa atc ttg aac acc gac gct gaa ggc cgc ctc att ctg gca gat gcc	528
Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala	
165 170 175	
att gct tac gct tct gaa gat aag cct gac tac ctc att gat gcg gca	576
Ile Ala Tyr Ala Ser Glu Asp Lys Pro Asp Tyr Leu Ile Asp Ala Ala	
180 185 190	
acc ctg act ggt gct caa tta gtc gct tta ggc ctg cgg act tca ggt	624
Thr Leu Thr Gly Ala Gln Leu Val Ala Leu Gly Leu Arg Thr Ser Gly	
195 200 205	

gtc atg ggt acc gat gag ttc cgc gac agc gtt gcc aag act ggc cgc 672
 Val Met Gly Thr Asp Glu Phe Arg Asp Ser Val Ala Lys Thr Gly Arg
 210 215 220
 gag gtt ggc gag caa gca tgg gca atg cct ctt cct gaa gag ctc gat 720
 Glu Val Gly Glu Gln Ala Trp Ala Met Pro Leu Pro Glu Glu Leu Asp
 225 230 235 240
 gag cag gtt aag tcc cct gtc gct gac ctg cgc aat gtc acc aat tcc 768
 Glu Gln Val Lys Ser Pro Val Ala Asp Leu Arg Asn Val Thr Asn Ser
 245 250 255
 cgt ttc gca gga atg tct gct gcg ggt cgt tac ttg cag gaa ttc gtt 816
 Arg Phe Ala Gly Met Ser Ala Ala Gly Arg Tyr Leu Gln Glu Phe Val
 260 265 270
 ggt gcc gac atc gag tgg gct cac gtc gat atc gct ggc cct gca tac 864
 Gly Ala Asp Ile Glu Trp Ala His Val Asp Ile Ala Gly Pro Ala Tyr
 275 280 285
 aac act gct ggt gaa ttc ggt tac acg cca aag cgc gca acc gga caa 912
 Asn Thr Ala Gly Glu Phe Gly Tyr Thr Pro Lys Arg Ala Thr Gly Gln
 290 295 300
 cca gtg cgc acc ttc gtt cag gtt ctg aag gat ctg tcg gaa agc 957
 Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser
 305 310 315
 taaacgctag ttaaagatca gga 980

<210> 148

<211> 319

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 148

Ser Val Leu Leu Ala Arg Asp Leu Val Asn Thr Pro Ser Ser His Leu
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Tyr Pro Glu Ser Tyr Ser Val Ile Ala Ser Asn Glu Ala Ser Lys His
 20 25 30

Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly
 35 40 45

Phe Gly Gly Ile Leu Ala Val Gly Asn Gly Ser Ser Arg Lys Pro Arg
 50 55 60

Leu Leu Arg Ile Asp Trp Lys Pro Arg Lys Ala Lys Lys Ser Ile Ala
 65 70 75 80

Leu Val Gly Lys Gly Ile Thr Phe Asp Thr Gly Gly Ile Ser Ile Lys
 85 90 95

Pro Gly Ala Ser Met Glu Asn Met Ile Ser Asp Met Gly Gly Ser Ala
 100 105 110

Ser Val Leu Ala Thr Ile Ile Ala Ala Ala Arg Leu Asn Leu Ser Ile
 115 120 125

Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp
 130 135 140
 Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser
 145 150 155 160
 Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala
 165 170 175
 Ile Ala Tyr Ala Ser Glu Asp Lys Pro Asp Tyr Leu Ile Asp Ala Ala
 180 185 190
 Thr Leu Thr Gly Ala Gln Leu Val Ala Leu Gly Leu Arg Thr Ser Gly
 195 200 205
 Val Met Gly Thr Asp Glu Phe Arg Asp Ser Val Ala Lys Thr Gly Arg
 210 215 220
 Glu Val Gly Glu Gln Ala Trp Ala Met Pro Leu Pro Glu Glu Leu Asp
 225 230 235 240
 Glu Gln Val Lys Ser Pro Val Ala Asp Leu Arg Asn Val Thr Asn Ser
 245 250 255
 Arg Phe Ala Gly Met Ser Ala Ala Gly Arg Tyr Leu Gln Glu Phe Val
 260 265 270
 Gly Ala Asp Ile Glu Trp Ala His Val Asp Ile Ala Gly Pro Ala Tyr
 275 280 285
 Asn Thr Ala Gly Glu Phe Gly Tyr Thr Pro Lys Arg Ala Thr Gly Gln
 290 295 300
 Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser
 305 310 315

<210> 149

<211> 980

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(957)

<223> FRXA01181

<400> 149

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 Ser Val Leu Leu Ala Arg Asp Leu Val Asn Thr Pro Ser Ser His Leu
 1 5 10 15
 tac cca gag tcc tac tca gta att gca tcc aac gaa gcg tcc aag cac 96
 Tyr Pro Glu Ser Tyr Ser Val Ile Ala Ser Asn Glu Ala Ser Lys His
 20 25 30
 ggc ttg cag acc acc atc ctg gat gag aag cag ctt gct gat caa ggt 144
 Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly
 35 40 45
 ttc ggc ggc atc ctc gca gtc ggt aac ggc tcc tcc cgc aag cct cgt 192

Phe	Gly	Gly	Ile	Leu	Ala	Val	Gly	Asn	Gly	Ser	Ser	Arg	Lys	Pro	Arg		
	50					55					60						
ctg	ctg	cgc	atc	gat	tgg	aag	cca	cgc	aag	gct	aag	aag	tcg	atc	gct	240	
Leu	Leu	Arg	Ile	Asp	Trp	Lys	Pro	Arg	Lys	Ala	Lys	Lys	Ser	Ile	Ala	80	
	65				70				75								
ttg	gtt	ggc	aag	ggc	atc	acc	ttt	gac	acc	ggc	gga	att	tcc	atc	aag	288	
Leu	Val	Gly	Lys	Gly	Ile	Thr	Phe	Asp	Thr	Gly	Gly	Ile	Ser	Ile	Lys	95	
				85					90								
cct	ggc	gca	agc	atg	gag	aac	atg	atc	tcc	gac	atg	ggg	gga	tcc	gca	336	
Pro	Gly	Ala	Ser	Met	Glu	Asn	Met	Ile	Ser	Asp	Met	Gly	Gly	Ser	Ala	110	
			100					105									
tcc	gta	ttg	gcc	acc	att	atc	gct	gca	gct	cgt	ttg	aac	ctg	tcg	atc	384	
Ser	Val	Leu	Ala	Thr	Ile	Ile	Ala	Ala	Ala	Arg	Leu	Asn	Leu	Ser	Ile	125	
		115					120					125					
aac	gtc	ttc	gcg	ttc	cta	cca	atg	gct	gag	aac	atg	cca	tcc	ggg	gac	432	
Asn	Val	Phe	Ala	Phe	Leu	Pro	Met	Ala	Glu	Asn	Met	Pro	Ser	Gly	Asp	140	
	130					135											
gct	ttc	cgc	ccc	ggc	gat	gtc	atc	act	cat	ttc	ggg	ggg	atc	acc	tcc	480	
Ala	Phe	Arg	Pro	Gly	Asp	Val	Ile	Thr	His	Phe	Gly	Gly	Ile	Thr	Ser	160	
	145				150					155							
gaa	atc	ttg	aac	acc	gac	gct	gaa	ggc	cgc	ctc	att	ctg	gca	gat	gcc	528	
Glu	Ile	Leu	Asn	Thr	Asp	Ala	Glu	Gly	Arg	Leu	Ile	Leu	Ala	Asp	Ala	175	
				165				170									
att	gct	tac	gct	tct	gaa	gat	aag	cct	gac	tac	ctc	att	gat	gcg	gca	576	
Ile	Ala	Tyr	Ala	Ser	Glu	Asp	Lys	Pro	Asp	Tyr	Leu	Ile	Asp	Ala	Ala	190	
			180					185									
acc	ctg	act	ggg	gct	caa	tta	gtc	gct	tta	ggc	ctg	cgg	act	tca	ggg	624	
Thr	Leu	Thr	Gly	Ala	Gln	Leu	Val	Ala	Leu	Gly	Leu	Arg	Thr	Ser	Gly	205	
		195					200					205					
gtc	atg	ggg	acc	gat	gag	ttc	cgc	gac	agc	gtt	gcc	aag	act	ggc	cgc	672	
Val	Met	Gly	Thr	Asp	Glu	Phe	Arg	Asp	Ser	Val	Ala	Lys	Thr	Gly	Arg	220	
	210					215					220						
gag	gtt	ggc	gag	caa	gca	tgg	gca	atg	cct	ctt	cct	gaa	gag	ctc	gat	720	
Glu	Val	Gly	Glu	Gln	Ala	Trp	Ala	Met	Pro	Leu	Pro	Glu	Glu	Leu	Asp	240	
	225				230					235							
gag	cag	gtt	aag	tcc	cct	gtc	gct	gac	ctg	cgc	aat	gtc	acc	aat	tcc	768	
Glu	Gln	Val	Lys	Ser	Pro	Val	Ala	Asp	Leu	Arg	Asn	Val	Thr	Asn	Ser	255	
				245					250								
cgt	ttc	gca	gga	atg	tct	gct	gcg	ggg	cgt	tac	ttg	cag	gaa	ttc	gtt	816	
Arg	Phe	Ala	Gly	Met	Ser	Ala	Ala	Gly	Arg	Tyr	Leu	Gln	Glu	Phe	Val	270	
			260					265					270				
ggg	gcc	gac	atc	gag	tgg	gct	cac	gtc	gat	atc	gct	ggc	cct	gca	tac	864	
Gly	Ala	Asp	Ile	Glu	Trp	Ala	His	Val	Asp	Ile	Ala	Gly	Pro	Ala	Tyr	285	
		275					280					285					
aac	act	gct	ggg	gaa	ttc	ggg	tac	acg	cca	aag	cgc	gca	acc	gga	caa	912	
Asn	Thr	Ala	Gly	Glu	Phe	Gly	Tyr	Thr	Pro	Lys	Arg	Ala	Thr	Gly	Gln		

290 295 300
 cca gtg cgc acc ttc gtt cag gtt ctg aag gat ctg tcg gaa agc 957
 Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser
 305 310 315

 taaacgctag ttaaagatca gga 980

 <210> 150
 <211> 319
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 150
 Ser Val Leu Leu Ala Arg Asp Leu Val Asn Thr Pro Ser Ser His Leu
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 Tyr Pro Glu Ser Tyr Ser Val Ile Ala Ser Asn Glu Ala Ser Lys His
 20 25 30
 Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly
 35 40 45
 Phe Gly Gly Ile Leu Ala Val Gly Asn Gly Ser Ser Arg Lys Pro Arg
 50 55 60
 Leu Leu Arg Ile Asp Trp Lys Pro Arg Lys Ala Lys Lys Ser Ile Ala
 65 70 75 80
 Leu Val Gly Lys Gly Ile Thr Phe Asp Thr Gly Gly Ile Ser Ile Lys
 85 90 95
 Pro Gly Ala Ser Met Glu Asn Met Ile Ser Asp Met Gly Gly Ser Ala
 100 105 110
 Ser Val Leu Ala Thr Ile Ile Ala Ala Ala Arg Leu Asn Leu Ser Ile
 115 120 125
 Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp
 130 135 140
 Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser
 145 150 155 160
 Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala
 165 170 175
 Ile Ala Tyr Ala Ser Glu Asp Lys Pro Asp Tyr Leu Ile Asp Ala Ala
 180 185 190
 Thr Leu Thr Gly Ala Gln Leu Val Ala Leu Gly Leu Arg Thr Ser Gly
 195 200 205
 Val Met Gly Thr Asp Glu Phe Arg Asp Ser Val Ala Lys Thr Gly Arg
 210 215 220
 Glu Val Gly Glu Gln Ala Trp Ala Met Pro Leu Pro Glu Glu Leu Asp
 225 230 235 240
 Glu Gln Val Lys Ser Pro Val Ala Asp Leu Arg Asn Val Thr Asn Ser

	245		250		255
Arg Phe Ala Gly Met Ser Ala Ala Gly Arg Tyr Leu Gln Glu Phe Val					
	260		265		270
Gly Ala Asp Ile Glu Trp Ala His Val Asp Ile Ala Gly Pro Ala Tyr					
	275		280		285
Asn Thr Ala Gly Glu Phe Gly Tyr Thr Pro Lys Arg Ala Thr Gly Gln					
	290		295		300
Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser					
305	310		315		

<210> 151
 <211> 2724
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2701)
 <223> RXN01014

<400> 151
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 tctaagggta gcgccccctc aaatttcaag gagcattaaa ttg acg tcc act aat 115.
 Leu Thr Ser Thr Asn
 1 5
 ctc acc cga cag gaa gct tcg gat cgt tcg agg tta ctg agt gta gaa 163
 Leu Thr Arg Gln Glu Ala Ser Asp Arg Ser Arg Leu Leu Ser Val Glu
 10 15 20
 aac tat gac att gca ctt gat ctc aac aac ggt gat gag ttt ttt agt 211
 Asn Tyr Asp Ile Ala Leu Asp Leu Asn Asn Gly Asp Glu Phe Phe Ser
 25 30 35
 tcc tcc acc gtt gtc agc ttc act gtc agg aag gct ggc gat acc ttt 259
 Ser Ser Thr Val Val Ser Phe Thr Val Arg Lys Ala Gly Asp Thr Phe
 40 45 50
 att gat ctc cgc gca gca agc gtt gag gag gtt cgc ctg gac aat gtg 307
 Ile Asp Leu Arg Ala Ala Ser Val Glu Glu Val Arg Leu Asp Asn Val
 55 60 65
 tcc atc aaa gat gag gct cta acc ctt ggc aag aac ggc tac gac gag 355
 Ser Ile Lys Asp Glu Ala Leu Thr Leu Gly Lys Asn Gly Tyr Asp Glu
 70 75 80 85
 acg ttc ggc atc gcc ctg aag ggt ctt act ccc ggc gcg cac acc ttg 403
 Thr Phe Gly Ile Ala Leu Lys Gly Leu Thr Pro Gly Ala His Thr Leu
 90 95 100
 cgg gta acg gcg tct atc ccc tat tcc cgc acc ggt gaa ggc ctg cac 451
 Arg Val Thr Ala Ser Ile Pro Tyr Ser Arg Thr Gly Glu Gly Leu His
 105 110 115
 cgc atg gtg gat cca gca gac aat gag gtg tat ttg tac acc cag ttt 499

Arg	Met	Val	Asp	Pro	Ala	Asp	Asn	Glu	Val	Tyr	Leu	Tyr	Thr	Gln	Phe	
		120					125					130				
gag	acc	gcc	gat	gcc	aag	cgt	atg	ttc	gcg	tgt	ttc	gat	cag	cca	gac	547
Glu	Thr	Ala	Asp	Ala	Lys	Arg	Met	Phe	Ala	Cys	Phe	Asp	Gln	Pro	Asp	
		135				140					145					
ctc	aag	gct	acc	tat	gat	ctg	aac	atc	aaa	act	cct	aag	ggt	tgg	aag	595
Leu	Lys	Ala	Thr	Tyr	Asp	Leu	Asn	Ile	Lys	Thr	Pro	Lys	Gly	Trp	Lys	
					155					160					165	
atc	att	tcc	aac	tct	gag	cag	cag	gtt	tcc	act	cag	cac	act	gat	tac	643
Ile	Ile	Ser	Asn	Ser	Glu	Gln	Gln	Val	Ser	Thr	Gln	His	Thr	Asp	Tyr	
				170					175					180		
gat	acc	cac	att	tcc	cga	gtg	gac	tat	ccc	ctc	tcc	acc	tac	ctg	att	691
Asp	Thr	His	Ile	Ser	Arg	Val	Asp	Tyr	Pro	Leu	Ser	Thr	Tyr	Leu	Ile	
			185					190					195			
gcg	gtg	tgc	gcg	ggt	cgt	tac	cac	gag	gtg	tgc	gat	gtc	tgg	aag	ggt	739
Ala	Val	Cys	Ala	Gly	Arg	Tyr	His	Glu	Val	Cys	Asp	Val	Trp	Lys	Gly	
		200					205					210				
acg	ctc	acc	cac	cat	gca	gaa	aca	cct	gcc	gat	cag	cca	act	gag	ctg	787
Thr	Leu	Thr	His	His	Ala	Glu	Thr	Pro	Ala	Asp	Gln	Pro	Thr	Glu	Leu	
		215				220					225					
act	gtt	ccg	ctt	gct	ctc	tac	tgc	cgc	agt	tct	ttg	gct	aaa	gat	ctt	835
Thr	Val	Pro	Leu	Ala	Leu	Tyr	Cys	Arg	Ser	Ser	Leu	Ala	Lys	Asp	Leu	
					235					240					245	
gat	gcg	gtg	cgt	ctg	ttt	acc	gaa	acg	aag	cag	ggc	ttt	gat	tgg	tac	883
Asp	Ala	Val	Arg	Leu	Phe	Thr	Glu	Thr	Lys	Gln	Gly	Phe	Asp	Trp	Tyr	
				250					255					260		
cac	cgc	aac	ttc	ggt	gtg	gcg	tac	cca	ttc	ggc	aag	tac	gat	cag	atc	931
His	Arg	Asn	Phe	Gly	Val	Ala	Tyr	Pro	Phe	Gly	Lys	Tyr	Asp	Gln	Ile	
			265					270					275			
ttc	gtc	cct	gaa	ttt	aat	gct	ggc	gcg	atg	gag	aac	gcc	ggc	gct	gtc	979
Phe	Val	Pro	Glu	Phe	Asn	Ala	Gly	Ala	Met	Glu	Asn	Ala	Gly	Ala	Val	
		280					285					290				
acc	atc	cgc	gat	gag	tac	gtt	ttt	gca	tcc	aag	gca	acc	cgt	tac	cgc	1027
Thr	Ile	Arg	Asp	Glu	Tyr	Val	Phe	Ala	Ser	Lys	Ala	Thr	Arg	Tyr	Arg	
		295				300					305					
tac	gag	cgc	cgc	gct	gaa	acc	atc	ctt	cac	gag	ctc	gct	cac	atg	tgg	1075
Tyr	Glu	Arg	Arg	Ala	Glu	Thr	Ile	Leu	His	Glu	Leu	Ala	His	Met	Trp	
					315					320					325	
ttc	ggt	gtg	ctg	gtg	acc	atg	cag	tgg	tgg	gat	gat	ctg	tgg	ctc	aac	1123
Phe	Gly	Val	Leu	Val	Thr	Met	Gln	Trp	Trp	Asp	Asp	Leu	Trp	Leu	Asn	
				330				335						340		
gag	tcc	ttc	gcc	act	tgg	tcc	gcg	gca	att	tct	cag	gct	gag	gaa	act	1171
Glu	Ser	Phe	Ala	Thr	Trp	Ser	Ala	Ala	Ile	Ser	Gln	Ala	Glu	Glu	Thr	
			345					350					355			
gaa	tac	aac	act	gca	tgg	gtg	act	ttc	gcc	aat	gtg	gag	aag	tcg	tgg	1219
Glu	Tyr	Asn	Thr	Ala	Trp	Val	Thr	Phe	Ala	Asn	Val	Glu	Lys	Ser	Trp	

360					365					370						
gcg	tac	cag	cag	gat	cag	ctg	cct	tcc	acc	cac	ccg	gtg	ttc	tct	gac	1267
Ala	Tyr	Gln	Gln	Asp	Gln	Leu	Pro	Ser	Thr	His	Pro	Val	Phe	Ser	Asp	
	375					380					385					
gga	tac	gac	att	gag	act	gtc	gac	cag	aac	ttc	gac	ggc	atc	acc	tac	1315
Gly	Tyr	Asp	Ile	Glu	Thr	Val	Asp	Gln	Asn	Phe	Asp	Gly	Ile	Thr	Tyr	
	390				395					400					405	
gca	aag	ggc	gcc	tcg	gtg	ctc	aag	cag	ctg	cag	gca	tac	gtt	ggc	cgt	1363
Ala	Lys	Gly	Ala	Ser	Val	Leu	Lys	Gln	Leu	Gln	Ala	Tyr	Val	Gly	Arg	
				410					415					420		
gag	gaa	ttc	ctg	gca	ggc	gta	cgc	agg	cac	ttt	gcc	aac	cac	gca	tgg	1411
Glu	Glu	Phe	Leu	Ala	Gly	Val	Arg	Arg	His	Phe	Ala	Asn	His	Ala	Trp	
			425					430					435			
ggc	aac	gcc	agc	ttt	gat	gat	ctg	ctc	ggc	gcc	ctc	gag	cag	tcc	tcc	1459
Gly	Asn	Ala	Ser	Phe	Asp	Asp	Leu	Leu	Gly	Ala	Leu	Glu	Gln	Ser	Ser	
		440					445					450				
ggc	cgc	gac	ctc	tcc	gac	tgg	gca	aac	cag	tgg	ctc	aag	acc	acc	ggc	1507
Gly	Arg	Asp	Leu	Ser	Asp	Trp	Ala	Asn	Gln	Trp	Leu	Lys	Thr	Thr	Gly	
	455					460					465					
atc	aac	acc	ctc	ggc	gca	aag	ttc	acc	acc	gac	aac	ggc	aaa	tac	acc	1555
Ile	Asn	Thr	Leu	Gly	Ala	Lys	Phe	Thr	Thr	Asp	Asn	Gly	Lys	Tyr	Thr	
	470				475					480					485	
tcc	ttc	tcc	gtc	acc	cag	acc	ggc	gcc	gcg	ccg	ggt	gcc	ggt	gag	ctg	1603
Ser	Phe	Ser	Val	Thr	Gln	Thr	Gly	Ala	Ala	Pro	Gly	Ala	Gly	Glu	Leu	
				490					495					500		
cgg	act	cac	cgc	atc	gcg	gtg	ggt	ctt	tat	aag	ctt	gtc	gac	gga	tcc	1651
Arg	Thr	His	Arg	Ile	Ala	Val	Gly	Leu	Tyr	Lys	Leu	Val	Asp	Gly	Ser	
			505					510					515			
ctc	aac	cgc	tac	gca	cga	gta	gaa	ctt	gac	tgc	agt	ggc	gcg	tcg	aca	1699
Leu	Asn	Arg	Tyr	Ala	Arg	Val	Glu	Leu	Asp	Cys	Ser	Gly	Ala	Ser	Thr	
		520					525					530				
agc	gtt	gaa	gag	atc	gtt	gga	ctt	gag	cag	gct	gac	ttc	gtg	ctg	gtc	1747
Ser	Val	Glu	Glu	Ile	Val	Gly	Leu	Glu	Gln	Ala	Asp	Phe	Val	Leu	Val	
	535					540					545					
aac	gat	gat	gat	ctg	acg	tat	gcg	ctg	ctg	gat	ctg	gat	gat	gat	tca	1795
Asn	Asp	Asp	Asp	Leu	Thr	Tyr	Ala	Leu	Leu	Asp	Leu	Asp	Asp	Asp	Ser	
	550				555					560					565	
cgc	aat	ttt	gtc	atc	gac	aat	att	gat	aag	ttc	agc	gac	cct	atg	cct	1843
Arg	Asn	Phe	Val	Ile	Asp	Asn	Ile	Asp	Lys	Phe	Ser	Asp	Pro	Met	Pro	
			570						575					580		
cgc	acg	ctg	gtg	tgg	tcc	gct	gcg	tgg	gag	atg	act	cgc	gct	ggt	cag	1891
Arg	Thr	Leu	Val	Trp	Ser	Ala	Ala	Trp	Glu	Met	Thr	Arg	Ala	Gly	Gln	
			585					590					595			
atg	aag	gct	cgt	gat	ttc	atc	gcg	ctg	gtt	gct	cgt	ggc	gct	gct	gcg	1939
Met	Lys	Ala	Arg	Asp	Phe	Ile	Ala	Leu	Val	Ala	Arg	Gly	Ala	Ala	Ala	
		600					605					610				

gaa act gaa att gct gtg ctg gag cgc att ctc gcg cag gct acc tct Glu Thr Glu Ile Ala Val Leu Glu Arg Ile Leu Ala Gln Ala Thr Ser 615 620 625	1987
gcg ctg aag agc tac gcc gac cca gcg tgg gca gaa gca act gga aat Ala Leu Lys Ser Tyr Ala Asp Pro Ala Trp Ala Glu Ala Thr Gly Asn 630 635 640 645	2035
gac ctg ctg gcc gat gct ttc ctt gag ggt gct cgc tcc gca gaa cca Asp Leu Leu Ala Asp Ala Phe Leu Glu Gly Ala Arg Ser Ala Glu Pro 650 655 660	2083
gac tcc gac act cag ttg gcg ttc att cag gct ctg gca aaa gca acg Asp Ser Asp Thr Gln Leu Ala Phe Ile Gln Ala Leu Ala Lys Ala Thr 665 670 675	2131
ctc aat gat gct gct gcc gat tac ttc cgc gac att ctt gcc ggc aac Leu Asn Asp Ala Ala Ala Asp Tyr Phe Arg Asp Ile Leu Ala Gly Asn 680 685 690	2179
gtc gaa ggc ctg acc gtg gat cct gac ctg cgt tgg tgg gca ctg act Val Glu Gly Leu Thr Val Asp Pro Asp Leu Arg Trp Trp Ala Leu Thr 695 700 705	2227
gcg ctt atc gcc cgt ggt gac atc gag gct gtc gaa gat gca atc gcc Ala Leu Ile Ala Arg Gly Asp Ile Glu Ala Val Glu Asp Ala Ile Ala 710 715 720 725	2275
gct gaa ctt tcc cgc gac aac tcc agt gcc tcc ttc ctc gca tca ctt Ala Glu Leu Ser Arg Asp Asn Ser Ser Ala Ser Phe Leu Ala Ser Leu 730 735 740	2323
cga gcc ggt gcc gct gtg aac act gaa gaa gtg aag gct gct gca tac Arg Ala Gly Ala Ala Val Asn Thr Glu Glu Val Lys Ala Ala Tyr 745 750 755	2371
aag cat gtc acg gca gtt gat agt ggc cta tcc aac ctg gag ctg cgc Lys His Val Thr Ala Val Asp Ser Gly Leu Ser Asn Leu Glu Leu Arg 760 765 770	2419
cac aag att gaa ggc ctc aca ttc act ggc tct tct gaa ctg ctg caa His Lys Ile Glu Gly Leu Thr Phe Thr Gly Ser Ser Glu Leu Leu Gln 775 780 785	2467
gcc tac aac gag cag tac ttc gaa atc ctt gat gat gtg tgg gcg aac Ala Tyr Asn Glu Gln Tyr Phe Glu Ile Leu Asp Asp Val Trp Ala Asn 790 795 800 805	2515
ttc tcc ggc gaa atg gca cag cag atc gtc ctc gga ctg ttc cct tca Phe Ser Gly Glu Met Ala Gln Gln Ile Val Leu Gly Leu Phe Pro Ser 810 815 820	2563
tgg aac gtt tcc gaa gag ggt ctc aag cgt acc gac gag ttt ctt gat Trp Asn Val Ser Glu Glu Gly Leu Lys Arg Thr Asp Glu Phe Leu Asp 825 830 835	2611
ggc gaa cat gtc gca ggc atc aag cga att gtt tcc gaa tcc ctc gac Gly Glu His Val Ala Gly Ile Lys Arg Ile Val Ser Glu Ser Leu Asp 840 845 850	2659

cgc act gcc cgt gct ctg cgc aac cgt gcg gca gat gct gcg 2701
 Arg Thr Ala Arg Ala Leu Arg Asn Arg Ala Ala Asp Ala Ala
 855 860 865

taagtaaaag attctcaatc cca 2724

<210> 152

<211> 867

<212> PRT

<213> Corynebacterium glutamicum

<400> 152

Leu Thr Ser Thr Asn Leu Thr Arg Gln Glu Ala Ser Asp Arg Ser Arg
 1 5 10 15

Leu Leu Ser Val Glu Asn Tyr Asp Ile Ala Leu Asp Leu Asn Asn Gly
 20 25 30

Asp Glu Phe Phe Ser Ser Ser Thr Val Val Ser Phe Thr Val Arg Lys
 35 40 45

Ala Gly Asp Thr Phe Ile Asp Leu Arg Ala Ala Ser Val Glu Glu Val
 50 55 60

Arg Leu Asp Asn Val Ser Ile Lys Asp Glu Ala Leu Thr Leu Gly Lys
 65 70 75 80

Asn Gly Tyr Asp Glu Thr Phe Gly Ile Ala Leu Lys Gly Leu Thr Pro
 85 90 95

Gly Ala His Thr Leu Arg Val Thr Ala Ser Ile Pro Tyr Ser Arg Thr
 100 105 110

Gly Glu Gly Leu His Arg Met Val Asp Pro Ala Asp Asn Glu Val Tyr
 115 120 125

Leu Tyr Thr Gln Phe Glu Thr Ala Asp Ala Lys Arg Met Phe Ala Cys
 130 135 140

Phe Asp Gln Pro Asp Leu Lys Ala Thr Tyr Asp Leu Asn Ile Lys Thr
 145 150 155 160

Pro Lys Gly Trp Lys Ile Ile Ser Asn Ser Glu Gln Gln Val Ser Thr
 165 170 175

Gln His Thr Asp Tyr Asp Thr His Ile Ser Arg Val Asp Tyr Pro Leu
 180 185 190

Ser Thr Tyr Leu Ile Ala Val Cys Ala Gly Arg Tyr His Glu Val Cys
 195 200 205

Asp Val Trp Lys Gly Thr Leu Thr His His Ala Glu Thr Pro Ala Asp
 210 215 220

Gln Pro Thr Glu Leu Thr Val Pro Leu Ala Leu Tyr Cys Arg Ser Ser
 225 230 235 240

Leu Ala Lys Asp Leu Asp Ala Val Arg Leu Phe Thr Glu Thr Lys Gln
 245 250 255

Gly Phe Asp Trp Tyr His Arg Asn Phe Gly Val Ala Tyr Pro Phe Gly
 260 265 270
 Lys Tyr Asp Gln Ile Phe Val Pro Glu Phe Asn Ala Gly Ala Met Glu
 275 280 285
 Asn Ala Gly Ala Val Thr Ile Arg Asp Glu Tyr Val Phe Ala Ser Lys
 290 295 300
 Ala Thr Arg Tyr Arg Tyr Glu Arg Arg Ala Glu Thr Ile Leu His Glu
 305 310 315 320
 Leu Ala His Met Trp Phe Gly Val Leu Val Thr Met Gln Trp Trp Asp
 325 330 335
 Asp Leu Trp Leu Asn Glu Ser Phe Ala Thr Trp Ser Ala Ala Ile Ser
 340 345 350
 Gln Ala Glu Glu Thr Glu Tyr Asn Thr Ala Trp Val Thr Phe Ala Asn
 355 360 365
 Val Glu Lys Ser Trp Ala Tyr Gln Gln Asp Gln Leu Pro Ser Thr His
 370 375 380
 Pro Val Phe Ser Asp Gly Tyr Asp Ile Glu Thr Val Asp Gln Asn Phe
 385 390 395 400
 Asp Gly Ile Thr Tyr Ala Lys Gly Ala Ser Val Leu Lys Gln Leu Gln
 405 410 415
 Ala Tyr Val Gly Arg Glu Glu Phe Leu Ala Gly Val Arg Arg His Phe
 420 425 430
 Ala Asn His Ala Trp Gly Asn Ala Ser Phe Asp Asp Leu Leu Gly Ala
 435 440 445
 Leu Glu Gln Ser Ser Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln Trp
 450 455 460
 Leu Lys Thr Thr Gly Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr Asp
 465 470 475 480
 Asn Gly Lys Tyr Thr Ser Phe Ser Val Thr Gln Thr Gly Ala Ala Pro
 485 490 495
 Gly Ala Gly Glu Leu Arg Thr His Arg Ile Ala Val Gly Leu Tyr Lys
 500 505 510
 Leu Val Asp Gly Ser Leu Asn Arg Tyr Ala Arg Val Glu Leu Asp Cys
 515 520 525
 Ser Gly Ala Ser Thr Ser Val Glu Glu Ile Val Gly Leu Glu Gln Ala
 530 535 540
 Asp Phe Val Leu Val Asn Asp Asp Asp Leu Thr Tyr Ala Leu Leu Asp
 545 550 555 560
 Leu Asp Asp Asp Ser Arg Asn Phe Val Ile Asp Asn Ile Asp Lys Phe
 565 570 575
 Ser Asp Pro Met Pro Arg Thr Leu Val Trp Ser Ala Ala Trp Glu Met

580										585					590				
Thr	Arg	Ala	Gly	Gln	Met	Lys	Ala	Arg	Asp	Phe	Ile	Ala	Leu	Val	Ala				
		595					600					605							
Arg	Gly	Ala	Ala	Ala	Glu	Thr	Glu	Ile	Ala	Val	Leu	Glu	Arg	Ile	Leu				
	610					615					620								
Ala	Gln	Ala	Thr	Ser	Ala	Leu	Lys	Ser	Tyr	Ala	Asp	Pro	Ala	Trp	Ala				
625					630					635					640				
Glu	Ala	Thr	Gly	Asn	Asp	Leu	Leu	Ala	Asp	Ala	Phe	Leu	Glu	Gly	Ala				
			645						650					655					
Arg	Ser	Ala	Glu	Pro	Asp	Ser	Asp	Thr	Gln	Leu	Ala	Phe	Ile	Gln	Ala				
		660						665					670						
Leu	Ala	Lys	Ala	Thr	Leu	Asn	Asp	Ala	Ala	Ala	Asp	Tyr	Phe	Arg	Asp				
		675					680					685							
Ile	Leu	Ala	Gly	Asn	Val	Glu	Gly	Leu	Thr	Val	Asp	Pro	Asp	Leu	Arg				
	690					695					700								
Trp	Trp	Ala	Leu	Thr	Ala	Leu	Ile	Ala	Arg	Gly	Asp	Ile	Glu	Ala	Val				
705					710					715					720				
Glu	Asp	Ala	Ile	Ala	Ala	Glu	Leu	Ser	Arg	Asp	Asn	Ser	Ser	Ala	Ser				
			725						730					735					
Phe	Leu	Ala	Ser	Leu	Arg	Ala	Gly	Ala	Ala	Val	Asn	Thr	Glu	Glu	Val				
		740					745						750						
Lys	Ala	Ala	Ala	Tyr	Lys	His	Val	Thr	Ala	Val	Asp	Ser	Gly	Leu	Ser				
	755						760					765							
Asn	Leu	Glu	Leu	Arg	His	Lys	Ile	Glu	Gly	Leu	Thr	Phe	Thr	Gly	Ser				
	770					775					780								
Ser	Glu	Leu	Leu	Gln	Ala	Tyr	Asn	Glu	Gln	Tyr	Phe	Glu	Ile	Leu	Asp				
785				790						795					800				
Asp	Val	Trp	Ala	Asn	Phe	Ser	Gly	Glu	Met	Ala	Gln	Gln	Ile	Val	Leu				
			805						810					815					
Gly	Leu	Phe	Pro	Ser	Trp	Asn	Val	Ser	Glu	Glu	Gly	Leu	Lys	Arg	Thr				
		820						825					830						
Asp	Glu	Phe	Leu	Asp	Gly	Glu	His	Val	Ala	Gly	Ile	Lys	Arg	Ile	Val				
	835						840					845							
Ser	Glu	Ser	Leu	Asp	Arg	Thr	Ala	Arg	Ala	Leu	Arg	Asn	Arg	Ala	Ala				
	850					855					860								
Asp	Ala	Ala																	
865																			

<210> 153

<211> 1578

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1578)

<223> FRXA01014

<400> 153

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Asp Asp Leu Trp Leu Asn Glu Ser Phe Ala Thr Trp Ser Ala Ala Ile	
1 5 10 15	
tct cag gct gag gaa act gaa tac aac act gca tgg gtg act ttc gcc	96
Ser Gln Ala Glu Glu Thr Glu Tyr Asn Thr Ala Trp Val Thr Phe Ala	
20 25 30	
aat gtg gag aag tcg tgg gcg tac cag cag gat cag ctg cct tcc acc	144
Asn Val Glu Lys Ser Trp Ala Tyr Gln Gln Asp Gln Leu Pro Ser Thr	
35 40 45	
cac ccg gtg ttc tct gac gga tac gac att gag act gtc gac cag aac	192
His Pro Val Phe Ser Asp Gly Tyr Asp Ile Glu Thr Val Asp Gln Asn	
50 55 60	
ttc gac ggc atc acc tac gca aag ggc gcc tcg gtg ctc aag cag ctg	240
Phe Asp Gly Ile Thr Tyr Ala Lys Gly Ala Ser Val Leu Lys Gln Leu	
65 70 75 80	
cag gca tac gtt ggc cgt gag gaa ttc ctg gca ggc gta cgc agg cac	288
Gln Ala Tyr Val Gly Arg Glu Glu Phe Leu Ala Gly Val Arg Arg His	
85 90 95	
ttt gcc aac cac gca tgg ggc aac gcc agc ttt gat gat ctg ctc ggc	336
Phe Ala Asn His Ala Trp Gly Asn Ala Ser Phe Asp Asp Leu Leu Gly	
100 105 110	
gcc ctc gag cag tcc tcc ggc cgc gac ctc tcc gac tgg gca aac cag	384
Ala Leu Glu Gln Ser Ser Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln	
115 120 125	
tgg ctc aag acc acc ggc atc aac acc ctc ggc gca aag ttc acc acc	432
Trp Leu Lys Thr Thr Gly Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr	
130 135 140	
gac aac ggc aaa tac acc tcc ttc tcc gtc acc cag acc ggc gcc gcg	480
Asp Asn Gly Lys Tyr Thr Ser Phe Ser Val Thr Gln Thr Gly Ala Ala	
145 150 155 160	
ccg ggt gcc ggt gag ctg cgg act cac cgc atc gcg gtg ggt ctt tat	528
Pro Gly Ala Gly Glu Leu Arg Thr His Arg Ile Ala Val Gly Leu Tyr	
165 170 175	
aag ctt gtc gac gga tcc ctc aac cgc tac gca cga gta gaa ctt gac	576
Lys Leu Val Asp Gly Ser Leu Asn Arg Tyr Ala Arg Val Glu Leu Asp	
180 185 190	
tgc agt ggc gcg tcg aca agc gtt gaa gag atc gtt gga ctt gag cag	624
Cys Ser Gly Ala Ser Thr Ser Val Glu Glu Ile Val Gly Leu Glu Gln	
195 200 205	
gct gac ttc gtg ctg gtc aac gat gat gat ctg acg tat gcg ctg ctg	672
Ala Asp Phe Val Leu Val Asn Asp Asp Asp Leu Thr Tyr Ala Leu Leu	

210	215	220	
gat ctg gat gat gat tca cgc aat ttt gtc atc gac aat att gat aag 720 Asp Leu Asp Asp Asp Ser Arg Asn Phe Val Ile Asp Asn Ile Asp Lys 225 230 235 240			
ttc agc gac cct atg cct cgc acg ctg gtg tgg tcc gct gcg tgg gag 768 Phe Ser Asp Pro Met Pro Arg Thr Leu Val Trp Ser Ala Ala Trp Glu 245 250 255			
atg act cgc gct ggt cag atg aag gct cgt gat ttc atc gcg ctg gtt 816 Met Thr Arg Ala Gly Gln Met Lys Ala Arg Asp Phe Ile Ala Leu Val 260 265 270			
gct cgt ggc gct gct gcg gaa act gaa att gct gtg ctg gag cgc att 864 Ala Arg Gly Ala Ala Ala Glu Thr Glu Ile Ala Val Leu Glu Arg Ile 275 280 285			
ctc gcg cag gct acc tct gcg ctg aag agc tac gcc gac cca gcg tgg 912 Leu Ala Gln Ala Thr Ser Ala Leu Lys Ser Tyr Ala Asp Pro Ala Trp 290 295 300			
gca gaa gca act gga aat gac ctg ctg gcc gat gct ttc ctt gag ggt 960 Ala Glu Ala Thr Gly Asn Asp Leu Leu Ala Asp Ala Phe Leu Glu Gly 305 310 315 320			
gct cgc tcc gca gaa cca gac tcc gac act cag ttg gcg ttc att cag 1008 Ala Arg Ser Ala Glu Pro Asp Ser Asp Thr Gln Leu Ala Phe Ile Gln 325 330 335			
gct ctg gca aaa gca acg ctc aat gat gct gct gcc gat tac ttc cgc 1056 Ala Leu Ala Lys Ala Thr Leu Asn Asp Ala Ala Ala Asp Tyr Phe Arg 340 345 350			
gac att ctt gcc ggc aac gtc gaa ggc ctg acc gtg gat cct gac ctg 1104 Asp Ile Leu Ala Gly Asn Val Glu Gly Leu Thr Val Asp Pro Asp Leu 355 360 365			
cgt tgg tgg gca ctg act gcg ctt atc gcc cgt ggt gac atc gag gct 1152 Arg Trp Trp Ala Leu Thr Ala Leu Ile Ala Arg Gly Asp Ile Glu Ala 370 375 380			
gtc gaa gat gca atc gcc gct gaa ctt tcc cgc gac aac tcc agt gcc 1200 Val Glu Asp Ala Ile Ala Ala Glu Leu Ser Arg Asp Asn Ser Ser Ala 385 390 395 400			
tcc ttc ctc gca tca ctt cga gcc ggt gcc gct gtg aac act gaa gaa 1248 Ser Phe Leu Ala Ser Leu Arg Ala Gly Ala Ala Val Asn Thr Glu Glu 405 410 415			
gtg aag gct gct gca tac aag cat gtc ccg gca gtt gat agt ggc cta 1296 Val Lys Ala Ala Tyr Lys His Val Pro Ala Val Asp Ser Gly Leu 420 425 430			
tcc aac ctg gag ctg cgc cac aag att gaa ggc ctc aca ttc act ggc 1344 Ser Asn Leu Glu Leu Arg His Lys Ile Glu Gly Leu Thr Phe Thr Gly 435 440 445			
tct ttt gaa ctg ctg caa gcc tac aac gag cag tac ttc gaa atc ctt 1392 Ser Phe Glu Leu Leu Gln Ala Tyr Asn Glu Gln Tyr Phe Glu Ile Leu 450 455 460			

gat gat gtg tgg gcg aac ttc tcc ggc gaa atg gca cag cag atc gtc 1440
 Asp Asp Val Trp Ala Asn Phe Ser Gly Glu Met Ala Gln Gln Ile Val
 465 470 475 480

ctc gga ctg ttc cct tca tgg aac gtt tcc gaa gag ggt ctc aag cgt 1488
 Leu Gly Leu Phe Pro Ser Trp Asn Val Ser Glu Glu Gly Leu Lys Arg
 485 490 495

acc gac gag ttt ctt gat ggc gaa cat gtc gca ggc atc aag cga att 1536
 Thr Asp Glu Phe Leu Asp Gly Glu His Val Ala Gly Ile Lys Arg Ile
 500 505 510

gtt tcc gaa tcc ctc gac cgc act gcc cgt gct ctg cgc aac 1578
 Val Ser Glu Ser Leu Asp Arg Thr Ala Arg Ala Leu Arg Asn
 515 520 525

<210> 154

<211> 526

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 154

Asp Asp Leu Trp Leu Asn Glu Ser Phe Ala Thr Trp Ser Ala Ala Ile
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Ser Gln Ala Glu Glu Thr Glu Tyr Asn Thr Ala Trp Val Thr Phe Ala
 20 25 30

Asn Val Glu Lys Ser Trp Ala Tyr Gln Gln Asp Gln Leu Pro Ser Thr
 35 40 45

His Pro Val Phe Ser Asp Gly Tyr Asp Ile Glu Thr Val Asp Gln Asn
 50 55 60

Phe Asp Gly Ile Thr Tyr Ala Lys Gly Ala Ser Val Leu Lys Gln Leu
 65 70 75 80

Gln Ala Tyr Val Gly Arg Glu Glu Phe Leu Ala Gly Val Arg Arg His
 85 90 95

Phe Ala Asn His Ala Trp Gly Asn Ala Ser Phe Asp Asp Leu Leu Gly
 100 105 110

Ala Leu Glu Gln Ser Ser Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln
 115 120 125

Trp Leu Lys Thr Thr Gly Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr
 130 135 140

Asp Asn Gly Lys Tyr Thr Ser Phe Ser Val Thr Gln Thr Gly Ala Ala
 145 150 155 160

Pro Gly Ala Gly Glu Leu Arg Thr His Arg Ile Ala Val Gly Leu Tyr
 165 170 175

Lys Leu Val Asp Gly Ser Leu Asn Arg Tyr Ala Arg Val Glu Leu Asp
 180 185 190

Cys Ser Gly Ala Ser Thr Ser Val Glu Glu Ile Val Gly Leu Glu Gln

195					200					205					
Ala	Asp	Phe	Val	Leu	Val	Asn	Asp	Asp	Asp	Leu	Thr	Tyr	Ala	Leu	Leu
210					215					220					
Asp	Leu	Asp	Asp	Asp	Ser	Arg	Asn	Phe	Val	Ile	Asp	Asn	Ile	Asp	Lys
225					230					235					240
Phe	Ser	Asp	Pro	Met	Pro	Arg	Thr	Leu	Val	Trp	Ser	Ala	Ala	Trp	Glu
				245					250					255	
Met	Thr	Arg	Ala	Gly	Gln	Met	Lys	Ala	Arg	Asp	Phe	Ile	Ala	Leu	Val
			260					265					270		
Ala	Arg	Gly	Ala	Ala	Ala	Glu	Thr	Glu	Ile	Ala	Val	Leu	Glu	Arg	Ile
		275					280					285			
Leu	Ala	Gln	Ala	Thr	Ser	Ala	Leu	Lys	Ser	Tyr	Ala	Asp	Pro	Ala	Trp
	290					295					300				
Ala	Glu	Ala	Thr	Gly	Asn	Asp	Leu	Leu	Ala	Asp	Ala	Phe	Leu	Glu	Gly
305					310					315					320
Ala	Arg	Ser	Ala	Glu	Pro	Asp	Ser	Asp	Thr	Gln	Leu	Ala	Phe	Ile	Gln
				325					330					335	
Ala	Leu	Ala	Lys	Ala	Thr	Leu	Asn	Asp	Ala	Ala	Ala	Asp	Tyr	Phe	Arg
			340					345					350		
Asp	Ile	Leu	Ala	Gly	Asn	Val	Glu	Gly	Leu	Thr	Val	Asp	Pro	Asp	Leu
		355					360					365			
Arg	Trp	Trp	Ala	Leu	Thr	Ala	Leu	Ile	Ala	Arg	Gly	Asp	Ile	Glu	Ala
	370					375					380				
Val	Glu	Asp	Ala	Ile	Ala	Ala	Glu	Leu	Ser	Arg	Asp	Asn	Ser	Ser	Ala
385						390					395				400
Ser	Phe	Leu	Ala	Ser	Leu	Arg	Ala	Gly	Ala	Ala	Val	Asn	Thr	Glu	Glu
				405					410					415	
Val	Lys	Ala	Ala	Ala	Tyr	Lys	His	Val	Pro	Ala	Val	Asp	Ser	Gly	Leu
			420					425					430		
Ser	Asn	Leu	Glu	Leu	Arg	His	Lys	Ile	Glu	Gly	Leu	Thr	Phe	Thr	Gly
		435					440					445			
Ser	Phe	Glu	Leu	Leu	Gln	Ala	Tyr	Asn	Glu	Gln	Tyr	Phe	Glu	Ile	Leu
		450				455					460				
Asp	Asp	Val	Trp	Ala	Asn	Phe	Ser	Gly	Glu	Met	Ala	Gln	Gln	Ile	Val
465						470					475				480
Leu	Gly	Leu	Phe	Pro	Ser	Trp	Asn	Val	Ser	Glu	Glu	Gly	Leu	Lys	Arg
				485					490					495	
Thr	Asp	Glu	Phe	Leu	Asp	Gly	Glu	His	Val	Ala	Gly	Ile	Lys	Arg	Ile
			500					505					510		
Val	Ser	Glu	Ser	Leu	Asp	Arg	Thr	Ala	Arg	Ala	Leu	Arg	Asn		
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<210> 155
 <211> 964
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(964)
 <223> FRXA01018

<400> 155
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 Leu Thr Ser Thr Asn
 1 5
 ctc acc cga cag gaa gct tcg gat cgt tcg agg tta ctg agt gta gaa 163
 Leu Thr Arg Gln Glu Ala Ser Asp Arg Ser Arg Leu Leu Ser Val Glu
 10 15 20
 aac tat gac att gca ctt gat ctc aac aac ggt gat gag ttt ttt agt 211
 Asn Tyr Asp Ile Ala Leu Asp Leu Asn Asn Gly Asp Glu Phe Phe Ser
 25 30 35
 tcc tcc acc gtt gtc agc ttc act gtc agg aag gct ggc gat acc ttt 259
 Ser Ser Thr Val Val Ser Phe Thr Val Arg Lys Ala Gly Asp Thr Phe
 40 45 50
 att gat ctc cgc gca gca agc gtt gag gag gtt cgc ctg gac aat gtg 307
 Ile Asp Leu Arg Ala Ala Ser Val Glu Glu Val Arg Leu Asp Asn Val
 55 60 65
 tcc atc aaa gat gag gct cta acc ctt ggc aag aac ggc tac gac gag 355
 Ser Ile Lys Asp Glu Ala Leu Thr Leu Gly Lys Asn Gly Tyr Asp Glu
 70 75 80 85
 acg ttc ggc atc gcc ctg aag ggt ctt act ccc ggc gcg cac acc ttg 403
 Thr Phe Gly Ile Ala Leu Lys Gly Leu Thr Pro Gly Ala His Thr Leu
 90 95 100
 cgg gta acg gcg tct atc ccc tat tcc cgc acc ggt gaa ggc ctg cac 451
 Arg Val Thr Ala Ser Ile Pro Tyr Ser Arg Thr Gly Glu Gly Leu His
 105 110 115
 cgc atg gtg gat cca gca gac aat gag gtg tat ttg tac acc cag ttt 499
 Arg Met Val Asp Pro Ala Asp Asn Glu Val Tyr Leu Tyr Thr Gln Phe
 120 125 130
 gag acc gcc gat gcc aag cgt atg ttc gcg tgt ttc gat cag cca gac 547
 Glu Thr Ala Asp Ala Lys Arg Met Phe Ala Cys Phe Asp Gln Pro Asp
 135 140 145
 ctc aag gct acc tat gat ctg aac atc aaa act cct aag ggt tgg aag 595
 Leu Lys Ala Thr Tyr Asp Leu Asn Ile Lys Thr Pro Lys Gly Trp Lys
 150 155 160 165
 atc att tcc aac tct gag cag cag gtt tcc act cag cac act gat tac 643
 Ile Ile Ser Asn Ser Glu Gln Gln Val Ser Thr Gln His Thr Asp Tyr

170										175					180					
gat	acc	cac	att	tcc	cga	gtg	gac	tat	ccc	ctc	tcc	acc	tac	ctg	att	691				
Asp	Thr	His	Ile	Ser	Arg	Val	Asp	Tyr	Pro	Leu	Ser	Thr	Tyr	Leu	Ile					
			185					190					195							
gcg	gtg	tgc	gcg	ggg	cgt	tac	cac	gag	gtg	tgc	gat	gtc	tgg	aag	ggg	739				
Ala	Val	Cys	Ala	Gly	Arg	Tyr	His	Glu	Val	Cys	Asp	Val	Trp	Lys	Gly					
		200					205					210								
acg	ctc	acc	cac	cat	gca	gaa	aca	cct	gcc	gat	cag	cca	act	gag	ctg	787				
Thr	Leu	Thr	His	His	Ala	Glu	Thr	Pro	Ala	Asp	Gln	Pro	Thr	Glu	Leu					
		215				220					225									
act	gtt	ccg	ctt	gct	ctc	tac	tgc	cgc	agt	tct	ttg	gct	aaa	gat	ctt	835				
Thr	Val	Pro	Leu	Ala	Leu	Tyr	Cys	Arg	Ser	Ser	Leu	Ala	Lys	Asp	Leu					
		230			235					240					245					
gat	gcg	gtg	cgt	ctg	ttt	acc	gaa	acg	aag	cag	ggc	ttt	gat	tgg	tac	883				
Asp	Ala	Val	Arg	Leu	Phe	Thr	Glu	Thr	Lys	Gln	Gly	Phe	Asp	Trp	Tyr					
			250						255					260						
cac	cgc	aac	ttc	ggg	gtg	gcg	tac	cca	ttc	ggc	aag	tac	gat	cag	atc	931				
His	Arg	Asn	Phe	Gly	Val	Ala	Tyr	Pro	Phe	Gly	Lys	Tyr	Asp	Gln	Ile					
			265					270						275						
ttc	gtc	cct	gaa	ttt	aat	gct	ggc	gcg	atg	gag						964				
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<213> Corynebacterium glutamicum

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Asp	Glu	Phe	Phe	Ser	Ser	Ser	Thr	Val	Val	Ser	Phe	Thr	Val	Arg	Lys
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Ala	Gly	Asp	Thr	Phe	Ile	Asp	Leu	Arg	Ala	Ala	Ser	Val	Glu	Glu	Val
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Arg	Leu	Asp	Asn	Val	Ser	Ile	Lys	Asp	Glu	Ala	Leu	Thr	Leu	Gly	Lys
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Asn	Gly	Tyr	Asp	Glu	Thr	Phe	Gly	Ile	Ala	Leu	Lys	Gly	Leu	Thr	Pro
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Gly	Ala	His	Thr	Leu	Arg	Val	Thr	Ala	Ser	Ile	Pro	Tyr	Ser	Arg	Thr
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Gly	Glu	Gly	Leu	His	Arg	Met	Val	Asp	Pro	Ala	Asp	Asn	Glu	Val	Tyr
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Leu Tyr Thr Gln Phe Glu Thr Ala Asp Ala Lys Arg Met Phe Ala Cys
 130 135 140
 Phe Asp Gln Pro Asp Leu Lys Ala Thr Tyr Asp Leu Asn Ile Lys Thr
 145 150 155 160
 Pro Lys Gly Trp Lys Ile Ile Ser Asn Ser Glu Gln Gln Val Ser Thr
 165 170 175
 Gln His Thr Asp Tyr Asp Thr His Ile Ser Arg Val Asp Tyr Pro Leu
 180 185 190
 Ser Thr Tyr Leu Ile Ala Val Cys Ala Gly Arg Tyr His Glu Val Cys
 195 200 205
 Asp Val Trp Lys Gly Thr Leu Thr His His Ala Glu Thr Pro Ala Asp
 210 215 220
 Gln Pro Thr Glu Leu Thr Val Pro Leu Ala Leu Tyr Cys Arg Ser Ser
 225 230 235 240
 Leu Ala Lys Asp Leu Asp Ala Val Arg Leu Phe Thr Glu Thr Lys Gln
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 Met Ile Pro Phe Pro
 1 5
 ggg caa ccg cag cag caa agc gca ccc aat gac gag acc cgt ttc atc 163
 Gly Gln Pro Gln Gln Gln Ser Ala Pro Asn Asp Glu Thr Arg Phe Ile
 10 15 20
 gac ctt aac gaa cgt cat aaa gat gat gaa cca gcc ctg ttt cgc gat 211
 Asp Leu Asn Glu Arg His Lys Asp Asp Glu Pro Ala Leu Phe Arg Asp
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 gat gtt att gat caa act ctc gct att ttg atc agt aaa aat aag ccc 259
 Asp Val Ile Asp Gln Thr Leu Ala Ile Leu Ile Ser Lys Asn Lys Pro
 40 45 50
 aat gcg cta ctc gtt ggg cct gcc ggt aca ggt aaa tcc cgt atc gca 307

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Glu	Asp	Ile	Ala	Arg	Arg	Leu	Ala	Asn	Asp	Asp	Val	Ser	Ile	Pro	Asp	85	
70					75					80							
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Gln	Leu	Val	Gly	His	Arg	Ile	Leu	Asp	Val	Ser	Ile	Ala	Glu	Leu	Val	100	
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Ala	Gly	Ala	Gly	Val	Val	Gly	Gln	Leu	Lys	Lys	Arg	Ile	Leu	Asp	Leu	115	
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Glu	Ile	His	Gln	Ile	Ala	Gly	Asp	Gln	Ser	Ser	His	Ser	Gly	Ser	Gln	145	
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Arg	Val	Ile	Gly	Ala	Thr	Thr	Thr	Gln	Glu	Ala	Arg	Asp	Phe	Asp	His	180	
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gat	cca	gcc	ctc	aaa	cgc	cgt	ttt	agc	aga	gta	aat	gtc	gat	gaa	ttt	691	
Asp	Pro	Ala	Leu	Lys	Arg	Arg	Phe	Ser	Arg	Val	Asn	Val	Asp	Glu	Phe	195	
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Leu	Lys	His	Phe	Asn	Asn	Ala	Val	Thr	Val	Ser	Asp	Asp	Val	Leu	Gly	225	
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Pro	Asp	Ala	Ala	Leu	Thr	Leu	Phe	Asp	Lys	Ala	Leu	Ala	Ser	Leu	Thr	260	
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Met	Glu	Lys	Gln	Arg	Leu	Ile	Asn	Asn	His	Val	Ile	Ala	Pro	Ser	Leu	275	
			265				270										
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Lys	Phe	Pro	Val	Ser	Glu	Arg	His	Ile	His	Asn	Thr	Ala	Arg	Lys	Leu	290	
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atc aat ggt ccc gaa tac att agt cct gag tcc att act ggc ctt atc Ile Asn Gly Pro Glu Tyr Ile Ser Pro Glu Ser Ile Thr Gly Leu Ile 375 380 385			1267
gga tca tcc gat ggc tat atc ggc tct aat tct aag cgt gct aaa cca Gly Ser Ser Asp Gly Tyr Ile Gly Ser Asn Ser Lys Arg Ala Lys Pro 390 395 400 405			1315
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cag gcc att atc att gcc acc acc aat gca gcc cgc gac aaa atc ggt Gln Ala Ile Ile Ile Ala Thr Thr Asn Ala Ala Arg Asp Lys Ile Gly 455 460 465			1507
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ttg cct tca acc gca ttg atg cag gca cct acc gtg aga ttc tgg aca Leu Pro Ser Thr Ala Leu Met Gln Ala Pro Thr Val Arg Phe Trp Thr 520 525 530			1699
atc tct acc agc gtc gcc gtg acg ccg tgc tgc tta gcc acc ccg cat Ile Ser Thr Ser Val Ala Val Thr Pro Cys Cys Leu Ala Thr Pro His 535 540 545			1747

tac gca gca cag atc cct gca gat att gat tca gac act ctt gat cag 1795
 Tyr Ala Ala Gln Ile Pro Ala Asp Ile Asp Ser Asp Thr Leu Asp Gln
 550 555 560 565

ctg gtg gaa acc acc ttt atc tca gat ttt ggt gca cgt cct gct gca 1843
 Leu Val Glu Thr Thr Phe Ile Ser Asp Phe Gly Ala Arg Pro Ala Ala
 570 575 580

cgc acc atc gaa gac cac atc gca tcc ttg ctg atg tgaccaacct 1889
 Arg Thr Ile Glu Asp His Ile Ala Ser Leu Leu Met
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tttaggagta cat 1902

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<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45

Ser Lys Asn Lys Pro Asn Ala Leu Leu Val Gly Pro Ala Gly Thr Gly
 50 55 60

Lys Ser Arg Ile Ala Glu Asp Ile Ala Arg Arg Leu Ala Asn Asp Asp
 65 70 75 80

Val Ser Ile Pro Asp Gln Leu Val Gly His Arg Ile Leu Asp Val Ser
 85 90 95

Ile Ala Glu Leu Val Ala Gly Ala Gly Val Val Gly Gln Leu Lys Lys
 100 105 110

Arg Ile Leu Asp Leu Ile Lys Tyr Ala Thr Asp Pro Ser Asn Lys Val
 115 120 125

Ile Ile Phe Ile Asp Glu Ile His Gln Ile Ala Gly Asp Gln Ser Ser
 130 135 140

His Ser Gly Ser Gln Ala Lys Val Ala Gln Ile Leu Lys Pro Tyr Leu
 145 150 155 160

Ala Arg Gly Asp Leu Arg Val Ile Gly Ala Thr Thr Thr Gln Glu Ala
 165 170 175

Arg Asp Phe Asp His Asp Pro Ala Leu Lys Arg Arg Phe Ser Arg Val
 180 185 190

Asn Val Asp Glu Phe Asp Arg Asp Gln Thr Leu Thr Ile Leu His Ala
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Ala	Arg	Asp	Gly	Tyr	Leu	Lys	His	Phe	Asn	Asn	Ala	Val	Thr	Val	Ser	210	215	220
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Gly	Asn	Thr	Ala	Gln	Pro	Asp	Ala	Ala	Leu	Thr	Leu	Phe	Asp	Lys	Ala	245	250	255
Leu	Ala	Ser	Leu	Thr	Met	Glu	Lys	Gln	Arg	Leu	Ile	Asn	Asn	His	Val	260	265	270
Ile	Ala	Pro	Ser	Leu	Lys	Phe	Pro	Val	Ser	Glu	Arg	His	Ile	His	Asn	275	280	285
Thr	Ala	Arg	Lys	Leu	Ala	Phe	Gly	Ser	Gln	Val	Pro	Ala	Ser	Ile	Asn	290	295	300
Thr	Asp	Asp	Ala	Arg	Asp	Lys	Leu	Glu	Thr	Leu	Phe	Gly	Gln	Asp	His	305	310	315
Ile	Ile	Glu	Pro	Val	Leu	Thr	Ala	Ile	Lys	Arg	Glu	Gln	Leu	Gly	Ile	325	330	335
Phe	Pro	Arg	Thr	Lys	Pro	Leu	Ser	Trp	Val	Phe	Ala	Gly	Ser	Ser	Gly	340	345	350
Val	Gly	Lys	Thr	Glu	Met	Ala	Arg	Ile	Leu	Ser	Arg	Ala	Ile	Asn	Gly	355	360	365
Gly	Asp	Pro	Ile	Ile	Ile	Asn	Gly	Pro	Glu	Tyr	Ile	Ser	Pro	Glu	Ser	370	375	380
Ile	Thr	Gly	Leu	Ile	Gly	Ser	Ser	Asp	Gly	Tyr	Ile	Gly	Ser	Asn	Ser	385	390	395
Lys	Arg	Ala	Lys	Pro	Leu	Asp	Pro	Leu	Ile	Ser	Asn	Pro	Arg	Gln	Val	405	410	415
Ile	Val	Leu	Asp	Glu	Phe	Glu	Lys	Ser	His	Pro	His	Phe	Gln	Gln	Leu	420	425	430
Phe	Met	Ala	Ala	Leu	Asp	Thr	Gly	Thr	Met	Ala	Met	Ala	Asn	Gly	Thr	435	440	445
Thr	Leu	Asn	Phe	Ser	Gln	Ala	Ile	Ile	Ile	Ala	Thr	Thr	Asn	Ala	Ala	450	455	460
Arg	Asp	Lys	Ile	Gly	Arg	Asp	Ser	Phe	Gly	Phe	Asp	Ser	Asp	Asn	Ser	465	470	475
Gly	Val	Leu	Gly	Ser	Ala	Gln	Ala	Ala	Thr	Asp	Pro	Arg	Ala	Gln	Glu	485	490	495
Arg	Leu	Lys	Ser	Leu	Met	Ser	Lys	Asp	Phe	Leu	Leu	Asn	Cys	Ser	Thr	500	505	510
Val	Ser	Arg	Ile	Ser	Leu	Pro	Ser	Thr	Ala	Leu	Met	Gln	Ala	Pro	Thr	515	520	525
Val	Arg	Phe	Trp	Thr	Ile	Ser	Thr	Ser	Val	Ala	Val	Thr	Pro	Cys	Cys			

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Met Thr Gln Val Val																5
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Ala Gly Thr Leu Val Gly Glu Ser Ile Asn Arg Glu Ile Asp Glu Asp																20
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Lys Tyr Pro Tyr Leu Ser Ser Tyr Ala Ala Pro Val Ala Val Pro Val																35
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Arg Glu Ile Ile Gly Arg Glu Glu Glu Val Asn Lys Ile Met Ala Ala																50
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Leu Met Arg Pro Glu Ile Ser Asn Val Met Leu Val Gly Pro Ala Gly																65
55 60																
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Ser Gly Lys Thr Thr Leu Val Gln Gln Ala Leu Val Lys Asp Pro Glu																85
70 75 80																
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Arg Asn Tyr Ile Glu Val Asp Val Ala Lys Met Val Ala Asp Leu Ser																100
90 95																
acc ccg gcg caa atg gct gcg cgt att aaa ggt gtg ttt gag gac gcc																451
Thr Pro Ala Gln Met Ala Ala Arg Ile Lys Gly Val Phe Glu Asp Ala																115
105 110																
att gcc tat cgc aag cac gaa ggt cat gaa ttg gtg ctg ttc gtt gat																499

Ile	Ala	Tyr	Arg	Lys	His	Glu	Gly	His	Glu	Leu	Val	Leu	Phe	Val	Asp		
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gag	ttt	cac	caa	att	gtg	cag	ctg	tct	aat	gct	gcg	gta	gag	gca	atc	547	
Glu	Phe	His	Gln	Ile	Val	Gln	Leu	Ser	Asn	Ala	Ala	Val	Glu	Ala	Ile		
	135					140					145						
aag	ccg	att	ttg	gcg	atg	tct	ggg	gtc	ctt	ggg	gtg	cgc	gtt	atc	gct	595	
Lys	Pro	Ile	Leu	Ala	Met	Ser	Gly	Val	Leu	Gly	Val	Arg	Val	Ile	Ala		
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Ala	Thr	Thr	Leu	Glu	Glu	Phe	His	Glu	His	Ile	Arg	Pro	Asn	Gln	Ala		
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Leu	Thr	Glu	Arg	Leu	Gln	Glu	Ile	Arg	Leu	Thr	Pro	Thr	Asp	Gln	Lys		
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acc	act	gtg	gcg	att	ttg	cgt	ggg	atg	gca	gat	cgt	tat	ggc	gta	agt	739	
Thr	Thr	Val	Ala	Ile	Leu	Arg	Gly	Met	Ala	Asp	Arg	Tyr	Gly	Val	Ser		
		200					205					210					
gat	cag	ttc	tat	gac	gac	cac	gtt	ttt	gag	cag	att	tac	tcc	acc	act	787	
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gag	cgt	ttt	atg	ccg	agt	tct	gtc	cag	cct	cgt	aaa	tcc	att	cgt	gtc	835	
Glu	Arg	Phe	Met	Pro	Ser	Ser	Val	Gln	Pro	Arg	Lys	Ser	Ile	Arg	Val		
230					235					240				245			
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Leu	Asp	Ala	Met	Val	Gly	Trp	His	Arg	Leu	Ser	Gly	Lys	Pro	Met	Asp		
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Met	Asp	Leu	Leu	Gly	Asp	Val	Leu	His	Asp	Ala	Ile	Gly	Val	Asp	Ile		
			265				270						275				
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Ala	Phe	Lys	Val	Asp	Gly	Thr	Ser	Ile	Lys	Asp	Lys	Leu	Asp	Glu	Lys		
		280					285					290					
gta	atg	gcg	caa	agt	ctt	gcc	acc	act	gtg	gta	gca	cgt	cgt	ttg	cag	1027	
Val	Met	Ala	Gln	Ser	Leu	Ala	Thr	Thr	Val	Val	Ala	Arg	Arg	Leu	Gln		
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gat gag gtt gag aaa gct gat cga gct att gcg cgg ttg tta ctg cag Asp Glu Val Glu Lys Ala Asp Arg Ala Ile Ala Arg Leu Leu Leu Gln 390 395 400 405			1315
gta ctt gat gat ggc cga cta tct gac gat tac aac cgt gag gtg agt Val Leu Asp Asp Gly Arg Leu Ser Asp Asp Tyr Asn Arg Glu Val Ser 410 415 420			1363
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cag gat gtg gct act gag gtc tat gaa cgc cac ggc gtg aaa ctg cac Gln Asp Val Ala Thr Glu Val Tyr Glu Arg His Gly Val Lys Leu His 505 510 515			1651
tgt tca caa aag gtt atg gag ttt ctg ctt gtg gat cag gtg gag gaa Cys Ser Gln Lys Val Met Glu Phe Leu Leu Val Asp Gln Val Glu Glu 520 525 530			1699
agt gct gaa tct ggt ggt gcc cgt ggt gcg gtg cgg tct ttg cag cgg Ser Ala Glu Ser Gly Gly Ala Arg Gly Ala Val Arg Ser Leu Gln Arg 535 540 545			1747
gaa gtg gtc act gaa gtg gcg acc ttt att aat acc tac cca gaa gtg Glu Val Val Thr Glu Val Ala Thr Phe Ile Asn Thr Tyr Pro Glu Val 550 555 560 565			1795
cgt gac att tac gtt gat gtc gat ggt cag atg cgt aat aag act aac Arg Asp Ile Tyr Val Asp Val Asp Gly Gln Met Arg Asn Lys Thr Asn 570 575 580			1843
cgt gtg tct acg gcc cgt gtg gtg ata aag cgt gtc gaa ggt Arg Val Ser Thr Ala Arg Val Val Ile Lys Arg Val Glu Gly 585 590 595			1885
taattactct ggggtcgctt aaa			1908

<210> 160

<211> 595

<212> PRT

<213> Corynebacterium glutamicum

<400> 160

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Glu Ile Asp Glu Asp Lys Tyr Pro Tyr Leu Ser Ser Tyr Ala Ala Pro
 20 25 30

Val Ala Val Pro Val Arg Glu Ile Ile Gly Arg Glu Glu Glu Val Asn
 35 40 45

Lys Ile Met Ala Ala Leu Met Arg Pro Glu Ile Ser Asn Val Met Leu
 50 55 60

Val Gly Pro Ala Gly Ser Gly Lys Thr Thr Leu Val Gln Gln Ala Leu
 65 70 75 80

Val Lys Asp Pro Glu Arg Asn Tyr Ile Glu Val Asp Val Ala Lys Met
 85 90 95

Val Ala Asp Leu Ser Thr Pro Ala Gln Met Ala Ala Arg Ile Lys Gly
 100 105 110

Val Phe Glu Asp Ala Ile Ala Tyr Arg Lys His Glu Gly His Glu Leu
 115 120 125

Val Leu Phe Val Asp Glu Phe His Gln Ile Val Gln Leu Ser Asn Ala
 130 135 140

Ala Val Glu Ala Ile Lys Pro Ile Leu Ala Met Ser Gly Val Leu Gly
 145 150 155 160

Val Arg Val Ile Ala Ala Thr Thr Leu Glu Glu Phe His Glu His Ile
 165 170 175

Arg Pro Asn Gln Ala Leu Thr Glu Arg Leu Gln Glu Ile Arg Leu Thr
 180 185 190

Pro Thr Asp Gln Lys Thr Thr Val Ala Ile Leu Arg Gly Met Ala Asp
 195 200 205

Arg Tyr Gly Val Ser Asp Gln Phe Tyr Asp Asp His Val Phe Glu Gln
 210 215 220

Ile Tyr Ser Thr Thr Glu Arg Phe Met Pro Ser Ser Val Gln Pro Arg
 225 230 235 240

Lys Ser Ile Arg Val Leu Asp Ala Met Val Gly Trp His Arg Leu Ser
 245 250 255

Gly Lys Pro Met Asp Met Asp Leu Leu Gly Asp Val Leu His Asp Ala
 260 265 270

Ile Gly Val Asp Ile Ala Phe Lys Val Asp Gly Thr Ser Ile Lys Asp
 275 280 285

Lys Leu Asp Glu Lys Val Met Ala Gln Ser Leu Ala Thr Thr Val Val

290	295	300
Ala Arg Arg Leu Gln 305	Leu Val Val Ala Asp 310	Leu His Asp Lys Ser Arg 315 320
Pro Leu Ser Asn Phe 325	Leu Phe Thr Gly 330	Pro Thr Gly Val Gly Lys Thr 335
Glu Leu Val Lys Gln 340	Leu Ala Arg Val 345	Leu Phe Gly Asp Asp Thr Gly 350
Arg Leu Ile Arg Phe 355	Asp Met Ser Glu Phe 360	Ala Leu Glu Ser Ser Leu 365
Asp Leu Phe Arg Ser 370	Glu Leu Thr Arg Arg 375	Val Ala Asp Gln Gly Asn 380
Ala Ile Val Leu Leu 385	Asp Glu Val Glu Lys 390	Ala Asp Arg Ala Ile Ala 395 400
Arg Leu Leu Leu Gln 405	Val Leu Asp Asp Gly 410	Arg Leu Ser Asp Asp Tyr 415
Asn Arg Glu Val Ser 420	Phe Leu Asn Thr Tyr 425	Ile Val Met Thr Thr Asn 430
Ala Gly Ser Glu Ile 435	Phe Glu Thr Ile Ser 440	Asn Tyr Ala Thr Asp Asp 445
Thr Gly Asp Gly Arg 450	Ala Ile Lys Asp Phe 455	Val Lys Asn Ile His Thr 460
Ser Ile Lys Asn Lys 465	Gly Phe Pro Pro Glu 470	Leu Leu Gly Arg Val Asp 475 480
Glu Ile Val Pro Phe 485	Gln Pro Leu Ser Glu 490	Thr Thr Gln Asp Arg Ile 495
Ile Ser Lys Lys Leu 500	Gln Asp Val Ala Thr 505	Glu Val Tyr Glu Arg His 510
Gly Val Lys Leu His 515	Cys Ser Gln Lys Val 520	Met Glu Phe Leu Leu Val 525
Asp Gln Val Glu Glu 530	Ser Ala Glu Ser Gly 535	Gly Ala Arg Gly Ala Val 540
Arg Ser Leu Gln Arg 545	Glu Val Val Thr Glu 550	Val Ala Thr Phe Ile Asn 555 560
Thr Tyr Pro Glu Val 565	Arg Asp Ile Tyr Val 570	Asp Val Asp Gly Gln Met 575
Arg Asn Lys Thr Asn 580	Arg Val Ser Thr Ala 585	Arg Val Val Ile Lys Arg 590
Val Glu Gly 595		

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agtaaattctt ttcaatcgtg gaagcgggtc tcacagtcta atg gca cgt atg cag 115																
Met Ala Arg Met Gln 5																
gaa agc gcc gat ctg ctc aaa tgt tcc ttc tgc gga aag agc caa aag 163																
Glu Ser Ala Asp Leu Leu Lys Cys Ser Phe Cys Gly Lys Ser Gln Lys 20																
cag gta aaa aaa ctc atc gcg ggt ggc gcc gta tat atc tgt gat gag 211																
Gln Val Lys Lys Leu Ile Ala Gly Gly Ala Val Tyr Ile Cys Asp Glu 35																
tgc att gag ctg tgc aac gag att att gaa gaa gaa ctc ggt caa gct 259																
Cys Ile Glu Leu Cys Asn Glu Ile Ile Glu Glu Glu Leu Gly Gln Ala 50																
caa cac gac gag cag gag cgc aac gag ctc ccc aag ccg tcg gag att 307																
Gln His Asp Glu Gln Glu Arg Asn Glu Leu Pro Lys Pro Ser Glu Ile 65																
tca gcc ttc ctt gat act tat gtc atc ggg cag gac cca gca aaa cgt 355																
Ser Ala Phe Leu Asp Thr Tyr Val Ile Gly Gln Asp Pro Ala Lys Arg 85																
atc ctg tcg gtt gcg gtg tac aac cat tac aag cgt ctc cgc gca tcg 403																
Ile Leu Ser Val Ala Val Tyr Asn His Tyr Lys Arg Leu Arg Ala Ser 100																
gaa acc atc ggt cgt cgc agg aat gac gag cct gaa acc gaa ctg gtt 451																
Glu Thr Ile Gly Arg Arg Arg Asn Asp Glu Pro Glu Thr Glu Leu Val 115																
aag tcc aat att ttg atg ctc ggc ccc act ggc tcc ggc aag act ttc 499																
Lys Ser Asn Ile Leu Met Leu Gly Pro Thr Gly Ser Gly Lys Thr Phe 130																
ctt gcc cag act ttg gca aag ctg ctg gat gtt cct ttt gct atc gcg 547																
Leu Ala Gln Thr Leu Ala Lys Leu Leu Asp Val Pro Phe Ala Ile Ala 145																
gat gcc acc tca ctg acc gag gct ggt tat gtg ggc gag gat gtg gaa 595																
Asp Ala Thr Ser Leu Thr Glu Ala Gly Tyr Val Gly Glu Asp Val Glu 165																
aac atc ttg ctc aag ctg ctt cag gct gct gat ttt gat gtg gaa cgt 643																
Asn Ile Leu Leu Lys Leu Leu Gln Ala Ala Asp Phe Asp Val Glu Arg 180																
gca caq cqc qqc atc att tac atc gat gaa gtg gac aag att tcc cgc 691																

Ala	Gln	Arg	Gly	Ile	Ile	Tyr	Ile	Asp	Glu	Val	Asp	Lys	Ile	Ser	Arg	
			185					190					195			
aag	tct	gaa	aac	cca	tcg	atc	act	cgc	gat	gtt	tcc	ggc	gaa	ggc	gtg	739
Lys	Ser	Glu	Asn	Pro	Ser	Ile	Thr	Arg	Asp	Val	Ser	Gly	Glu	Gly	Val	
		200					205					210				
cag	cag	gca	ctg	ctg	aaa	att	ttg	gaa	ggc	act	gtc	gcc	gca	atc	cca	787
Gln	Gln	Ala	Leu	Leu	Lys	Ile	Leu	Glu	Gly	Thr	Val	Ala	Ala	Ile	Pro	
		215				220					225					
ccg	cag	gga	gga	cgc	aag	cac	ccc	aac	cag	gat	ttc	atc	cag	ctg	gat	835
Pro	Gln	Gly	Gly	Arg	Lys	His	Pro	Asn	Gln	Asp	Phe	Ile	Gln	Leu	Asp	
230					235					240					245	
acc	acc	aac	att	ttg	ttc	atc	gtt	gct	ggc	gcg	ttc	tct	ggc	ctg	gag	883
Thr	Thr	Asn	Ile	Leu	Phe	Ile	Val	Ala	Gly	Ala	Phe	Ser	Gly	Leu	Glu	
				250					255					260		
aag	gtc	atc	gcg	gac	cgc	aat	ggc	aag	aaa	ggc	ttg	ggc	ttc	ggc	gtg	931
Lys	Val	Ile	Ala	Asp	Arg	Asn	Gly	Lys	Lys	Gly	Leu	Gly	Phe	Gly	Val	
			265					270					275			
gag	gtc	tct	tcc	aag	aag	gaa	gaa	gcc	aac	att	gtg	gat	atc	ttc	aag	979
Glu	Val	Ser	Ser	Lys	Lys	Glu	Glu	Ala	Asn	Ile	Val	Asp	Ile	Phe	Lys	
							285					290				
gat	gtc	ctc	cct	gag	gac	ctg	gtg	aag	ttt	ggc	ctc	atc	cca	gaa	ttc	1027
Asp	Val	Leu	Pro	Glu	Asp	Leu	Val	Lys	Phe	Gly	Leu	Ile	Pro	Glu	Phe	
						300					305					
att	ggg	cgt	ctg	cca	gtc	gtt	gcc	acc	gta	tcc	aac	ctg	gat	cag	aaa	1075
Ile	Gly	Arg	Leu	Pro	Val	Val	Ala	Thr	Val	Ser	Asn	Leu	Asp	Gln	Lys	
310					315					320					325	
tct	ctg	gtc	aag	gtt	ctc	acg	gag	cct	cgt	aac	tca	ttg	gtg	aag	cag	1123
Ser	Leu	Val	Lys	Val	Leu	Thr	Glu	Pro	Arg	Asn	Ser	Leu	Val	Lys	Gln	
				330					335					340		
tat	cga	cgt	ctg	ttt	gaa	atg	gat	gac	gct	gtg	ttg	acc	ttt	act	gat	1171
Tyr	Arg	Arg	Leu	Phe	Glu	Met	Asp	Asp	Ala	Val	Leu	Thr	Phe	Thr	Asp	
				345				350					355			
gat	gct	ttg	gag	gag	atc	gct	aat	cag	gca	ctc	gag	cgc	aaa	act	ggc	1219
Asp	Ala	Leu	Glu	Glu	Ile	Ala	Asn	Gln	Ala	Leu	Glu	Arg	Lys	Thr	Gly	
		360					365					370				
gcc	cgt	ggc	ctg	cgc	gcg	atc	atg	gaa	gag	atc	ctg	gtt	ccg	atc	atg	1267
Ala	Arg	Gly	Leu	Arg	Ala	Ile	Met	Glu	Glu	Ile	Leu	Val	Pro	Ile	Met	
		375				380					385					
tat	gac	ctc	cca	gac	cgt	aaa	gac	gtt	ggc	gaa	gtc	atc	atc	aac	ggc	1315
Tyr	Asp	Leu	Pro	Asp	Arg	Lys	Asp	Val								

425

<210> 162

<211> 426

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 162

Met Ala Arg Met Gln Glu Ser Ala Asp Leu Leu Lys Cys Ser Phe Cys
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Gly Lys Ser Gln Lys Gln Val Lys Lys Leu Ile Ala Gly Gly Ala Val
 20 25 30

Tyr Ile Cys Asp Glu Cys Ile Glu Leu Cys Asn Glu Ile Ile Glu Glu
 35 40 45

Glu Leu Gly Gln Ala Gln His Asp Glu Gln Glu Arg Asn Glu Leu Pro
 50 55 60

Lys Pro Ser Glu Ile Ser Ala Phe Leu Asp Thr Tyr Val Ile Gly Gln
 65 70 75 80

Asp Pro Ala Lys Arg Ile Leu Ser Val Ala Val Tyr Asn His Tyr Lys
 85 90 95

Arg Leu Arg Ala Ser Glu Thr Ile Gly Arg Arg Arg Asn Asp Glu Pro
 100 105 110

Glu Thr Glu Leu Val Lys Ser Asn Ile Leu Met Leu Gly Pro Thr Gly
 115 120 125

Ser Gly Lys Thr Phe Leu Ala Gln Thr Leu Ala Lys Leu Leu Asp Val
 130 135 140

Pro Phe Ala Ile Ala Asp Ala Thr Ser Leu Thr Glu Ala Gly Tyr Val
 145 150 155 160

Gly Glu Asp Val Glu Asn Ile Leu Leu Lys Leu Leu Gln Ala Ala Asp
 165 170 175

Phe Asp Val Glu Arg Ala Gln Arg Gly Ile Ile Tyr Ile Asp Glu Val
 180 185 190

Asp Lys Ile Ser Arg Lys Ser Glu Asn Pro Ser Ile Thr Arg Asp Val
 195 200 205

Ser Gly Glu Gly Val Gln Gln Ala Leu Leu Lys Ile Leu Glu Gly Thr
 210 215 220

Val Ala Ala Ile Pro Pro Gln Gly Gly Arg Lys His Pro Asn Gln Asp
 225 230 235 240

Phe Ile Gln Leu Asp Thr Thr Asn Ile Leu Phe Ile Val Ala Gly Ala
 245 250 255

Phe Ser Gly Leu Glu Lys Val Ile Ala Asp Arg Asn Gly Lys Lys Gly
 260 265 270

Leu Gly Phe Gly Val Glu Val Ser Ser Lys Lys Glu Glu Ala Asn Ile

55	60	65	
tca gcc ttc ctt gat act tat gtc atc ggg cag gac cca gca aaa cgt Ser Ala Phe Leu Asp Thr Tyr Val Ile Gly Gln Asp Pro Ala Lys Arg 70 75 80 85			355
atc ctg tcg gtt gcg gtg tac aac cat tac aag cgt ctc cgc gca tcg Ile Leu Ser Val Ala Val Tyr Asn His Tyr Lys Arg Leu Arg Ala Ser 90 95 100			403
gaa acc atc ggt cgt cgc agg aat gac gag cct gaa acc gaa ctg gtt Glu Thr Ile Gly Arg Arg Arg Asn Asp Glu Pro Glu Thr Glu Leu Val 105 110 115			451
aag tcc aat att ttg atg ctc ggc ccc act ggc tcc ggc aag act ttc Lys Ser Asn Ile Leu Met Leu Gly Pro Thr Gly Ser Gly Lys Thr Phe 120 125 130			499
ctt gcc cag act ttg gca aag ctg ctg gat gtt cct ttt gct atc gcg Leu Ala Gln Thr Leu Ala Lys Leu Leu Asp Val Pro Phe Ala Ile Ala 135 140 145			547
gat gcc acc tca ctg acc gag gct ggt tat gtg ggc gag gat gtg gaa Asp Ala Thr Ser Leu Thr Glu Ala Gly Tyr Val Gly Glu Asp Val Glu 150 155 160 165			595
aac atc ttg ctc aag ctg ctt cag gct gct gat ttt gat gtg gaa cgt Asn Ile Leu Leu Lys Leu Leu Gln Ala Ala Asp Phe Asp Val Glu Arg 170 175 180			643
gca cag cgc ggc atc att tac atc gat gaa gtg gac aag att tcc cgc Ala Gln Arg Gly Ile Ile Tyr Ile Asp Glu Val Asp Lys Ile Ser Arg 185 190 195			691
aag tct gaa aac cca tcg atc act cgc gat gtt tcc ggt gaa ggc gtg Lys Ser Glu Asn Pro Ser Ile Thr Arg Asp Val Ser Gly Glu Gly Val 200 205 210			739
cag cag gca ctg ctg aaa att ttg gaa ggc act gtc gcc gca atc cca Gln Gln Ala Leu Leu Lys Ile Leu Glu Gly Thr Val Ala Ala Ile Pro 215 220 225			787
ccg cag gga gga cgc aag cac ccc aac cag gat ttc atc cag ctg gat Pro Gln Gly Gly Arg Lys His Pro Asn Gln Asp Phe Ile Gln Leu Asp 230 235 240 245			835
acc acc aac att ttg ttc atc gtt gct ggt gcg ttc tct ggt ctg gag Thr Thr Asn Ile Leu Phe Ile Val Ala Gly Ala Phe Ser Gly Leu Glu 250 255 260			883
aag gtc atc gcg gac cgc aat ggc aag aaa ggc ttg ggc ttc ggt gtg Lys Val Ile Ala Asp Arg Asn Gly Lys Lys Gly Leu Gly Phe Gly Val 265 270 275			931
gag gtc tct tcc aag aag gaa gaa gcc aac att gtg gat atc ttc aag Glu Val Ser Ser Lys Lys Glu Glu Ala Asn Ile Val Asp Ile Phe Lys 280 285 290			979
gat gtc ctc cct gag gac ctg gtg aag ttt ggt ctc atc cca gaa ttc Asp Val Leu Pro Glu Asp Leu Val Lys Phe Gly Leu Ile Pro Glu Phe 295 300 305			1027

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att ggg cgt ctg cca gtc gtt gcc acc gta tcc aac ctg gat cag aaa 1075
Ile Gly Arg Leu Pro Val Val Ala Thr Val Ser Asn Leu Asp Gln Lys
310                      315                      320                      325

tct ctg gtc aag gtt ctc acg gag cct cgt aac tca ttg gtg aag cag 1123
Ser Leu Val Lys Val Leu Thr Glu Pro Arg Asn Ser Leu Val Lys Gln
                      330                      335                      340

tat cga cgt ctg ttt gaa atg gat gac gct gtg ttg acc ttt act gat 1171
Tyr Arg Arg Leu Phe Glu Met Asp Asp Ala Val Leu Thr Phe Thr Asp
                      345                      350                      355

gat gct ttg gag gag atc gct aat cag gca ctc gag cgc aaa act ggc 1219
Asp Ala Leu Glu Glu Ile Ala Asn Gln Ala Leu Glu Arg Lys Thr Gly
                      360                      365                      370

gcc cgt ggc ctg cgc gcg atc atg gaa gag atc ctg gtt ccg atc atg 1267
Ala Arg Gly Leu Arg Ala Ile Met Glu Glu Ile Leu Val Pro Ile Met
                      375                      380                      385

tat gac ctc cca gac cgt aaa gac gtt ggc gaa gtc atc atc aac ggt 1315
Tyr Asp Leu Pro Asp Arg Lys Asp Val Gly Glu Val Ile Ile Asn Gly
390                      395                      400                      405

gcc gtt gcc cgt ggc gaa gcc gaa cca gag atg ttg gaa gct gtc gca 1363
Ala Val Ala Arg Gly Glu Ala Glu Pro Glu Met Leu Glu Ala Val Ala
                      410                      415                      420

gaa gaa aag acc gcg tagttggcag gagttatcac cgg 1401
Glu Glu Lys Thr Ala
425

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<210> 164

<211> 426

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 164

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Met Ala Arg Met Gln Glu Ser Ala Asp Leu Leu Lys Cys Ser Phe Cys
  1                      5                      10                      15

Gly Lys Ser Gln Lys Gln Val Lys Lys Leu Ile Ala Gly Gly Ala Val
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Tyr Ile Cys Asp Glu Cys Ile Glu Leu Cys Asn Glu Ile Ile Glu Glu
    35                      40                      45

Glu Leu Gly Gln Ala Gln His Asp Glu Gln Glu Arg Asn Glu Leu Pro
    50                      55                      60

Lys Pro Ser Glu Ile Ser Ala Phe Leu Asp Thr Tyr Val Ile Gly Gln
    65                      70                      75                      80

Asp Pro Ala Lys Arg Ile Leu Ser Val Ala Val Tyr Asn His Tyr Lys
                85                      90                      95

Arg Leu Arg Ala Ser Glu Thr Ile Gly Arg Arg Arg Asn Asp Glu Pro
                100                      105                      110

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Glu Thr Glu Leu Val Lys Ser Asn Ile Leu Met Leu Gly Pro Thr Gly
 115 120 125
 Ser Gly Lys Thr Phe Leu Ala Gln Thr Leu Ala Lys Leu Leu Asp Val
 130 135 140
 Pro Phe Ala Ile Ala Asp Ala Thr Ser Leu Thr Glu Ala Gly Tyr Val
 145 150 155 160
 Gly Glu Asp Val Glu Asn Ile Leu Leu Lys Leu Leu Gln Ala Ala Asp
 165 170 175
 Phe Asp Val Glu Arg Ala Gln Arg Gly Ile Ile Tyr Ile Asp Glu Val
 180 185 190
 Asp Lys Ile Ser Arg Lys Ser Glu Asn Pro Ser Ile Thr Arg Asp Val
 195 200 205
 Ser Gly Glu Gly Val Gln Gln Ala Leu Leu Lys Ile Leu Glu Gly Thr
 210 215 220
 Val Ala Ala Ile Pro Pro Gln Gly Gly Arg Lys His Pro Asn Gln Asp
 225 230 235 240
 Phe Ile Gln Leu Asp Thr Thr Asn Ile Leu Phe Ile Val Ala Gly Ala
 245 250 255
 Phe Ser Gly Leu Glu Lys Val Ile Ala Asp Arg Asn Gly Lys Lys Gly
 260 265 270
 Leu Gly Phe Gly Val Glu Val Ser Ser Lys Lys Glu Glu Ala Asn Ile
 275 280 285
 Val Asp Ile Phe Lys Asp Val Leu Pro Glu Asp Leu Val Lys Phe Gly
 290 295 300
 Leu Ile Pro Glu Phe Ile Gly Arg Leu Pro Val Val Ala Thr Val Ser
 305 310 315 320
 Asn Leu Asp Gln Lys Ser Leu Val Lys Val Leu Thr Glu Pro Arg Asn
 325 330 335
 Ser Leu Val Lys Gln Tyr Arg Arg Leu Phe Glu Met Asp Asp Ala Val
 340 345 350
 Leu Thr Phe Thr Asp Asp Ala Leu Glu Glu Ile Ala Asn Gln Ala Leu
 355 360 365
 Glu Arg Lys Thr Gly Ala Arg Gly Leu Arg Ala Ile Met Glu Glu Ile
 370 375 380
 Leu Val Pro Ile Met Tyr Asp Leu Pro Asp Arg Lys Asp Val Gly Glu
 385 390 395 400
 Val Ile Ile Asn Gly Ala Val Ala Arg Gly Glu Ala Glu Pro Glu Met
 405 410 415
 Leu Glu Ala Val Ala Glu Glu Lys Thr Ala
 420 425

<210> 165
 <211> 924
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(901)
 <223> RXN00397

<400> 165
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 Leu Ser Leu Thr Glu
 1 5
 ggg gag atc att ccc atc caa aca aag ctc ggc cac tgg cgt gac gtg 163
 Gly Glu Ile Ile Pro Ile Gln Thr Lys Leu Gly His Trp Arg Asp Val
 10 15 20
 cgg gat tcc gaa gat ctg cca ttc caa gta atc gca tcg cgc acc aac 211
 Arg Asp Ser Glu Asp Leu Pro Phe Gln Val Ile Ala Ser Arg Thr Asn
 25 30 35
 gtg acc att atg gaa aac acc ctg gaa tgg acc aac agc cgc ctt gag 259
 Val Thr Ile Met Glu Asn Thr Leu Glu Trp Thr Asn Ser Arg Leu Glu
 40 45 50
 cgt ggc gaa gag ttc acc gag ctc gac att tat gct cac tac ttg gaa 307
 Arg Gly Glu Glu Phe Thr Glu Leu Asp Ile Tyr Ala His Tyr Leu Glu
 55 60 65
 gag ttg gaa gat tac gcc ctc caa ttc acc ttc gat gtc gag ccc tac 355
 Glu Leu Glu Asp Tyr Ala Leu Gln Phe Thr Phe Asp Val Glu Pro Tyr
 70 75 80 85
 ttc acc aac ctg cac tcc tcc aac aga atg ctc ttc cct gga cct cct 403
 Phe Thr Asn Leu His Ser Ser Asn Arg Met Leu Phe Pro Gly Pro Pro
 90 95 100
 gtg gat ttc ccg atc aac gca gaa acc cga tgc att cag ctc gac gcc 451
 Val Asp Phe Pro Ile Asn Ala Glu Thr Arg Cys Ile Gln Leu Asp Ala
 105 110 115
 ggt gtt gca gta aag aag gac ggc gtg gtg ctg ggt acc tca gat atg 499
 Gly Val Ala Val Lys Lys Asp Gly Val Val Leu Gly Thr Ser Asp Met
 120 125 130
 gcg agg tcc ctg cct cga acc gcc gct ggc caa gaa gcc tat gag tac 547
 Ala Arg Ser Leu Pro Arg Thr Ala Ala Gly Gln Glu Ala Tyr Glu Tyr
 135 140 145
 ttc ttc aag gtg gtt cgt gaa ggc atc atc ggg cag ctg cgc ccg ggc 595
 Phe Phe Lys Val Val Arg Glu Gly Ile Ile Gly Gln Leu Arg Pro Gly
 150 155 160 165
 gtg atc tgc gct gac gtg cac gaa gca acc ctt gat tac cta agc ccg 643
 Val Ile Cys Ala Asp Val His Glu Ala Thr Leu Asp Tyr Leu Ser Pro
 170 175 180

cag cta cct cgc atg att gac atc gga atg ctg ggt gcc gac acc gat 691
 Gln Leu Pro Arg Met Ile Asp Ile Gly Met Leu Gly Ala Asp Thr Asp
 185 190 195

 ttc aac acc atc tac cgc aag cgc aat gtt ggc cac ctc atg ggc aag 739
 Phe Asn Thr Ile Tyr Arg Lys Arg Asn Val Gly His Leu Met Gly Lys
 200 205 210

 cag gaa tcc ttt gcc aat gag ctt cgc cct gga tac aag cac att ctt 787
 Gln Glu Ser Phe Ala Asn Glu Leu Arg Pro Gly Tyr Lys His Ile Leu
 215 220 225

 cac cac ggc tcc tat ggt gcc gcg gag atc cct tgg cgc tac aac ggt 835
 His His Gly Ser Tyr Gly Ala Ala Glu Ile Pro Trp Arg Tyr Asn Gly
 230 235 240 245

 gta gcc att ggt acc gag gat ctg tgg tac atc ggc gca gac aag acc 883
 Val Ala Ile Gly Thr Glu Asp Leu Trp Tyr Ile Gly Ala Asp Lys Thr
 250 255 260

 tac att ttg agc cag cgc taaggagaac ccagtgacag aaa 924
 Tyr Ile Leu Ser Gln Arg
 265

<210> 166

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 166

Leu Ser Leu Thr Glu Gly Glu Ile Ile Pro Ile Gln Thr Lys Leu Gly
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 His Trp Arg Asp Val Arg Asp Ser Glu Asp Leu Pro Phe Gln Val Ile
 20 25 30

 Ala Ser Arg Thr Asn Val Thr Ile Met Glu Asn Thr Leu Glu Trp Thr
 35 40 45

 Asn Ser Arg Leu Glu Arg Gly Glu Glu Phe Thr Glu Leu Asp Ile Tyr
 50 55 60

 Ala His Tyr Leu Glu Glu Leu Glu Asp Tyr Ala Leu Gln Phe Thr Phe
 65 70 75 80

 Asp Val Glu Pro Tyr Phe Thr Asn Leu His Ser Ser Asn Arg Met Leu
 85 90 95

 Phe Pro Gly Pro Pro Val Asp Phe Pro Ile Asn Ala Glu Thr Arg Cys
 100 105 110

 Ile Gln Leu Asp Ala Gly Val Ala Val Lys Lys Asp Gly Val Val Leu
 115 120 125

 Gly Thr Ser Asp Met Ala Arg Ser Leu Pro Arg Thr Ala Ala Gly Gln
 130 135 140

 Glu Ala Tyr Glu Tyr Phe Phe Lys Val Val Arg Glu Gly Ile Ile Gly
 145 150 155 160

Gln Leu Arg Pro Gly Val Ile Cys Ala Asp Val His Glu Ala Thr Leu
 165 170 175

Asp Tyr Leu Ser Pro Gln Leu Pro Arg Met Ile Asp Ile Gly Met Leu
 180 185 190

Gly Ala Asp Thr Asp Phe Asn Thr Ile Tyr Arg Lys Arg Asn Val Gly
 195 200 205

His Leu Met Gly Lys Gln Glu Ser Phe Ala Asn Glu Leu Arg Pro Gly
 210 215 220

Tyr Lys His Ile Leu His His Gly Ser Tyr Gly Ala Ala Glu Ile Pro
 225 230 235 240

Trp Arg Tyr Asn Gly Val Ala Ile Gly Thr Glu Asp Leu Trp Tyr Ile
 245 250 255

Gly Ala Asp Lys Thr Tyr Ile Leu Ser Gln Arg
 260 265

<210> 167
 <211> 2049
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2026)
 <223> RXN01868

<400> 167
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ccacaaaccc tgtggcggta aatcccctag agtaggccac atg aag gat ctt tat 115
 Met Lys Asp Leu Tyr
 1 5

cgc ttt gtc aat ggc ctg tgg ctt gac acc cac atc att ccc gac gat 163
 Arg Phe Val Asn Gly Leu Trp Leu Asp Thr His Ile Ile Pro Asp Asp
 10 15 20

cgc gcg gtg gac ggc acg ttc cac aag ctg cgc gat gat gct gaa gaa 211
 Arg Ala Val Asp Gly Thr Phe His Lys Leu Arg Asp Asp Ala Glu Glu
 25 30 35

gac gtc cat gag atc gtc aag gaa gac act gga cgc gca ggc aca ctt 259
 Asp Val His Glu Ile Val Lys Glu Asp Thr Gly Arg Ala Gly Thr Leu
 40 45 50

tat gcc tca ttt atg gat act gac gcc atc aac gct gct ggt gtt gca 307
 Tyr Ala Ser Phe Met Asp Thr Asp Ala Ile Asn Ala Ala Gly Val Ala
 55 60 65

ccg ctc gat gcg gat ctg aac agg ctg tct gtt gct aac tca tcg ttt 355
 Pro Leu Asp Ala Asp Leu Asn Arg Leu Ser Val Ala Asn Ser Ser Phe
 70 75 80 85

ttc gca gct gct ctc ggc gaa ctg gac cgt gaa ggc gtt ggc gcg cca 403
 Phe Ala Ala Ala Leu Gly Glu Leu Asp Arg Glu Gly Val Gly Ala Pro

ccc gcc acc cgc gag cgt gcc ctg gaa aag ttg ggc aaa ttc aac gcg	1171
Pro Ala Thr Arg Glu Arg Ala Leu Glu Lys Leu Gly Lys Phe Asn Ala	
345 350 355	
aaa atc ggc tac ccc gac aag tgg cgc tcc tac gaa ggc ctc gaa ttc	1219
Lys Ile Gly Tyr Pro Asp Lys Trp Arg Ser Tyr Glu Gly Leu Glu Phe	
360 365 370	
ggc tcc gac ctg gtg gac aac tcc cgc aag ggc tcc gcg ttc ctc cat	1267
Gly Ser Asp Leu Val Asp Asn Ser Arg Lys Gly Ser Ala Phe Leu His	
375 380 385	
gac tat gag ctg ggc aag atc ggc aaa cca gcc gac cgc gac gaa tgg	1315
Asp Tyr Glu Leu Gly Lys Ile Gly Lys Pro Ala Asp Arg Asp Glu Trp	
390 395 400 405	
gtc acc acc cca caa acc gtc aac gcc ttc tac aac ccc gtg gtc aac	1363
Val Thr Thr Pro Gln Thr Val Asn Ala Phe Tyr Asn Pro Val Val Asn	
410 415 420	
gac atc acc ttc ccc gca gcc atc ctg cgc gca cca ttc ttc gac ccc	1411
Asp Ile Thr Phe Pro Ala Ala Ile Leu Arg Ala Pro Phe Phe Asp Pro	
425 430 435	
gaa gca gaa gcc gca gaa aac ttc ggt gca atc ggt gct gtg atc gga	1459
Glu Ala Glu Ala Ala Glu Asn Phe Gly Ala Ile Gly Ala Val Ile Gly	
440 445 450	
cac gaa atc ggc cac ggc ttt gac gat caa ggc agc caa tac gac ggc	1507
His Glu Ile Gly His Gly Phe Asp Asp Gln Gly Ser Gln Tyr Asp Gly	
455 460 465	
gac ggc aac ctc aac tcc tgg tgg acc gac gaa gac cgc tcc gca ttc	1555
Asp Gly Asn Leu Asn Ser Trp Trp Thr Asp Glu Asp Arg Ser Ala Phe	
470 475 480 485	
gag cag ctc acc tca cgt ctg gtc acc caa ttc agc gga ctc gtc cct	1603
Glu Gln Leu Thr Ser Arg Leu Val Thr Gln Phe Ser Gly Leu Val Pro	
490 495 500	
gcc gtc ctg acc tct gaa gga atc gac acc gac ggc gtc aac ggt gaa	1651
Ala Val Leu Thr Ser Glu Gly Ile Asp Thr Asp Gly Val Asn Gly Glu	
505 510 515	
ttc act ctc ggc gaa aac atc ggt gac ctc ggc gga ttg ggc atc gct	1699
Phe Thr Leu Gly Glu Asn Ile Gly Asp Leu Gly Gly Leu Gly Ile Ala	
520 525 530	
gtc gtt gcc tac gaa aag tac ctc gca gac cgt ggc caa acc ttt gaa	1747
Val Val Ala Tyr Glu Lys Tyr Leu Ala Asp Arg Gly Gln Thr Phe Glu	
535 540 545	
acc tca cca gtc caa aaa ttc gaa gca gaa ggc gcc gag gaa ggc ctg	1795
Thr Ser Pro Val Gln Lys Phe Glu Ala Glu Gly Ala Glu Glu Gly Leu	
550 555 560 565	
gcc gag caa gaa ttc aac ggt ctc caa cgc ctc ttc ctg tcc tgg gct	1843
Ala Glu Gln Glu Phe Asn Gly Leu Gln Arg Leu Phe Leu Ser Trp Ala	
570 575 580	

cgc gtg tgg cgc acc aaa atc cgc cca cag atg gcc gtc caa tac ctg 1891
 Arg Val Trp Arg Thr Lys Ile Arg Pro Gln Met Ala Val Gln Tyr Leu
 585 590 595

gcc atc gac cca cac tcc cct gca gaa ttc cgc tgc aat gtc atc gcc 1939
 Ala Ile Asp Pro His Ser Pro Ala Glu Phe Arg Cys Asn Val Ile Ala
 600 605 610

gga aac gtc gct gaa ttc tac gaa gca ttc gac gtc ccc gaa gat gca 1987
 Gly Asn Val Ala Glu Phe Tyr Glu Ala Phe Asp Val Pro Glu Asp Ala
 615 620 625

cct gtg tac atc aag cca gaa gag cgc cta gct atc tgg tagttgtag 2036
 Pro Val Tyr Ile Lys Pro Glu Glu Arg Leu Ala Ile Trp
 630 635 640

ttggtattga aaa 2049

<210> 168

<211> 642

<212> PRT

<213> Corynebacterium glutamicum

<400> 168

Met Lys Asp Leu Tyr Arg Phe Val Asn Gly Leu Trp Leu Asp Thr His
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Ile Ile Pro Asp Asp Arg Ala Val Asp Gly Thr Phe His Lys Leu Arg
 20 25 30

Asp Asp Ala Glu Glu Asp Val His Glu Ile Val Lys Glu Asp Thr Gly
 35 40 45

Arg Ala Gly Thr Leu Tyr Ala Ser Phe Met Asp Thr Asp Ala Ile Asn
 50 55 60

Ala Ala Gly Val Ala Pro Leu Asp Ala Asp Leu Asn Arg Leu Ser Val
 65 70 75 80

Ala Asn Ser Ser Phe Phe Ala Ala Ala Leu Gly Glu Leu Asp Arg Glu
 85 90 95

Gly Val Gly Ala Pro Val Gly Phe Trp Val Glu Lys Asp Ser Ser Ser
 100 105 110

Asn Glu Ser Val Ala Tyr Val Ile Gln Ser Gly Leu Gly Leu Pro Asp
 115 120 125

Glu Ala Tyr Tyr Arg Glu Glu Ala His Ala Glu Thr Leu Ala Ala Tyr
 130 135 140

Lys Glu His Val Glu Arg Met Leu Gly Tyr Leu Asp Asn Ser Arg Leu
 145 150 155 160

Phe Gly Leu Ser Ala Ala Ser Ala Ala Arg Ile Val Ala Leu Glu
 165 170 175

Thr Glu Ile Ala Ala Gly His Trp Asp Val Val Lys Thr Arg Asp Ala
 180 185 190

Val	Ala	Thr	Tyr	Asn	Pro	Thr	Glu	Leu	Gly	Ala	Leu	Pro	Pro	Lys	Val
		195					200					205			
Arg	Thr	Leu	Leu	Ser	Ser	Ala	Gly	Leu	Pro	Asp	Gln	Arg	Leu	Val	Ser
	210					215					220				
Met	Met	Pro	Ser	Tyr	Leu	Asp	His	Leu	Asn	Gly	Leu	Leu	Val	Asp	Asp
225					230					235					240
Arg	Leu	Pro	Asp	Trp	Gln	Leu	Trp	Ala	Thr	Trp	His	Ile	Leu	Arg	Ser
				245					250					255	
Arg	Ala	Gly	Leu	Leu	Thr	Glu	Glu	Ile	Ser	Gln	Ala	Asn	Phe	Asp	Phe
			260					265					270		
Tyr	Gly	Thr	Lys	Leu	Ser	Gly	Ala	Thr	Glu	Gln	Lys	Asp	Arg	Trp	Lys
		275					280					285			
Arg	Ala	Val	Gly	Leu	Ala	Glu	Arg	Met	Val	Gly	Glu	Glu	Ile	Gly	Gln
	290					295					300				
Arg	Phe	Val	Glu	Arg	His	Phe	Pro	Ala	Ser	Ser	Lys	Glu	His	Met	Leu
305					310					315					320
Glu	Leu	Val	Asp	Tyr	Leu	Val	Ala	Ala	Tyr	Arg	Asp	Arg	Ile	Ser	Asn
				325					330					335	
Leu	Glu	Trp	Met	Thr	Pro	Ala	Thr	Arg	Glu	Arg	Ala	Leu	Glu	Lys	Leu
			340					345					350		
Gly	Lys	Phe	Asn	Ala	Lys	Ile	Gly	Tyr	Pro	Asp	Lys	Trp	Arg	Ser	Tyr
		355					360					365			
Glu	Gly	Leu	Glu	Phe	Gly	Ser	Asp	Leu	Val	Asp	Asn	Ser	Arg	Lys	Gly
	370					375					380				
Ser	Ala	Phe	Leu	His	Asp	Tyr	Glu	Leu	Gly	Lys	Ile	Gly	Lys	Pro	Ala
385					390					395					400
Asp	Arg	Asp	Glu	Trp	Val	Thr	Thr	Pro	Gln	Thr	Val	Asn	Ala	Phe	Tyr
				405					410					415	
Asn	Pro	Val	Val	Asn	Asp	Ile	Thr	Phe	Pro	Ala	Ala	Ile	Leu	Arg	Ala
			420					425					430		
Pro	Phe	Phe	Asp	Pro	Glu	Ala	Glu	Ala	Ala	Glu	Asn	Phe	Gly	Ala	Ile
		435				440						445			
Gly	Ala	Val	Ile	Gly	His	Glu	Ile	Gly	His	Gly	Phe	Asp	Asp	Gln	Gly
	450					455					460				
Ser	Gln	Tyr	Asp	Gly	Asp	Gly	Asn	Leu	Asn	Ser	Trp	Trp	Thr	Asp	Glu
465					470					475					480
Asp	Arg	Ser	Ala	Phe	Glu	Gln	Leu	Thr	Ser	Arg	Leu	Val	Thr	Gln	Phe
				485					490					495	
Ser	Gly	Leu	Val	Pro	Ala	Val	Leu	Thr	Ser	Glu	Gly	Ile	Asp	Thr	Asp
			500					505					510		
Gly	Val	Asn	Gly	Glu	Phe	Thr	Leu	Gly	Glu	Asn	Ile	Gly	Asp	Leu	Gly

515						520						525					
Gly	Leu	Gly	Ile	Ala	Val	Val	Ala	Tyr	Glu	Lys	Tyr	Leu	Ala	Asp	Arg		
530						535						540					
Gly	Gln	Thr	Phe	Glu	Thr	Ser	Pro	Val	Gln	Lys	Phe	Glu	Ala	Glu	Gly		
545						550						555					
Ala	Glu	Glu	Gly	Leu	Ala	Glu	Gln	Glu	Phe	Asn	Gly	Leu	Gln	Arg	Leu		
560						565						570					
Phe	Leu	Ser	Trp	Ala	Arg	Val	Trp	Arg	Thr	Lys	Ile	Arg	Pro	Gln	Met		
575						580						585					
Ala	Val	Gln	Tyr	Leu	Ala	Ile	Asp	Pro	His	Ser	Pro	Ala	Glu	Phe	Arg		
590						595						600					
Cys	Asn	Val	Ile	Ala	Gly	Asn	Val	Ala	Glu	Phe	Tyr	Glu	Ala	Phe	Asp		
605						610						615					
Val	Pro	Glu	Asp	Ala	Pro	Val	Tyr	Ile	Lys	Pro	Glu	Glu	Arg	Leu	Ala		
620						625						630					
Ile	Trp																

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<210> 169
<211> 1734
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1711)
<223> FRXA01868
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<400> 169
atgcggatct gaacaggctg tctgttgcta actcatcggtt ttcgcagctg ctctcggcga 60

actggaccgt gaaggcggtt ggcgcgccagt aggtttcttg  gtg gag aag gat tct 115
                                         Val Glu Lys Asp Ser
                                           1                     5

tcc tcc aac gaa tcc gtc gcc tat gtc atc cag tcc ggc ctc ggc ctg 163
Ser Ser Asn Glu Ser Val Ala Tyr Val Ile Gln Ser Gly Leu Gly Leu
                        10                        15                        20

ccc gat gag gct tat tac cgc gag gag gca cac gcc gaa act ctc gcg 211
Pro Asp Glu Ala Tyr Tyr Arg Glu Glu Ala His Ala Glu Thr Leu Ala
                        25                        30                        35

gcc tac aaa gag cac gtt gag cgc atg ctc ggc tac ttg gat aac agc 259
Ala Tyr Lys Glu His Val Glu Arg Met Leu Gly Tyr Leu Asp Asn Ser
                        40                        45                        50

cgc ctc ttc ggt ctg tcg gct gct tcc gct gcc gca cga att gtc gcc 307
Arg Leu Phe Gly Leu Ser Ala Ala Ser Ala Ala Ala Arg Ile Val Ala
                        55                        60                        65

ctg gaa acg gaa atc gct gct ggc cac tgg gat gtc gtg aag acc cgc 355

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Leu 70	Glu	Thr	Glu	Ile	Ala 75	Ala	Gly	His	Trp	Asp 80	Val	Val	Lys	Thr	Arg 85	
gac Asp	gcc Ala	gta Val	gcc Ala	acc Thr 90	tac Tyr	aac Asn	ccc Pro	acc Thr	gaa Glu 95	ctc Leu	ggc Gly	gcg Ala	ctg Leu	cca Pro 100	cca Pro	403
aag Lys	gtc Val	cgc Arg	acg Thr 105	ctg Leu	ctc Leu	agt Ser	tcc Ser	gca Ala 110	ggc Gly	ctc Leu	ccg Pro	gac Asp	cag Gln 115	cgc Arg	ctg Leu	451
gta Val	tcg Ser	atg Met 120	atg Met	ccg Pro	tca Ser	tac Tyr	ctc Leu 125	gac Asp	cac His	ctc Leu	aac Asn	ggc Gly 130	ttg Leu	ctt Leu	gtc Val	499
gac Asp	gac Asp 135	cgc Arg	ctc Leu	ccc Pro	gat Asp	tgg Trp 140	cag Gln	cta Leu	tgg Trp	gca Ala	acc Thr 145	tgg Trp	cac His	atc Ile	ttg Leu	547
agg Arg 150	tct Ser	cga Arg	gca Ala	gga Gly 155	ctg Leu	ttg Leu	acc Thr	gag Glu	gaa Glu	att Ile 160	agc Ser	caa Gln	gca Ala	aac Asn	ttc Phe 165	595
gac Asp	ttc Phe	tat Tyr	ggc Gly 170	acc Thr	aaa Lys	ctg Leu	tcc Ser	ggc Gly 175	gcc Ala	acc Thr	gag Glu	caa Gln	aaa Lys	gat Asp 180	cga Arg	643
tgg Trp	aag Lys	cgt Arg	gct Ala 185	gtc Val	ggc Gly	ctg Leu	gca Ala	gag Glu 190	cgc Arg	atg Met	gtg Val	ggc Gly 195	gag Glu	gaa Glu	atc Ile	691
ggg Gly	caa Gln 200	cga Arg	ttc Phe	gtc Val	gaa Glu	agg Arg	cat His 205	ttt Phe	cct Pro	gca Ala	agc Ser	tcc Ser 210	aag Lys	gag Glu	cac His	739
atg Met	ctt Leu 215	gag Glu	ctc Leu	gtc Val	gac Asp	tac Tyr 220	ctg Leu	gtt Val	gcc Ala	gcc Ala	tac Tyr 225	cgt Arg	gat Asp	cgc Arg	att Ile	787
tcc Ser 230	aac Asn	ctc Leu	gaa Glu	tgg Trp 235	atg Met	acg Thr	ccc Pro	gcc Ala	acc Thr	cgc Arg	gag Glu 240	cgt Arg	gcc Ala	ctg Leu	gaa Glu 245	835
aag Lys	ttg Leu	ggc Gly	aaa Lys 250	ttc Phe	aac Asn	gcg Ala	aaa Lys	atc Ile	ggc Gly 255	tac Tyr	ccc Pro	gac Asp	aag Lys	tgg Trp 260	cgc Arg	883
tcc Ser	tac Tyr	gaa Glu	ggc Gly 265	ctc Leu	gaa Glu	ttc Phe	ggc Gly 270	tcc Ser	gac Asp	ctg Leu	gtg Val	gac Asp	aac Asn	tcc Ser	cgc Arg	931
aag Lys	ggc Gly	tcc Ser 280	gcg Ala	ttc Phe	ctc Leu	cat His	gac Asp 285	tat Tyr	gag Glu	ctg Leu	ggc Gly 290	aag Lys	atc Ile	ggc Gly	aaa Lys	979
cca Pro	gcc Ala 295	gac Asp	cgc Arg	gac Asp	gaa Glu	tgg Trp 300	gtc Val	acc Thr	acc Thr	cca Pro	caa Gln 305	acc Thr	gtc Val	aac Asn	gcc Ala	1027
ttc Phe	tac Tyr	aac Asn	ccc Pro	gtg Val	gtc Val	aac Asn	gac Asp	atc Ile	acc Thr	ttc Phe	ccc Pro	gca Ala	gcc Ala	atc Ile	ctg Leu	1075

310	315	320	325	
cgc gca cca ttc ttc gac ccc gaa gca gaa gcc gca gaa aac ttc ggt				1123
Arg Ala Pro Phe Phe Asp Pro Glu Ala Glu Ala Ala Glu Asn Phe Gly				
	330	335	340	
gca atc ggt gct gtg atc gga cac gaa atc ggc cac ggc ttt gac gat				1171
Ala Ile Gly Ala Val Ile Gly His Glu Ile Gly His Gly Phe Asp Asp				
	345	350	355	
caa ggc agc caa tac gac ggc gac ggc aac ctc aac tcc tgg tgg acc				1219
Gln Gly Ser Gln Tyr Asp Gly Asp Gly Asn Leu Asn Ser Trp Trp Thr				
	360	365	370	
gac gaa gac cgc tcc gca ttc gag cag ctc acc tca cgt ctg gtc acc				1267
Asp Glu Asp Arg Ser Ala Phe Glu Gln Leu Thr Ser Arg Leu Val Thr				
	375	380	385	
caa ttc agc gga ctc gtc cct gcc gtc ctg acc tct gaa gga atc gac				1315
Gln Phe Ser Gly Leu Val Pro Ala Val Leu Thr Ser Glu Gly Ile Asp				
	390	395	400	405
acc gac ggc gtc aac ggt gaa ttc act ctc ggc gaa aac atc ggt gac				1363
Thr Asp Gly Val Asn Gly Glu Phe Thr Leu Gly Glu Asn Ile Gly Asp				
	410	415	420	
ctc ggc gga ttg ggc atc gct gtc gtt gcc tac gaa aag tac ctc gca				1411
Leu Gly Gly Leu Gly Ile Ala Val Val Ala Tyr Glu Lys Tyr Leu Ala				
	425	430	435	
gac cgt ggc caa acc ttt gaa acc tca cca gtc caa aaa ttc gaa gca				1459
Asp Arg Gly Gln Thr Phe Glu Thr Ser Pro Val Gln Lys Phe Glu Ala				
	440	445	450	
gaa ggc gcc gag gaa ggc ctg gcc gag caa gaa ttc aac ggt ctc caa				1507
Glu Gly Ala Glu Glu Gly Leu Ala Glu Gln Glu Phe Asn Gly Leu Gln				
	455	460	465	
cgc ctc ttc ctg tcc tgg gct cgc gtg tgg cgc acc aaa atc cgc cca				1555
Arg Leu Phe Leu Ser Trp Ala Arg Val Trp Arg Thr Lys Ile Arg Pro				
	470	475	480	485
cag atg gcc gtc caa tac ctg gcc atc gac cca cac tcc cct gca gaa				1603
Gln Met Ala Val Gln Tyr Leu Ala Ile Asp Pro His Ser Pro Ala Glu				
	490	495	500	
ttc cgc tgc aat gtc atc gcc gga aac gtc gct gaa ttc tac gaa gca				1651
Phe Arg Cys Asn Val Ile Ala Gly Asn Val Ala Glu Phe Tyr Glu Ala				
	505	510	515	
ttc gac gtc ccc gaa gat gca cct gtg tac atc aag cca gaa gag cgc				1699
Phe Asp Val Pro Glu Asp Ala Pro Val Tyr Ile Lys Pro Glu Glu Arg				
	520	525	530	
cta gct atc tgg tagttgttag ttggtattga aaa				1734
Leu Ala Ile Trp				
	535			

<210> 170

<211> 537

Gly Lys Ile Gly Lys Pro Ala Asp Arg Asp Glu Trp Val Thr Thr Pro
290 295 300

Gln Thr Val Asn Ala Phe Tyr Asn Pro Val Val Asn Asp Ile Thr Phe
 305 310 315 320
 Pro Ala Ala Ile Leu Arg Ala Pro Phe Phe Asp Pro Glu Ala Glu Ala
 325 330 335
 Ala Glu Asn Phe Gly Ala Ile Gly Ala Val Ile Gly His Glu Ile Gly
 340 345 350
 His Gly Phe Asp Asp Gln Gly Ser Gln Tyr Asp Gly Asp Gly Asn Leu
 355 360 365
 Asn Ser Trp Trp Thr Asp Glu Asp Arg Ser Ala Phe Glu Gln Leu Thr
 370 375 380
 Ser Arg Leu Val Thr Gln Phe Ser Gly Leu Val Pro Ala Val Leu Thr
 385 390 395 400
 Ser Glu Gly Ile Asp Thr Asp Gly Val Asn Gly Glu Phe Thr Leu Gly
 405 410 415
 Glu Asn Ile Gly Asp Leu Gly Gly Leu Gly Ile Ala Val Val Ala Tyr
 420 425 430
 Glu Lys Tyr Leu Ala Asp Arg Gly Gln Thr Phe Glu Thr Ser Pro Val
 435 440 445
 Gln Lys Phe Glu Ala Glu Gly Ala Glu Glu Gly Leu Ala Glu Gln Glu
 450 455 460
 Phe Asn Gly Leu Gln Arg Leu Phe Leu Ser Trp Ala Arg Val Trp Arg
 465 470 475 480
 Thr Lys Ile Arg Pro Gln Met Ala Val Gln Tyr Leu Ala Ile Asp Pro
 485 490 495
 His Ser Pro Ala Glu Phe Arg Cys Asn Val Ile Ala Gly Asn Val Ala
 500 505 510
 Glu Phe Tyr Glu Ala Phe Asp Val Pro Glu Asp Ala Pro Val Tyr Ile
 515 520 525
 Lys Pro Glu Glu Arg Leu Ala Ile Trp
 530 535

<210> 171

<211> 426

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(403)

<223> FRXA01869

<400> 171

tgacaggcta ccttctgggg tggacatgat cccaacgct caaccactt gtggcaccaa 60

 ccacaaaccc tgtggcggt aatcccctag agtaggccac atg aag gat ctt tat 115
 Met Lys Asp Leu Tyr

	1	5	
cgc ttt gtc aat ggc ctg tgg ctt gac acc cac atc att ccc gac gat			163
Arg Phe Val Asn Gly Leu Trp Leu Asp Thr His Ile Ile Pro Asp Asp			
	10	20	
cgc gcg gtg gac ggc acg ttc cac aag ctg cgc gat gat gct gaa gaa			211
Arg Ala Val Asp Gly Thr Phe His Lys Leu Arg Asp Asp Ala Glu Glu			
	25	35	
gac gtc cat gag atc gtc aag gaa gac act gga cgc gca ggc aca ctt			259
Asp Val His Glu Ile Val Lys Glu Asp Thr Gly Arg Ala Gly Thr Leu			
	40	50	
tat gcc tca ttt atg gat act gac gcc atc aac gct gct ggt gtt gca			307
Tyr Ala Ser Phe Met Asp Thr Asp Ala Ile Asn Ala Ala Gly Val Ala			
	55	65	
ccg ctc gat gcg gat ctg aac agg ctg tct gtt gct aac tca tcg ttt			355
Pro Leu Asp Ala Asp Leu Asn Arg Leu Ser Val Ala Asn Ser Ser Phe			
	70	85	
tcg cag ctg ctc tcg gcg aac tgg acc gtg aag gcg ttg gcg cgc cag			403
Ser Gln Leu Leu Ser Ala Asn Trp Thr Val Lys Ala Leu Ala Arg Gln			
	90	100	
taggtttctg ggtggagaag gat			426

<210> 172

<211> 101

<212> PRT

<213> Corynebacterium glutamicum

<400> 172

Met Lys Asp Leu Tyr Arg Phe Val Asn Gly Leu Trp Leu Asp Thr His			
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Ile Ile Pro Asp Asp Arg Ala Val Asp Gly Thr Phe His Lys Leu Arg			
	20	25	30
Asp Asp Ala Glu Glu Asp Val His Glu Ile Val Lys Glu Asp Thr Gly			
	35	40	45
Arg Ala Gly Thr Leu Tyr Ala Ser Phe Met Asp Thr Asp Ala Ile Asn			
	50	55	60
Ala Ala Gly Val Ala Pro Leu Asp Ala Asp Leu Asn Arg Leu Ser Val			
	65	70	75
Ala Asn Ser Ser Phe Ser Gln Leu Leu Ser Ala Asn Trp Thr Val Lys			
	85	90	95
Ala Leu Ala Arg Gln			
	100		

<210> 173

<211> 1404

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1381)

<223> RXN00499

<400> 173

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tgccaacagg ggatatgcca ctgtgtaccc cacggcgatg atcggtaaaa tcctcggcgc 60

gcagatattg ttcttgctgc tctaagggtga tttttgggca  gtg  gtg  ggg  gtg  gtg  115
                                           Val Val Gly Val Val
                                           1      5

tcc acc cct gcg cgt aac ctg gga agc atg act aaa aca ctt ggt tcc  163
Ser Thr Pro Ala Arg Asn Leu Gly Ser Met Thr Lys Thr Leu Gly Ser
                      10                      15                      20

ctt cag ctg gaa gaa atc acg ctg acc ctc cct ctg act gaa gat gtg  211
Leu Gln Leu Glu Glu Ile Thr Leu Thr Leu Pro Leu Thr Glu Asp Val
                      25                      30                      35

gcc gat gaa cgc acc att gat gtg ttc gca cgc att gcc aca cgc gtc  259
Ala Asp Glu Arg Thr Ile Asp Val Phe Ala Arg Ile Ala Thr Arg Val
                      40                      45                      50

ggg ggg gaa gac ctt cca tat tta gta ttc ctg cag ggt ggg cct ggc  307
Gly Gly Glu Asp Leu Pro Tyr Leu Val Phe Leu Gln Gly Gly Pro Gly
                      55                      60                      65

aat gaa gct cca cgt cca agc ctt aat ccc ctc aac ccc aat tgg ttg  355
Asn Glu Ala Pro Arg Pro Ser Leu Asn Pro Leu Asn Pro Asn Trp Leu
                      70                      75                      80                      85

ggc gtg gcc ttg gag gaa tac cgc gtg gtc atg ttg gat caa cgt ggc  403
Gly Val Ala Leu Glu Glu Tyr Arg Val Val Met Leu Asp Gln Arg Gly
                      90                      95                      100

acc ggc cgt tcc acc cca gtg ggt aat gat att ttg gaa aaa ccc aca  451
Thr Gly Arg Ser Thr Pro Val Gly Asn Asp Ile Leu Glu Lys Pro Thr
                      105                      110                      115

gca gaa gta gtg gag tac tta tcc cac ctg cgc gca gat ggc att gtg  499
Ala Glu Val Val Glu Tyr Leu Ser His Leu Arg Ala Asp Gly Ile Val
                      120                      125                      130

cga gat gct gaa gcc ctg cgt aag cat ttg ggt gtg aat cag tgg aac  547
Arg Asp Ala Glu Ala Leu Arg Lys His Leu Gly Val Asn Gln Trp Asn
                      135                      140                      145

ctt tta ggc cag tcc ttc gga ggt ttc acc acc ctg cat tac ttg tcc  595
Leu Leu Gly Gln Ser Phe Gly Gly Phe Thr Thr Leu His Tyr Leu Ser
                      150                      155                      160                      165

cgg cac gcc gat tcc ttg gac aac gtg ttt att acc ggc ggt ctc agc  643
Arg His Ala Asp Ser Leu Asp Asn Val Phe Ile Thr Gly Gly Leu Ser
                      170                      175                      180

gct att gat cgc cca gca gaa gac gtg tat gcc aac tgt tac aac cgc  691
Ala Ile Asp Arg Pro Ala Glu Asp Val Tyr Ala Asn Cys Tyr Asn Arg
                      185                      190                      195

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atg cgc cga aac tct gag gaa ttc tac cgt cgc ttc ccg caa tta cgg	739
Met Arg Arg Asn Ser Glu Glu Phe Tyr Arg Arg Phe Pro Gln Leu Arg	
200 205 210	
gaa act ttc cga ggg ttg gtt aat cgt gct cgc gcc ggg gag att gtg	787
Glu Thr Phe Arg Gly Leu Val Asn Arg Ala Arg Ala Gly Glu Ile Val	
215 220 225	
ctt ccc acc ggc gaa gtt gtg tca gaa acc agg ctg cga tcc ctt ggt	835
Leu Pro Thr Gly Glu Val Val Ser Glu Thr Arg Leu Arg Ser Leu Gly	
230 235 240 245	
cac ttg ttg ggt agc aat gac ggc tgg ttt gat ctg tac aac ctg ctg	883
His Leu Leu Gly Ser Asn Asp Gly Trp Phe Asp Leu Tyr Asn Leu Leu	
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gaa tta gat ccc acc tcc aac gct ttt gtc cat gac ctg gca gga ctt	931
Glu Leu Asp Pro Thr Ser Asn Ala Phe Val His Asp Leu Ala Gly Leu	
265 270 275	
ttg cct ttc ggc aac cgc aac cca att tat tac gtg ctc cat gag tcc	979
Leu Pro Phe Gly Asn Arg Asn Pro Ile Tyr Tyr Val Leu His Glu Ser	
280 285 290	
tct tac gcc gac ggt gtg gtg aca aat tgg gca gca gag cgt gtg ctt	1027
Ser Tyr Ala Asp Gly Val Val Thr Asn Trp Ala Ala Glu Arg Val Leu	
295 300 305	
cca gag gat ttc cgc gag gat cca aca ctg ctc acc ggt gag cac gtg	1075
Pro Glu Asp Phe Arg Glu Asp Pro Thr Leu Thr Gly Glu His Val	
310 315 320 325	
ttc cag gag tgg aca gac acc gtg ccg tcg ctc aag ccg tgg aag gac	1123
Phe Gln Glu Trp Thr Asp Thr Val Pro Ser Leu Lys Pro Trp Lys Asp	
330 335 340	
gtt gcc ctg gca ttg gct cag cag gaa tgg ccc aag ctt tat gat gcg	1171
Val Ala Leu Ala Leu Ala Gln Gln Glu Trp Pro Lys Leu Tyr Asp Ala	
345 350 355	
aag gca ttg gaa aac tca cag gcc aag ggc gct gca gca gtg tat gcc	1219
Lys Ala Leu Glu Asn Ser Gln Ala Lys Gly Ala Ala Ala Val Tyr Ala	
360 365 370	
aat gac gtt ttc gtc cca gtg gat tac tct ctg gaa acc gca caa cac	1267
Asn Asp Val Phe Val Pro Val Asp Tyr Ser Leu Glu Thr Ala Gln His	
375 380 385	
ctg ccc ggt gtg cag ctg ttt atc acc agc cag cat gaa cac aat gga	1315
Leu Pro Gly Val Gln Leu Phe Ile Thr Ser Gln His Glu His Asn Gly	
390 395 400 405	
ctt cgt gcc agc tca ggc gca gta ctg aag cac ctt ttc gat ctg gcc	1363
Leu Arg Ala Ser Ser Gly Ala Val Leu Lys His Leu Phe Asp Leu Ala	
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His Gly Arg Glu Val Arg	
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<210> 174

<211> 427

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 174

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Lys	Thr	Leu	Gly	Ser	Leu	Gln	Leu	Glu	Glu	Ile	Thr	Leu	Thr	Leu	Pro
			20					25					30		

Leu	Thr	Glu	Asp	Val	Ala	Asp	Glu	Arg	Thr	Ile	Asp	Val	Phe	Ala	Arg
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Ile	Ala	Thr	Arg	Val	Gly	Gly	Glu	Asp	Leu	Pro	Tyr	Leu	Val	Phe	Leu
	50					55					60				

Gln	Gly	Gly	Pro	Gly	Asn	Glu	Ala	Pro	Arg	Pro	Ser	Leu	Asn	Pro	Leu
65					70					75					80

Asn	Pro	Asn	Trp	Leu	Gly	Val	Ala	Leu	Glu	Glu	Tyr	Arg	Val	Val	Met
			85						90						95

Leu	Asp	Gln	Arg	Gly	Thr	Gly	Arg	Ser	Thr	Pro	Val	Gly	Asn	Asp	Ile
		100					105						110		

Leu	Glu	Lys	Pro	Thr	Ala	Glu	Val	Val	Glu	Tyr	Leu	Ser	His	Leu	Arg
		115					120					125			

Ala	Asp	Gly	Ile	Val	Arg	Asp	Ala	Glu	Ala	Leu	Arg	Lys	His	Leu	Gly
	130					135					140				

Val	Asn	Gln	Trp	Asn	Leu	Leu	Gly	Gln	Ser	Phe	Gly	Gly	Phe	Thr	Thr
145					150					155					160

Leu	His	Tyr	Leu	Ser	Arg	His	Ala	Asp	Ser	Leu	Asp	Asn	Val	Phe	Ile
				165					170					175	

Thr	Gly	Gly	Leu	Ser	Ala	Ile	Asp	Arg	Pro	Ala	Glu	Asp	Val	Tyr	Ala
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Asn	Cys	Tyr	Asn	Arg	Met	Arg	Arg	Asn	Ser	Glu	Glu	Phe	Tyr	Arg	Arg
		195					200					205			

Phe	Pro	Gln	Leu	Arg	Glu	Thr	Phe	Arg	Gly	Leu	Val	Asn	Arg	Ala	Arg
	210					215					220				

Ala	Gly	Glu	Ile	Val	Leu	Pro	Thr	Gly	Glu	Val	Val	Ser	Glu	Thr	Arg
225					230					235					240

Leu	Arg	Ser	Leu	Gly	His	Leu	Leu	Gly	Ser	Asn	Asp	Gly	Trp	Phe	Asp
				245					250					255	

Leu	Tyr	Asn	Leu	Leu	Glu	Leu	Asp	Pro	Thr	Ser	Asn	Ala	Phe	Val	His
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Asp	Leu	Ala	Gly	Leu	Leu	Pro	Phe	Gly	Asn	Arg	Asn	Pro	Ile	Tyr	Tyr
		275					280					285			

Val	Leu	His	Glu	Ser	Ser	Tyr	Ala	Asp	Gly	Val	Val	Thr	Asn	Trp	Ala
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290	295	300
Ala Glu Arg Val Leu Pro Glu Asp Phe Arg Glu Asp Pro Thr Leu Leu 305 310 315 320		
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Lys Pro Trp Lys Asp Val Ala Leu Ala Leu Ala Gln Gln Glu Trp Pro 340 345 350		
Lys Leu Tyr Asp Ala Lys Ala Leu Glu Asn Ser Gln Ala Lys Gly Ala 355 360 365		
Ala Ala Val Tyr Ala Asn Asp Val Phe Val Pro Val Asp Tyr Ser Leu 370 375 380		
Glu Thr Ala Gln His Leu Pro Gly Val Gln Leu Phe Ile Thr Ser Gln 385 390 395 400		
His Glu His Asn Gly Leu Arg Ala Ser Ser Gly Ala Val Leu Lys His 405 410 415		
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<211> 980

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(957)

<223> FRXA00499

<400> 175

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aag cat ttg ggt gtg aat cag tgg aac ctt tta ggc cag tcc ttc gga Lys His Leu Gly Val Asn Gln Trp Asn Leu Leu Gly Gln Ser Phe Gly 35 40 45	144
ggt ttc acc acc ctg cat tac ttg tcc cgg cac gcc gat tcc ttg gac Gly Phe Thr Thr Leu His Tyr Leu Ser Arg His Ala Asp Ser Leu Asp 50 55 60	192
aac gtg ttt att acc ggc ggt ctc agc gct att gat cgc cca gca gaa Asn Val Phe Ile Thr Gly Gly Leu Ser Ala Ile Asp Arg Pro Ala Glu 65 70 75 80	240
gac gtg tat gcc aac tgt tac aac cgc atg cgc cga aac tct gag gaa Asp Val Tyr Ala Asn Cys Tyr Asn Arg Met Arg Arg Asn Ser Glu Glu 85 90 95	288

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Phe Tyr Arg Arg Phe Pro Gln Leu Arg Glu Thr Phe Arg Gly Leu Val	
100 105 110	
aat cgt gct cgc gcc ggg gag att gtg ctt ccc acc ggc gaa gtt gtg	384
Asn Arg Ala Arg Ala Gly Glu Ile Val Leu Pro Thr Gly Glu Val Val	
115 120 125	
tca gaa acc agg ctg cga tcc ctt ggt cac ttg ttg ggt agc aat gac	432
Ser Glu Thr Arg Leu Arg Ser Leu Gly His Leu Gly Ser Asn Asp	
130 135 140	
ggc tgg ttt gat ctg tac aac ctg ctg gaa tta gat ccc acc tcc aac	480
Gly Trp Phe Asp Leu Tyr Asn Leu Leu Glu Leu Asp Pro Thr Ser Asn	
145 150 155 160	
gct ttt gtc cat gac ctg gca gga ctt ttg cct ttc ggc aac cgc aac	528
Ala Phe Val His Asp Leu Ala Gly Leu Leu Pro Phe Gly Asn Arg Asn	
165 170 175	
cca att tat tac gtg ctc cat gag tcc tct tac gcc gac ggt gtg gtg	576
Pro Ile Tyr Tyr Val Leu His Glu Ser Ser Tyr Ala Asp Gly Val Val	
180 185 190	
aca aat tgg gca gca gag cgt gtg ctt cca gag gat ttc cgc gag gat	624
Thr Asn Trp Ala Ala Glu Arg Val Leu Pro Glu Asp Phe Arg Glu Asp	
195 200 205	
cca aca ctg ctc acc ggt gag cac gtg ttc cag gag tgg aca gac acc	672
Pro Thr Leu Leu Thr Gly Glu His Val Phe Gln Glu Trp Thr Asp Thr	
210 215 220	
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Val Pro Ser Leu Lys Pro Trp Lys Asp Val Ala Leu Ala Leu Ala Gln	
225 230 235 240	
cag gaa tgg ccc aag ctt tat gat gcg aag gca ttg gaa aac tca cag	768
Gln Glu Trp Pro Lys Leu Tyr Asp Ala Lys Ala Leu Glu Asn Ser Gln	
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gcc aag ggc gct gca gca gtg tat gcc aat gac gtt ttc gtc cca gtg	816
Ala Lys Gly Ala Ala Ala Val Tyr Ala Asn Asp Val Phe Val Pro Val	
260 265 270	
gat tac tct ctg gaa acc gca caa cac ctg ccc ggt gtg cag ctg ttt	864
Asp Tyr Ser Leu Glu Thr Ala Gln His Leu Pro Gly Val Gln Leu Phe	
275 280 285	
atc acc agc cag cat gaa cac aat gga ctt cgt gcc agc tca ggc gca	912
Ile Thr Ser Gln His Glu His Asn Gly Leu Arg Ala Ser Ser Gly Ala	
290 295 300	
gta ctg aag cac ctt ttc gat ctg gcc cac ggc cga gag gta cgc	957
Val Leu Lys His Leu Phe Asp Leu Ala His Gly Arg Glu Val Arg	
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<211> 319

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 176

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Lys His Leu Gly Val Asn Gln Trp Asn Leu Leu Gly Gln Ser Phe Gly
      35           40           45

Gly Phe Thr Thr Leu His Tyr Leu Ser Arg His Ala Asp Ser Leu Asp
      50           55           60

Asn Val Phe Ile Thr Gly Gly Leu Ser Ala Ile Asp Arg Pro Ala Glu
      65           70           75           80

Asp Val Tyr Ala Asn Cys Tyr Asn Arg Met Arg Arg Asn Ser Glu Glu
      85           90           95

Phe Tyr Arg Arg Phe Pro Gln Leu Arg Glu Thr Phe Arg Gly Leu Val
      100          105          110

Asn Arg Ala Arg Ala Gly Glu Ile Val Leu Pro Thr Gly Glu Val Val
      115          120          125

Ser Glu Thr Arg Leu Arg Ser Leu Gly His Leu Leu Gly Ser Asn Asp
      130          135          140

Gly Trp Phe Asp Leu Tyr Asn Leu Leu Glu Leu Asp Pro Thr Ser Asn
      145          150          155          160

Ala Phe Val His Asp Leu Ala Gly Leu Leu Pro Phe Gly Asn Arg Asn
      165          170          175

Pro Ile Tyr Tyr Val Leu His Glu Ser Ser Tyr Ala Asp Gly Val Val
      180          185          190

Thr Asn Trp Ala Ala Glu Arg Val Leu Pro Glu Asp Phe Arg Glu Asp
      195          200          205

Pro Thr Leu Leu Thr Gly Glu His Val Phe Gln Glu Trp Thr Asp Thr
      210          215          220

Val Pro Ser Leu Lys Pro Trp Lys Asp Val Ala Leu Ala Leu Ala Gln
      225          230          235          240

Gln Glu Trp Pro Lys Leu Tyr Asp Ala Lys Ala Leu Glu Asn Ser Gln
      245          250          255

Ala Lys Gly Ala Ala Ala Val Tyr Ala Asn Asp Val Phe Val Pro Val
      260          265          270

Asp Tyr Ser Leu Glu Thr Ala Gln His Leu Pro Gly Val Gln Leu Phe
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Ile Thr Ser Gln His Glu His Asn Gly Leu Arg Ala Ser Ser Gly Ala
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Val Leu Lys His Leu Phe Asp Leu Ala His Gly Arg Glu Val Arg
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<210> 177

<211> 2127

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2104)

<223> RXN01277

<400> 177

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 Met Thr Asp Tyr Thr
 1 5
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 Phe Leu Glu Asp Ile Asp Thr Pro Glu Ala Leu Ala Trp Ala Glu Lys
 10 15 20
 tgg tcg ggg gaa agc gtc gaa aag cta aaa agc cca gcc aag gac gcc 211
 Trp Ser Gly Glu Ser Val Glu Lys Leu Lys Ser Pro Ala Lys Asp Ala
 25 30 35
 ctg gaa gcc agg ctg ctg gct gcg ttg gac acc gat gat cgc att gcc 259
 Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr Asp Asp Arg Ile Ala
 40 45 50
 tac gtg agc cgg cgc ggt gag aag ctg tac aac ttt tgg cgg gac gcg 307
 Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn Phe Trp Arg Asp Ala
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 Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr Leu Glu Ser Tyr Glu
 70 75 80 85
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 Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp Val Asp Ala Leu Ala
 90 95 100
 gag gat gag ggc gaa aac tgg gta tgg aag ggc gcg gtt gtg cgc tcg 451
 Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly Ala Val Val Arg Ser
 105 110 115
 ccg gag ttt gat cgg gcg ttg gtg aag ttc tcg cgg ggc ggg gct gat 499
 Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser Arg Gly Gly Ala Asp
 120 125 130
 gcg acg gtg att agg gag ttt gat ctg gcc acg gct gct ttc gtg gat 547
 Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr Ala Ala Phe Val Asp
 135 140 145
 gat tcg ccg ttt gaa ttg aag gag gcg aag tcc gat gtc acg tgg gtt 595
 Asp Ser Pro Phe Glu Leu Lys Glu Ala Lys Ser Asp Val Thr Trp Val
 150 155 160 165

gat	ctg	gat	acg	ttg	ctg	gtg	ggc	acg	gat	acc	ggc	gag	ggg	tca	ctg	643
Asp	Leu	Asp	Thr	Leu	Leu	Val	Gly	Thr	Asp	Thr	Gly	Glu	Gly	Ser	Leu	
			170						175					180		
acg	gat	tct	ggg	tac	ccg	gcg	cgg	gtg	ctc	acg	tgg	aag	cgt	ggg	act	691
Thr	Asp	Ser	Gly	Tyr	Pro	Ala	Arg	Val	Leu	Thr	Trp	Lys	Arg	Gly	Thr	
			185					190					195			
ccg	ctt	gag	cag	gcg	gag	ttg	ttc	ttt	gag	ggg	tcg	cgt	cag	gat	gtg	739
Pro	Leu	Glu	Gln	Ala	Glu	Leu	Phe	Phe	Glu	Gly	Ser	Arg	Gln	Asp	Val	
		200					205					210				
gcg	act	cat	gcg	tgg	cgg	gat	tca	aca	cct	ggt	ttt	gag	cgg	acg	ttt	787
Ala	Thr	His	Ala	Trp	Arg	Asp	Ser	Thr	Pro	Gly	Phe	Glu	Arg	Thr	Phe	
	215					220					225					
gtg	tca	agg	tcg	ttg	gat	ttc	tat	aat	tcg	gag	acg	tcg	ctg	gaa	acc	835
Val	Ser	Arg	Ser	Leu	Asp	Phe	Tyr	Asn	Ser	Glu	Thr	Ser	Leu	Glu	Thr	
230					235				240					245		
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Glu	Gly	Gly	Leu	Val	Lys	Leu	Asp	Val	Pro	Thr	Asp	Cys	Asp	Val	Ile	
			250					255						260		
gtg	aag	aag	cag	tgg	att	ttt	gtg	agt	cct	cgg	acg	gat	ttc	gct	ggg	931
Val	Lys	Lys	Gln	Trp	Ile	Phe	Val	Ser	Pro	Arg	Thr	Asp	Phe	Ala	Gly	
			265				270					275				
att	cca	gca	ggt	ggc	ttg	gga	gtg	ctg	ctg	tta	aag	gag	ttc	ctt	gag	979
Ile	Pro	Ala	Gly	Gly	Leu	Gly	Val	Leu	Leu	Leu	Lys	Glu	Phe	Leu	Glu	
		280				285						290				
ggc	ggg	cgc	gat	ttt	cag	cct	gtg	ttt	acg	cct	act	gag	tcg	acg	tcg	1027
Gly	Gly	Arg	Asp	Phe	Gln	Pro	Val	Phe	Thr	Pro	Thr	Glu	Ser	Thr	Ser	
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310				315					320					325		
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Asn	Asn	Val	Ser	Thr	Glu	Ile	Val	Thr	Val	Pro	Leu	Asn	Asp	Pro	Thr	
			330					335					340			
acg	gag	cat	gaa	cac	att	gac	ctc	cca	gag	cat	gtc	acc	gcg	cat	gtg	1171
Thr	Glu	His	Glu	His	Ile	Asp	Leu	Pro	Glu	His	Val	Thr	Ala	His	Val	
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Val	Ala	Thr	Ser	Pro	Leu	Asp	Gly	Asp	Glu	Ile	Trp	Val	Gln	Ala	Ala	
		360				365					370					
agt	ttc	acc	gaa	gcg	cca	acg	ttg	ctg	cgt	gcg	gag	ctg	cct	ggt	gcg	1267
Ser	Phe	Thr	Glu	Ala	Pro	Thr	Leu	Leu	Arg	Ala	Glu	Leu	Pro	Gly	Ala	
	375				380						385					
ctt	gag	gct	gtg	aag	aag	gcg	ccg	ttg	cag	ttt	gaa	aat	gct	ggt	cag	1315
Leu	Glu	Ala	Val	Lys	Lys	Ala	Pro	Leu	Gln	Phe	Glu	Asn	Ala	Gly	Gln	
390				395					400					405		

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Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp Gly Thr Lys Ile Pro	
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Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro Gln Asn Thr Leu Val	
425 430 435	
cac gcc tac ggc ggc ttc gag gtt tcc ctt acc cca agc cac tcc ccg	1459
His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr Pro Ser His Ser Pro	
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Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr Tyr Phe Val Glu Ala	
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Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp His Arg Ala Val Leu	
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Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro Glu Gln Ile Ala Ile	
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Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser Gly Ala Leu Thr Gln	
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Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln Val Pro Leu Ala Asp	
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550 555 560 565	
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Tyr Gly Asn Pro Asp Asp Pro Glu Glu Arg Ala Val Ile Glu Gln Tyr	
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Ser Pro Val Gln Ala Val Val Gly Val Glu Lys Arg Ile Tyr Pro Pro	
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Ala Leu Val Thr Thr Ser Thr Arg Asp Asp Arg Val His Pro Ala His	
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gcg cgc ctt ttt gct caa gct ttg ctt gat gcg ggc cag gcc gtg gat	1987
Ala Arg Leu Phe Ala Gln Ala Leu Leu Asp Ala Gly Gln Ala Val Asp	
615 620 625	
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Tyr Tyr Glu Asn Thr Glu Gly Gly His Ala Gly Ala Ala Asp Asn Lys	
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2127

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Pro	Ala	Lys 35	Asp	Ala	Leu	Glu	Ala 40	Arg	Leu	Leu	Ala	Ala 45	Leu	Asp	Thr	
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Phe 65	Trp	Arg	Asp	Ala	Gln 70	His	Pro	Arg	Gly	Val 75	Trp	Arg	Thr	Thr	Thr 80	
Leu	Glu	Ser	Tyr	Glu 85	Ser	Asp	Gln	Pro	Glu 90	Trp	Asp	Val	Leu	Ile 95	Asp	
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Ala 145	Ala	Phe	Val	Asp	Asp 150	Ser	Pro	Phe	Glu	Leu 155	Lys	Glu	Ala	Lys	Ser 160	
Asp	Val	Thr	Trp	Val 165	Asp	Leu	Asp	Thr	Leu 170	Leu	Val	Gly	Thr	Asp 175	Thr	
Gly	Glu	Gly	Ser 180	Leu	Thr	Asp	Ser	Gly 185	Tyr	Pro	Ala	Arg	Val 190	Leu	Thr	
Trp	Lys	Arg 195	Gly	Thr	Pro	Leu	Glu 200	Gln	Ala	Glu	Leu	Phe 205	Phe	Glu	Gly	
Ser	Arg 210	Gln	Asp	Val	Ala	Thr 215	His	Ala	Trp	Arg	Asp 220	Ser	Thr	Pro	Gly	
Phe 225	Glu	Arg	Thr	Phe	Val 230	Ser	Arg	Ser	Leu	Asp 235	Phe	Tyr	Asn	Ser	Glu 240	
Thr	Ser	Leu	Glu	Thr 245	Glu	Gly	Gly	Leu	Val 250	Lys	Leu	Asp	Val	Pro 255	Thr	

Asp Cys Asp Val Ile Val Lys Lys Gln Trp Ile Phe Val Ser Pro Arg
 260 265 270
 Thr Asp Phe Ala Gly Ile Pro Ala Gly Gly Leu Gly Val Leu Leu Leu
 275 280 285
 Lys Glu Phe Leu Glu Gly Gly Arg Asp Phe Gln Pro Val Phe Thr Pro
 290 295 300
 Thr Glu Ser Thr Ser Leu Gln Gly Leu Ala Thr Thr Lys Asn Phe Leu
 305 310 315 320
 Val Leu Thr Leu Leu Asn Asn Val Ser Thr Glu Ile Val Thr Val Pro
 325 330 335
 Leu Asn Asp Pro Thr Thr Glu His Glu His Ile Asp Leu Pro Glu His
 340 345 350
 Val Thr Ala His Val Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile
 355 360 365
 Trp Val Gln Ala Ala Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala
 370 375 380
 Glu Leu Pro Gly Ala Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe
 385 390 395 400
 Glu Asn Ala Gly Gln Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp
 405 410 415
 Gly Thr Lys Ile Pro Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro
 420 425 430
 Gln Asn Thr Leu Val His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr
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 Pro Ser His Ser Pro Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr
 450 455 460
 Tyr Phe Val Glu Ala Asn Leu Arg Gly Gly Gly Glu Phe Gly Pro Glu
 465 470 475 480
 Trp His Ser Gln Ala Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp
 485 490 495
 His Arg Ala Val Leu Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro
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 Glu Gln Ile Ala Ile Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser
 515 520 525
 Gly Ala Leu Thr Gln Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln
 530 535 540
 Val Pro Leu Ala Asp Met Leu Arg Tyr His Thr Trp Ser Ala Gly Ala
 545 550 555 560
 Ser Trp Met Ala Glu Tyr Gly Asn Pro Asp Asp Pro Glu Glu Arg Ala
 565 570 575

Val Ile Glu Gln Tyr Ser Pro Val Gln Ala Val Val Gly Val Glu Lys
 580 585 590

Arg Ile Tyr Pro Pro Ala Leu Val Thr Thr Ser Thr Arg Asp Asp Arg
 595 600 605

Val His Pro Ala His Ala Arg Leu Phe Ala Gln Ala Leu Leu Asp Ala
 610 615 620

Gly Gln Ala Val Asp Tyr Tyr Glu Asn Thr Glu Gly Gly His Ala Gly
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 <222> (101)..(1789)
 <223> FRXA01277

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 Met Thr Asp Tyr Thr
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 Phe Leu Glu Asp Ile Asp Thr Pro Glu Ala Leu Ala Trp Ala Glu Lys
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 Trp Ser Gly Glu Ser Val Glu Lys Leu Lys Ser Pro Ala Lys Asp Ala
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 Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr Asp Arg Arg Ile Ala
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 Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn Phe Trp Arg Asp Ala
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 Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr Leu Glu Ser Tyr Glu
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 Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp Val Asp Ala Leu Ala
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Pro	Glu	Phe	Asp	Arg	Ala	Leu	Val	Lys	Phe	Ser	Arg	Gly	Gly	Ala	Asp		
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gcg	acg	gtg	att	agg	gag	ttt	gat	ctg	gcc	acg	gct	gct	ttc	gtg	gat	547	
Ala	Thr	Val	Ile	Arg	Glu	Phe	Asp	Leu	Ala	Thr	Ala	Ala	Phe	Val	Asp		
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Asp	Ser	Pro	Phe	Glu	Leu	Lys	Glu	Ala	Lys	Ser	Asp	Val	Thr	Trp	Val		
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Asp	Leu	Asp	Thr	Leu	Leu	Val	Gly	Thr	Asp	Thr	Gly	Glu	Gly	Ser	Leu		
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Thr	Asp	Ser	Gly	Tyr	Pro	Ala	Arg	Val	Leu	Thr	Trp	Lys	Arg	Gly	Thr		
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Val	Ser	Arg	Ser	Leu	Asp	Phe	Tyr	Asn	Ser	Glu	Thr	Ser	Leu	Glu	Thr		
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Glu	Gly	Gly	Leu	Val	Lys	Leu	Asp	Val	Pro	Thr	Asp	Cys	Asp	Val	Ile		
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Val	Lys	Lys	Gln	Trp	Ile	Phe	Val	Ser	Pro	Arg	Thr	Asp	Phe	Ala	Gly		
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Ile	Pro	Ala	Gly	Gly	Leu	Gly	Val	Leu	Leu	Leu	Lys	Glu	Phe	Leu	Glu		
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Tyr	Pro	Glu	Ala	Phe	Gly	Ala	Ala	Val	Val	Gln	Val	Pro	Leu	Ala	Asp																								
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<212> PRT

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<400> 180

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Pro Ala Lys Asp Ala Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr
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Asp Asp Arg Ile Ala Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn
      50           55           60

Phe Trp Arg Asp Ala Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr
      65           70           75           80

Leu Glu Ser Tyr Glu Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp
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Val Asp Ala Leu Ala Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly
          100          105          110

Ala Val Val Arg Ser Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser
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Arg Gly Gly Ala Asp Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr
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Ala Ala Phe Val Asp Asp Ser Pro Phe Glu Leu Lys Glu Ala Lys Ser
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Asp Val Thr Trp Val Asp Leu Asp Thr Leu Leu Val Gly Thr Asp Thr
          165          170          175

Gly Glu Gly Ser Leu Thr Asp Ser Gly Tyr Pro Ala Arg Val Leu Thr
          180          185          190

Trp Lys Arg Gly Thr Pro Leu Glu Gln Ala Glu Leu Phe Phe Glu Gly
          195          200          205

Ser Arg Gln Asp Val Ala Thr His Ala Trp Arg Asp Ser Thr Pro Gly
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Phe Glu Arg Thr Phe Val Ser Arg Ser Leu Asp Phe Tyr Asn Ser Glu
      225           230          235          240

Thr Ser Leu Glu Thr Glu Gly Gly Leu Val Lys Leu Asp Val Pro Thr
          245          250          255

Asp Cys Asp Val Ile Val Lys Lys Gln Trp Ile Phe Val Ser Pro Arg
          260          265          270

Thr Asp Phe Ala Gly Ile Pro Ala Gly Gly Leu Gly Val Leu Leu Leu
      275           280          285

Lys Glu Phe Leu Glu Gly Gly Arg Asp Phe Gln Pro Val Phe Thr Pro
      290           295          300

Thr Glu Ser Thr Ser Leu Gln Gly Leu Ala Thr Thr Lys Asn Phe Leu
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Val Leu Thr Leu Leu Asn Asn Val Ser Thr Glu Ile Val Thr Val Pro
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Leu Asn Asp Pro Thr Thr Glu His Glu His Ile Asp Leu Pro Glu His
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Val Thr Ala His Val Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile
 355 360 365

Trp Val Gln Ala Ala Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala
 370 375 380

Glu Leu Pro Gly Ala Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe
 385 390 395 400

Glu Asn Ala Gly Gln Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp
 405 410 415

Gly Thr Lys Ile Pro Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro
 420 425 430

Gln Asn Thr Leu Val His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr
 435 440 445

Pro Ser His Ser Pro Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr
 450 455 460

Tyr Phe Val Glu Ala Asn Leu Arg Gly Gly Gly Glu Phe Gly Pro Glu
 465 470 475 480

Trp His Ser Gln Ala Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp
 485 490 495

His Arg Ala Val Leu Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro
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Glu Gln Ile Ala Ile Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser
 515 520 525

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Ser Trp Met

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<211> 915

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<222> (101)..(892)

<223> RXN00675

<400> 181

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Met Gly Phe Arg Ser
1 5
aag aag aag gtt att gcg gca aag acc gcc gct gag ctg gac gcg atg 163
Lys Lys Lys Val Ile Ala Ala Lys Thr Ala Ala Glu Leu Asp Ala Met
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Gln Ala Ala Gly Glu Ile Val Gly Lys Ala Leu Gln Ala Val Arg Ala
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Glu Ala Lys Ala Gly Met Ser Thr Trp Asp Leu Asp Gln Ile Ala Glu
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Gln Val Ile Arg Asp Ala Gly Ala Val Pro Thr Phe Leu Gly Tyr Gln
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Gly Phe Pro Ala Ser Val Cys Ala Ser Val Asn Glu Val Ile Val His
70 75 80 85
ggc att cca tcc aag gag acc atc ttg gag gaa ggc gat ctg gtg tcc 403
Gly Ile Pro Ser Lys Glu Thr Ile Leu Glu Glu Gly Asp Leu Val Ser
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Ile Asp Cys Gly Ala Thr Phe Asp Gly Trp Val Gly Asp Ser Ala Trp
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Ser Phe Gly Ile Gly Glu Leu Asp Glu Asp Val Gln Gly Leu Asn Leu
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Ala Thr Glu Trp Val Leu Met Glu Gly Met Lys Ala Met Val Pro Gly
135 140 145
aac cgt ttg acc gat gtc tcc cac gct ctc gag gtc gca acc cgc aag 595
Asn Arg Leu Thr Asp Val Ser His Ala Leu Glu Val Ala Thr Arg Lys
150 155 160 165
gct gag tcc aag ttc ggc gtc gcg ctc ggc atc gtc gat ggc tac ggc 643
Ala Glu Ser Lys Phe Gly Val Ala Leu Gly Ile Val Asp Gly Tyr Gly
170 175 180
gga cac ggc att ggc cgc cac atg cac gag gag cca tac ttg gct aat 691
Gly His Gly Ile Gly Arg His Met His Glu Glu Pro Tyr Leu Ala Asn
185 190 195
gag ggc aag gcc ggc aag ggc cct gtg att cag gag ggc tcc gtg ctc 739
Glu Gly Lys Ala Gly Lys Gly Pro Val Ile Gln Glu Gly Ser Val Leu
200 205 210
gcc att gag cct atg ctc acc ctc ggc acc gaa gat tcc gca gtg ctg 787
Ala Ile Glu Pro Met Leu Thr Leu Gly Thr Glu Asp Ser Ala Val Leu
215 220 225

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gaa gat gat tgg act gtc gtg act ctc gac ggt tca tgg gca tca cac 835
 Glu Asp Asp Trp Thr Val Val Thr Leu Asp Gly Ser Trp Ala Ser His
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tgg gag cac acc gtt gca gcc acc aag ggc ggc ccg cgc atc ctc acg 883
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<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 182

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Asp Gln Ile Ala Glu Gln Val Ile Arg Asp Ala Gly Ala Val Pro Thr
 50 55 60

Phe Leu Gly Tyr Gln Gly Phe Pro Ala Ser Val Cys Ala Ser Val Asn
 65 70 75 80

Glu Val Ile Val His Gly Ile Pro Ser Lys Glu Thr Ile Leu Glu Glu
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Gly Asp Leu Val Ser Ile Asp Cys Gly Ala Thr Phe Asp Gly Trp Val
 100 105 110

Gly Asp Ser Ala Trp Ser Phe Gly Ile Gly Glu Leu Asp Glu Asp Val
 115 120 125

Gln Gly Leu Asn Leu Ala Thr Glu Trp Val Leu Met Glu Gly Met Lys
 130 135 140

Ala Met Val Pro Gly Asn Arg Leu Thr Asp Val Ser His Ala Leu Glu
 145 150 155 160

Val Ala Thr Arg Lys Ala Glu Ser Lys Phe Gly Val Ala Leu Gly Ile
 165 170 175

Val Asp Gly Tyr Gly Gly His Gly Ile Gly Arg His Met His Glu Glu
 180 185 190

Pro Tyr Leu Ala Asn Glu Gly Lys Ala Gly Lys Gly Pro Val Ile Gln
 195 200 205

Glu Gly Ser Val Leu Ala Ile Glu Pro Met Leu Thr Leu Gly Thr Glu
 210 215 220

Asp Ser Ala Val Leu Glu Asp Asp Trp Thr Val Val Thr Leu Asp Gly
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Pro Arg Ile Leu Thr Pro Arg Tyr
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<223> FRXA00675

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 Gly Ile Gly Glu Leu Asp Glu Asp Val Gln Gly Leu Asn Leu Ala Thr
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gag tgg gtc ctc atg gaa ggc atg aag gcc atg gtt cca ggc aac cgt 144
 Glu Trp Val Leu Met Glu Gly Met Lys Ala Met Val Pro Gly Asn Arg
 35 40 45

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 85 90 95

aag gcc ggc aag ggc cct gtg att cag gag ggc tcc gtg ctc gcc att 336
 Lys Ala Gly Lys Gly Pro Val Ile Gln Glu Gly Ser Val Leu Ala Ile
 100 105 110

gag cct atg ctc acc ctc ggc acc gaa gat tcc gca gtg ctg gaa gat 384
 Glu Pro Met Leu Thr Leu Gly Thr Glu Asp Ser Ala Val Leu Glu Asp
 115 120 125

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 Asp Trp Thr Val Val Thr Leu Asp Gly Ser Trp Ala Ser His Trp Glu
 130 135 140

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Tyr

506

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<213> Corynebacterium glutamicum

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35 40 45
Leu Thr Asp Val Ser His Ala Leu Glu Val Ala Thr Arg Lys Ala Glu
50 55 60
Ser Lys Phe Gly Val Ala Leu Gly Ile Val Asp Gly Tyr Gly Gly His
65 70 75 80
Gly Ile Gly Arg His Met His Glu Glu Pro Tyr Leu Ala Asn Glu Gly
85 90 95
Lys Ala Gly Lys Gly Pro Val Ile Gln Glu Gly Ser Val Leu Ala Ile
100 105 110
Glu Pro Met Leu Thr Leu Gly Thr Glu Asp Ser Ala Val Leu Glu Asp
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Tyr

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<223> RXN00877

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Met Thr Val Glu His

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Ile	Lys	Val	Ala	Asp	Phe	Pro	Pro	Ala	Phe	Glu	Leu	Ala	Leu	Ala	Glu																
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cac	gat	gct	gaa	att	aca	gcg	atc	gct	acc	aat	gag	gac	gct	cct	acc	259															
His	Asp	Ala	Glu	Ile	Thr	Ala	Ile	Ala	Thr	Asn	Glu	Asp	Ala	Pro	Thr																
				40					45					50																	
tgg	gag	aac	acc	att	gag	gcc	ctg	gaa	cgc	gca	ggc	ctg	tcc	ctc	aac	307															
Trp	Glu	Asn	Thr	Ile	Glu	Ala	Leu	Glu	Arg	Ala	Gly	Leu	Ser	Leu	Asn																
				55					60					65																	
cgc	gtc	gcc	gcc	gta	ttc	ttc	aac	ttg	cag	ggc	acc	gat	tcc	tcc	cct	355															
Arg	Val	Ala	Ala	Val	Phe	Phe	Asn	Leu	Gln	Gly	Thr	Asp	Ser	Ser	Pro																
				70					75					80			85														
gaa	atg	gat	gaa	atc	gca	gcc	act	atc	gcg	ccg	aaa	ctc	tcc	gcg	cat	403															
Glu	Met	Asp	Glu	Ile	Ala	Ala	Thr	Ile	Ala	Pro	Lys	Leu	Ser	Ala	His																
				90					95					100																	
tcg	gat	gcg	att	ttc	cac	aat	gct	gcg	ctt	ttc	gcg	cgc	att	gag	gcc	451															
Ser	Asp	Ala	Ile	Phe	His	Asn	Ala	Ala	Leu	Phe	Ala	Arg	Ile	Glu	Ala																
				105					110					115																	
gta	gaa	gca	ccg	gcc	gac	gag	gaa	tcg	caa	cgc	ctg	ttg	tcc	cac	acc	499															
Val	Glu	Ala	Pro	Ala	Asp	Glu	Glu	Ser	Gln	Arg	Leu	Leu	Ser	His	Thr																
				120					125					130																	
aag	cgc	gct	ttt	cga	cgt	cgc	ggt	gca	gca	ctc	aac	gcc	gac	ggc	aag	547															
Lys	Arg	Ala	Phe	Arg	Arg	Arg	Gly	Ala	Ala	Leu	Asn	Ala	Asp	Gly	Lys																
				135					140					145																	
gcc	cga	ctg	agc	acc	atc	aac	cag	cgc	cta	tcg	gca	ctg	tcc	gaa	cag	595															
Ala	Arg	Leu	Ser	Thr	Ile	Asn	Gln	Arg	Leu	Ser	Ala	Leu	Ser	Glu	Gln																
				150					155					160			165														
ttc	ggc	cgc	aac	ctg	ctt	cag	gac	acc	cgc	gat	ctg	gcg	gtc	aac	ttt	643															
Phe	Gly	Arg	Asn	Leu	Leu	Gln	Asp	Thr	Arg	Asp	Leu	Ala	Val	Asn	Phe																
				170					175					180																	
gaa	gaa	tct	gaa	ctt	gcc	ggt	ttt	agc	gaa	gcc	cgc	ata	tcc	gcc	gcc	691															
Glu	Glu	Ser	Glu	Leu	Ala	Gly	Phe	Ser	Glu	Ala	Arg	Ile	Ser	Ala	Ala																
				185					190					195																	
gct	gac	tac	gca	gca	gca	gtt	ggc	acc	gaa	ggc	tac	gtg	gtt	cca	ctg	739															
Ala	Asp	Tyr	Ala	Ala	Ala	Val	Gly	Thr	Glu	Gly	Tyr	Val	Val	Pro	Leu																
				200					205					210																	
gaa	ctg	ccc	acc	gtg	cag	tca	gag	cag	gca	gta	tta	acc	gaa	tcc	gcc	787															
Glu	Leu	Pro	Thr	Val	Gln	Ser	Glu	Gln	Ala	Val	Leu	Thr	Glu	Ser	Ala																
				215					220					225																	
tcg	cgt	gca	aag	ctt	tat	gaa	gcc	tcc	cag	aag	cgt	ggc	gcc	agc	ctg	835															
Ser	Arg	Ala	Lys	Leu	Tyr	Glu	Ala	Ser	Gln	Lys	Arg	Gly	Ala	Ser	Leu																
				230					235					240			245														

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Asn Lys Asp Val Leu Leu Glu Thr Val Arg Leu Arg Ala Glu Arg Ala	
250 255 260	
aca ctt tta ggc tac gac acc cac gcc gat tac gtc atc gaa gaa gaa	931
Thr Leu Leu Gly Tyr Asp Thr His Ala Asp Tyr Val Ile Glu Glu Glu	
265 270 275	
acc gcc gat gac gtc gca gcc gtg cgc gcc ttg ctt tat gat ctc gcc	979
Thr Ala Asp Asp Val Ala Ala Val Arg Ala Leu Leu Tyr Asp Leu Ala	
280 285 290	
cca gcc gcc tct gcc aat gcg aaa gcc gaa tac aaa ctc tcc gca gaa	1027
Pro Ala Ala Ser Ala Asn Ala Lys Ala Glu Tyr Lys Leu Ser Ala Glu	
295 300 305	
gaa gca gaa gaa cac ggc caa aaa gtc ggc gca gct gac tgg agc ttc	1075
Glu Ala Glu Glu His Gly Gln Lys Val Gly Ala Ala Asp Trp Ser Phe	
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tgg gaa gcc aaa gtc cgc gcc cgc gac tac gcc ctg gac gaa acc gaa	1123
Trp Glu Ala Lys Val Arg Ala Arg Asp Tyr Ala Leu Asp Glu Thr Glu	
330 335 340	
ctg cgc aac tac ttc cca ttg aac caa gta ctc cgt gac ggc gtc ttc	1171
Leu Arg Asn Tyr Phe Pro Leu Asn Gln Val Leu Arg Asp Gly Val Phe	
345 350 355	
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Phe Ala Ala Asn Arg Leu Tyr Gly Ile Thr Val Glu Pro Arg Pro Asp	
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ctg cgc ggt tac gcc gag ggc gtg gac gtc tgg gaa gtc ctc gat tct	1267
Leu Arg Gly Tyr Ala Glu Gly Val Asp Val Trp Glu Val Leu Asp Ser	
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gac ggc tcc ggc atc ggc ctg atc ctt acc gac tac tac ggc cga cca	1315
Asp Gly Ser Gly Ile Gly Leu Ile Leu Thr Asp Tyr Tyr Gly Arg Pro	
390 395 400 405	
tcc aag cgg ggc ggc gct tgg atg tcc agc ttt gtc gac caa tcc gag	1363
Ser Lys Arg Gly Gly Ala Trp Met Ser Ser Phe Val Asp Gln Ser Glu	
410 415 420	
ctg cta ggc acc aag cca gtc gtg gtc aac gtt atg ggt att acc aaa	1411
Leu Leu Gly Thr Lys Pro Val Val Val Asn Val Met Gly Ile Thr Lys	
425 430 435	
cca acc acc ggc gaa gca cta ctc agc ctc gat gaa gta acc acc atc	1459
Pro Thr Thr Gly Glu Ala Leu Leu Ser Leu Asp Glu Val Thr Thr Ile	
440 445 450	
ttc cac gaa ttc ggc cac ggc ctg cac ggc ttg ctg tcc aag gtg cgc	1507
Phe His Glu Phe Gly His Gly Leu His Gly Leu Leu Ser Lys Val Arg	
455 460 465	
tac cca agc ttc tcc gga acc tcc gtg ccc cgc gac tac gta gaa ttc	1555
Tyr Pro Ser Phe Ser Gly Thr Ser Val Pro Arg Asp Tyr Val Glu Phe	
470 475 480 485	


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ccc tcc cag atc aac gaa aac tgg gca ttc gac cct gca gta gtc cgc 1603
Pro Ser Gln Ile Asn Glu Asn Trp Ala Phe Asp Pro Ala Val Val Arg
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aac tac gcc cgc cac gtg gac acc ggc gac atc att cca gac tcc ctg 1651
Asn Tyr Ala Arg His Val Asp Thr Gly Asp Ile Ile Pro Asp Ser Leu
          505                      510                      515

ctt gag gca gtg gaa gca tgt ggc att tca gac aga gtg gtg gaa cat 1699
Leu Glu Ala Val Glu Ala Cys Gly Ile Ser Asp Arg Val Val Glu His
          520                      525                      530

gtg agt act tgt ccc cat cta tta tgc acc tgc cct gtc tct ccc tgt 1747
Val Ser Thr Cys Pro His Leu Leu Ser Thr Cys Pro Val Ser Pro Cys
          535                      540                      545

cca cag cgg atg ccg cac tagtcaatga cattgaccaa tta 1788
Pro Gln Arg Met Pro His
550                      555

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<210> 186
<211> 555
<212> PRT
<213> Corynebacterium glutamicum

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Leu Ala Leu Ala Glu His Asp Ala Glu Ile Thr Ala Ile Ala Thr Asn
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Glu Asp Ala Pro Thr Trp Glu Asn Thr Ile Glu Ala Leu Glu Arg Ala
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Gly Leu Ser Leu Asn Arg Val Ala Ala Val Phe Phe Asn Leu Gln Gly
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Thr Asp Ser Ser Pro Glu Met Asp Glu Ile Ala Ala Thr Ile Ala Pro
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Lys Leu Ser Ala His Ser Asp Ala Ile Phe His Asn Ala Ala Leu Phe
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Ala Arg Ile Glu Ala Val Glu Ala Pro Ala Asp Glu Glu Ser Gln Arg
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Leu Leu Ser His Thr Lys Arg Ala Phe Arg Arg Arg Gly Ala Ala Leu
          130             135             140

Asn Ala Asp Gly Lys Ala Arg Leu Ser Thr Ile Asn Gln Arg Leu Ser
          145             150             155             160

Ala Leu Ser Glu Gln Phe Gly Arg Asn Leu Leu Gln Asp Thr Arg Asp
          165             170             175

Leu Ala Val Asn Phe Glu Glu Ser Glu Leu Ala Gly Phe Ser Glu Ala

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180					185					190					
Arg	Ile	Ser	Ala	Ala	Ala	Asp	Tyr	Ala	Ala	Ala	Val	Gly	Thr	Glu	Gly
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Leu	Thr	Glu	Ser	Ala	Ser	Arg	Ala	Lys	Leu	Tyr	Glu	Ala	Ser	Gln	Lys
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Arg	Gly	Ala	Ser	Leu	Asn	Lys	Asp	Val	Leu	Leu	Glu	Thr	Val	Arg	Leu
				245					250					255	
Arg	Ala	Glu	Arg	Ala	Thr	Leu	Leu	Gly	Tyr	Asp	Thr	His	Ala	Asp	Tyr
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Val	Ile	Glu	Glu	Glu	Thr	Ala	Asp	Asp	Val	Ala	Ala	Val	Arg	Ala	Leu
		275					280					285			
Leu	Tyr	Asp	Leu	Ala	Pro	Ala	Ala	Ser	Ala	Asn	Ala	Lys	Ala	Glu	Tyr
	290					295					300				
Lys	Leu	Ser	Ala	Glu	Glu	Ala	Glu	Glu	His	Gly	Gln	Lys	Val	Gly	Ala
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Ala	Asp	Trp	Ser	Phe	Trp	Glu	Ala	Lys	Val	Arg	Ala	Arg	Asp	Tyr	Ala
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Leu	Asp	Glu	Thr	Glu	Leu	Arg	Asn	Tyr	Phe	Pro	Leu	Asn	Gln	Val	Leu
			340					345					350		
Arg	Asp	Gly	Val	Phe	Phe	Ala	Ala	Asn	Arg	Leu	Tyr	Gly	Ile	Thr	Val
		355					360					365			
Glu	Pro	Arg	Pro	Asp	Leu	Arg	Gly	Tyr	Ala	Glu	Gly	Val	Asp	Val	Trp
	370					375					380				
Glu	Val	Leu	Asp	Ser	Asp	Gly	Ser	Gly	Ile	Gly	Leu	Ile	Leu	Thr	Asp
385					390					395					400
Tyr	Tyr	Gly	Arg	Pro	Ser	Lys	Arg	Gly	Gly	Ala	Trp	Met	Ser	Ser	Phe
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Val	Asp	Gln	Ser	Glu	Leu	Leu	Gly	Thr	Lys	Pro	Val	Val	Val	Asn	Val
			420					425					430		
Met	Gly	Ile	Thr	Lys	Pro	Thr	Thr	Gly	Glu	Ala	Leu	Leu	Ser	Leu	Asp
	435						440					445			
Glu	Val	Thr	Thr	Ile	Phe	His	Glu	Phe	Gly	His	Gly	Leu	His	Gly	Leu
	450					455					460				
Leu	Ser	Lys	Val	Arg	Tyr	Pro	Ser	Phe	Ser	Gly	Thr	Ser	Val	Pro	Arg
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Asp	Tyr	Val	Glu	Phe	Pro	Ser	Gln	Ile	Asn	Glu	Asn	Trp	Ala	Phe	Asp
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Pro	Ala	Val	Val	Arg	Asn	Tyr	Ala	Arg	His	Val	Asp	Thr	Gly	Asp	Ile
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acc	gtg	cag	tca	gag	cag	gca	gta	tta	acc	gaa	tcc	gcc	tcg	cgt	gca	96
Thr	Val	Gln	Ser	Glu	Gln	Ala	Val	Leu	Thr	Glu	Ser	Ala	Ser	Arg	Ala	
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aag	ctt	tat	gaa	gcc	tcc	cag	aag	cgt	ggc	gcc	agc	ctg	aac	aag	gac	144
Lys	Leu	Tyr	Glu	Ala	Ser	Gln	Lys	Arg	Gly	Ala	Ser	Leu	Asn	Lys	Asp	
35			40			45										
gtg	ctg	ctc	gaa	acc	gtg	cgt	ctg	cgt	gct	gaa	cgc	gcc	aca	ctt	tta	192
Val	Leu	Leu	Glu	Thr	Val	Arg	Leu	Arg	Ala	Glu	Arg	Ala	Thr	Leu	Leu	
50			55			60										
ggc	tac	gac	acc	cac	gcc	gat	tac	gtc	atc	gaa	gaa	gaa	acc	gcc	gat	240
Gly	Tyr	Asp	Thr	His	Ala	Asp	Tyr	Val	Ile	Glu	Glu	Glu	Thr	Ala	Asp	
65			70			75			80							
gac	gtc	gca	gcc	gtg	cgc	gcc	ttg	ctt	tat	gat	ctc	gcc	cca	gcc	gcc	288
Asp	Val	Ala	Ala	Val	Arg	Ala	Leu	Leu	Tyr	Asp	Leu	Ala	Pro	Ala	Ala	
85			90			95										
tct	gcc	aat	gcg	aaa	gcc	gaa	tac	aaa	ctc	tcc	gca	gaa	gaa	gca	gaa	336
Ser	Ala	Asn	Ala	Lys	Ala	Glu	Tyr	Lys	Leu	Ser	Ala	Glu	Glu	Ala	Glu	
100			105			110										
gaa	cac	ggc	caa	aaa	gtc	ggc	gca	gct	gac	tgg	agc	ttc	tgg	gaa	gcc	384
Glu	His	Gly	Gln	Lys	Val	Gly	Ala	Ala	Asp	Trp	Ser	Phe	Trp	Glu	Ala	
115			120			125										
aaa	gtc	cgc	gcc	cgc	gac	tac	gcc	ctg	gac	gaa	acc	gaa	ctg	cgc	aac	432
Lys	Val	Arg	Ala	Arg	Asp	Tyr	Ala	Leu	Asp	Glu	Thr	Glu	Leu	Arg	Asn	
130			135			140										
tac	ttc	cca	ttg	aac	caa	gta	ctc	cgt	gac	ggc	gtc	ttc	ttc	gct	gct	480
Tyr	Phe	Pro	Leu	Asn	Gln	Val	Leu	Arg	Asp	Gly	Val	Phe	Phe	Ala	Ala	
145			150			155			160							

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aac cgc ctc tac gga atc acc gtg gaa cca cgc cct gac ctg cgc ggt 528
Asn Arg Leu Tyr Gly Ile Thr Val Glu Pro Arg Pro Asp Leu Arg Gly
165 170 175

tac gcc gag ggc gtg gac gtc tgg gaa gtc ctc gat tct gac ggc tcc 576
Tyr Ala Glu Gly Val Asp Val Trp Glu Val Leu Asp Ser Asp Gly Ser
180 185 190

ggc atc ggc ctg atc ctt acc gac tac tac ggc cga cca tcc aag cgg 624
Gly Ile Gly Leu Ile Leu Thr Asp Tyr Tyr Gly Arg Pro Ser Lys Arg
195 200 205

ggc ggc gct tgg atg tcc agc ttt gtc gac caa tcc gag ctg cta ggc 672
Gly Gly Ala Trp Met Ser Ser Phe Val Asp Gln Ser Glu Leu Leu Gly
210 215 220

acc aag cca gtc gtg gtc aac gtt atg ggt att acc aaa cca acc acc 720
Thr Lys Pro Val Val Val Asn Val Met Gly Ile Thr Lys Pro Thr Thr
225 230 235

ggc gaa gca cta ctc agc ctc gat gaa gta acc acc atc ttc cac gaa 768
Gly Glu Ala Leu Leu Ser Leu Asp Glu Val Thr Thr Ile Phe His Glu
245 250 255

ttc ggc cac ggc ctg cac ggc ttg ctg tcc aag gtg cgc tac cca agc 816
Phe Gly His Gly Leu His Gly Leu Leu Ser Lys Val Arg Tyr Pro Ser
260 265 270

ttc tcc gga acc tcc gtg ccc cgc gac tac gta gaa ttc ccc tcc cag 864
Phe Ser Gly Thr Ser Val Pro Arg Asp Tyr Val Glu Phe Pro Ser Gln
275 280 285

atc aac gaa aac tgg gca ttc gac cct gca gta gtc cgc aac tac gcc 912
Ile Asn Glu Asn Trp Ala Phe Asp Pro Ala Val Val Arg Asn Tyr Ala
290 295 300

cgc cac gtg gac acc ggc gac atc att cca gac tcc ctg ctt gag gca 960
Arg His Val Asp Thr Gly Asp Ile Ile Pro Asp Ser Leu Leu Glu Ala
305 310 315

gtg gaa gca tgt ggc att tca gac aga gtg gtg gaa cat gtg agt act 1008
Val Glu Ala Cys Gly Ile Ser Asp Arg Val Val Glu His Val Ser Thr
325 330 335

tgt ccc cat cta tta tcg acc tgc cct gtc tct ccc tgt cca cag cgg 1056
Cys Pro His Leu Leu Ser Thr Cys Pro Val Ser Pro Cys Pro Gln Arg
340 345 350

atg ccg cac tagtcaatga cattgaccaa tta 1088
Met Pro His
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<210> 188

<211> 355

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

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Lys Leu Tyr Glu Ala Ser Gln Lys Arg Gly Ala Ser Leu Asn Lys Asp	35	40	45
Val Leu Leu Glu Thr Val Arg Leu Arg Ala Glu Arg Ala Thr Leu Leu	50	55	60
Gly Tyr Asp Thr His Ala Asp Tyr Val Ile Glu Glu Glu Thr Ala Asp	65	70	75
Asp Val Ala Ala Val Arg Ala Leu Leu Tyr Asp Leu Ala Pro Ala Ala	85	90	95
Ser Ala Asn Ala Lys Ala Glu Tyr Lys Leu Ser Ala Glu Glu Ala Glu	100	105	110
Glu His Gly Gln Lys Val Gly Ala Ala Asp Trp Ser Phe Trp Glu Ala	115	120	125
Lys Val Arg Ala Arg Asp Tyr Ala Leu Asp Glu Thr Glu Leu Arg Asn	130	135	140
Tyr Phe Pro Leu Asn Gln Val Leu Arg Asp Gly Val Phe Phe Ala Ala	145	150	155
Asn Arg Leu Tyr Gly Ile Thr Val Glu Pro Arg Pro Asp Leu Arg Gly	165	170	175
Tyr Ala Glu Gly Val Asp Val Trp Glu Val Leu Asp Ser Asp Gly Ser	180	185	190
Gly Ile Gly Leu Ile Leu Thr Asp Tyr Tyr Gly Arg Pro Ser Lys Arg	195	200	205
Gly Gly Ala Trp Met Ser Ser Phe Val Asp Gln Ser Glu Leu Leu Gly	210	215	220
Thr Lys Pro Val Val Val Asn Val Met Gly Ile Thr Lys Pro Thr Thr	225	230	235
Gly Glu Ala Leu Leu Ser Leu Asp Glu Val Thr Thr Ile Phe His Glu	245	250	255
Phe Gly His Gly Leu His Gly Leu Leu Ser Lys Val Arg Tyr Pro Ser	260	265	270
Phe Ser Gly Thr Ser Val Pro Arg Asp Tyr Val Glu Phe Pro Ser Gln	275	280	285
Ile Asn Glu Asn Trp Ala Phe Asp Pro Ala Val Val Arg Asn Tyr Ala	290	295	300
Arg His Val Asp Thr Gly Asp Ile Ile Pro Asp Ser Leu Leu Glu Ala	305	310	315
Val Glu Ala Cys Gly Ile Ser Asp Arg Val Val Glu His Val Ser Thr	325	330	335

Cys Pro His Leu Leu Ser Thr Cys Pro Val Ser Pro Cys Pro Gln Arg
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Met Pro His
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<210> 189

<211> 663

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(640)

<223> RXN01226

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 Met Gly Asp Val Asn
 1 5

aac tct ccc ctt tta gtt gtt ggc ctg gga aat ccc ggc ccg aaa tac 163
 Asn Ser Pro Leu Leu Val Val Gly Leu Gly Asn Pro Gly Pro Lys Tyr
 10 15 20

gtt ggc acc cgc cac aat att ggc ttt gag gtt gca gaa gaa cta gtg 211
 Val Gly Thr Arg His Asn Ile Gly Phe Glu Val Ala Glu Glu Leu Val
 25 30 35

tcg cgc agc ttt gga tca ttt agt gtg cac aag cgc tcc aac acc gat 259
 Ser Arg Ser Phe Gly Ser Phe Ser Val His Lys Arg Ser Asn Thr Asp
 40 45 50

atc gcg cag ctt cct ggg cta att gtg gcc aag ccg cgc agc ttt atg 307
 Ile Ala Gln Leu Pro Gly Leu Ile Val Ala Lys Pro Arg Ser Phe Met
 55 60 65

aac ctg tcg gga act ccg att cgg gcg ctg tgt gac ttc ttt aag att 355
 Asn Leu Ser Gly Thr Pro Ile Arg Ala Leu Cys Asp Phe Phe Lys Ile
 70 75 80 85

tcc cca gcc aat gtc atc gtg gtg cat gat gaa ttg gag ctt gat ttc 403
 Ser Pro Ala Asn Val Ile Val Val His Asp Glu Leu Glu Leu Asp Phe
 90 95 100

ggc tca gtg aag cta cgt cag ggt ggc ggg gat cat ggg cac aat ggt 451
 Gly Ser Val Lys Leu Arg Gln Gly Gly Gly Asp His Gly His Asn Gly
 105 110 115

ctg aaa tcc acg tcc aaa tct ttg gga act aag gac tat tgg aag ctc 499
 Leu Lys Ser Thr Ser Lys Ser Leu Gly Thr Lys Asp Tyr Trp Lys Leu
 120 125 130

agc atg ggt atc ggt agg cca ccg ggt cgg atg gat ccg gca agt ttt 547
 Ser Met Gly Ile Gly Arg Pro Pro Gly Arg Met Asp Pro Ala Ser Phe
 135 140 145

gtg ttg aag cct ttt ggc aag caa gaa ctg gcg gat att ccc atc atg 595
 Val Leu Lys Pro Phe Gly Lys Gln Glu Leu Ala Asp Ile Pro Ile Met
 150 155 160 165

gcg gct gac gct gca gat ctc gtc gaa aag cat ttg cag cag ggc 640
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 170 175 180

tagctacttg cgccgcgcct ctt 663

<210> 190

<211> 180

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 190

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Ala Glu Glu Leu Val Ser Arg Ser Phe Gly Ser Phe Ser Val His Lys
 35 40 45

Arg Ser Asn Thr Asp Ile Ala Gln Leu Pro Gly Leu Ile Val Ala Lys
 50 55 60

Pro Arg Ser Phe Met Asn Leu Ser Gly Thr Pro Ile Arg Ala Leu Cys
 65 70 75 80

Asp Phe Phe Lys Ile Ser Pro Ala Asn Val Ile Val Val His Asp Glu
 85 90 95

Leu Glu Leu Asp Phe Gly Ser Val Lys Leu Arg Gln Gly Gly Gly Asp
 100 105 110

His Gly His Asn Gly Leu Lys Ser Thr Ser Lys Ser Leu Gly Thr Lys
 115 120 125

Asp Tyr Trp Lys Leu Ser Met Gly Ile Gly Arg Pro Pro Gly Arg Met
 130 135 140

Asp Pro Ala Ser Phe Val Leu Lys Pro Phe Gly Lys Gln Glu Leu Ala
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Asp Ile Pro Ile Met Ala Ala Asp Ala Ala Asp Leu Val Glu Lys His
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Leu Gln Gln Gly
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<220>

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<222> (101)..(784)

<223> RXN01963

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                                   Met Lys Asn Arg Lys
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aaa atc atg tct acc ctc acc act gtc tgc gcc gta ctg ggt ata gtt 163
Lys Ile Met Ser Thr Leu Thr Thr Val Cys Ala Val Leu Gly Ile Val
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Ala Ala His Pro Phe His Ala Ser Ala Val Ile Gly Gly Ser Val Pro
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tca act gat tcc gtt gcc aac gct gtc gca aaa atc gga cca ggc gca 259
Ser Thr Asp Ser Val Ala Asn Ala Val Ala Lys Ile Gly Pro Gly Ala
                                   40 45 50

ttg aac tgc agc ggt gtc atg atc tca cca tcg tgg gca ctc acc gca 307
Leu Asn Cys Ser Gly Val Met Ile Ser Pro Ser Trp Ala Leu Thr Ala
                                   55 60 65

cgc cac tgt gtc gat gac atc aac ata ctc ggc gac atc gac acc atc 355
Arg His Cys Val Asp Asp Ile Asn Ile Leu Gly Asp Ile Asp Thr Ile
                                   70 75 80 85

acg cct att act cca ggt att cat cgc aat gaa ggt aac tat atg ggt 403
Thr Pro Ile Thr Pro Gly Ile His Arg Asn Glu Gly Asn Tyr Met Gly
                                   90 95 100

gag gtt tac cgc gca ccg tcc ggt gat cta gcg ctc att aat atc aac 451
Glu Val Tyr Arg Ala Pro Ser Gly Asp Leu Ala Leu Ile Asn Ile Asn
                                   105 110 115

ggc gtg cac aag ggc acc att gcg cag ctc ccc aca caa gaa tat cca 499
Gly Val His Lys Gly Thr Ile Ala Gln Leu Pro Thr Gln Glu Tyr Pro
                                   120 125 130

ctg gga acc gct gca cag tca gtc ggt ttt ggt ggc ggt ggt gtc aat 547
Leu Gly Thr Ala Ala Gln Ser Val Gly Phe Gly Gly Gly Gly Val Asn
                                   135 140 145

atc cgc acc gct gaa tcg gtc aac atg att ctc acc gac ata tat agc 595
Ile Arg Thr Ala Glu Ser Val Asn Met Ile Leu Thr Asp Ile Tyr Ser
                                   150 155 160 165

gtg agg tca ggg aaa ttc cat cac ggt gtc ggt cga tca cac tat ctc 643
Val Arg Ser Gly Lys Phe His His Gly Val Gly Arg Ser His Tyr Leu
                                   170 175 180

ctc ttt gat tat gac agt gct gaa act ggt cga atc cac aaa ggt gat 691
Leu Phe Asp Tyr Asp Ser Ala Glu Thr Gly Arg Ile His Lys Gly Asp
                                   185 190 195

tct ggg ggc ccc atc ttc att ggt gac gag gtt gtg ggc att atg tct 739
Ser Gly Gly Pro Ile Phe Ile Gly Asp Glu Val Val Gly Ile Met Ser
                                   200 205 210

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cac ggc aca ata aat aag aac gac ggg tct ttt gat gac gaa tcc 784
 His Gly Thr Ile Asn Lys Asn Asp Gly Ser Phe Asp Asp Glu Ser
 215 220 225

<210> 192
 <211> 228
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 192
 Met Lys Asn Arg Lys Lys Ile Met Ser Thr Leu Thr Thr Val Cys Ala
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 Val Leu Gly Ile Val Ala Ala His Pro Phe His Ala Ser Ala Val Ile
 20 25 30
 Gly Gly Ser Val Pro Ser Thr Asp Ser Val Ala Asn Ala Val Ala Lys
 35 40 45
 Ile Gly Pro Gly Ala Leu Asn Cys Ser Gly Val Met Ile Ser Pro Ser
 50 55 60
 Trp Ala Leu Thr Ala Arg His Cys Val Asp Asp Ile Asn Ile Leu Gly
 65 70 75 80
 Asp Ile Asp Thr Ile Thr Pro Ile Thr Pro Gly Ile His Arg Asn Glu
 85 90 95
 Gly Asn Tyr Met Gly Glu Val Tyr Arg Ala Pro Ser Gly Asp Leu Ala
 100 105 110
 Leu Ile Asn Ile Asn Gly Val His Lys Gly Thr Ile Ala Gln Leu Pro
 115 120 125
 Thr Gln Glu Tyr Pro Leu Gly Thr Ala Ala Gln Ser Val Gly Phe Gly
 130 135 140
 Gly Gly Gly Val Asn Ile Arg Thr Ala Glu Ser Val Asn Met Ile Leu
 145 150 155 160
 Thr Asp Ile Tyr Ser Val Arg Ser Gly Lys Phe His His Gly Val Gly
 165 170 175
 Arg Ser His Tyr Leu Leu Phe Asp Tyr Asp Ser Ala Glu Thr Gly Arg
 180 185 190
 Ile His Lys Gly Asp Ser Gly Gly Pro Ile Phe Ile Gly Asp Glu Val
 195 200 205
 Val Gly Ile Met Ser His Gly Thr Ile Asn Lys Asn Asp Gly Ser Phe
 210 215 220
 Asp Asp Glu Ser
 225

<210> 193
 <211> 906
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(883)

<223> RXN00621

<400> 193

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acgagcgtgc	agaagatgtg	cgtgactaag	atcggggggct	atg	tct	gaa	cg	cta	115
				Met	Ser	Glu	Arg	Leu	
				1				5	

aac	gct	ccg	caa	gca	cca	atc	cat	ccc	atc	acc	cga	acc	cac	cac	ggt	163
Asn	Ala	Pro	Gln	Ala	Pro	Ile	His	Pro	Ile	Thr	Arg	Thr	His	His	Gly	
			10						15					20		

att	gat	ttc	gta	gac	aac	tat	gaa	tgg	ctg	agg	gat	aaa	gaa	tcc	caa	211
Ile	Asp	Phe	Val	Asp	Asn	Tyr	Glu	Trp	Leu	Arg	Asp	Lys	Glu	Ser	Gln	
			25					30					35			

gaa	acc	ttg	gac	tac	ctg	gag	gcg	gag	aat	gcg	ttc	acc	aag	cag	gag	259
Glu	Thr	Leu	Asp	Tyr	Leu	Glu	Ala	Glu	Asn	Ala	Phe	Thr	Lys	Gln	Glu	
		40					45					50				

act	gaa	cag	cta	gcc	aca	ctg	cgg	gac	aac	atc	tat	gaa	gag	att	aag	307
Thr	Glu	Gln	Leu	Ala	Thr	Leu	Arg	Asp	Asn	Ile	Tyr	Glu	Glu	Ile	Lys	
	55					60					65					

tca	cg	gtt	aaa	gaa	acc	gac	atg	tcc	atc	cca	gtg	cgt	gcc	gga	aag	355
Ser	Arg	Val	Lys	Glu	Thr	Asp	Met	Ser	Ile	Pro	Val	Arg	Ala	Gly	Lys	
	70				75					80					85	

cac	tgg	tat	tac	tct	cg	act	gaa	gaa	ggc	aag	agc	tac	ggc	tat	tcc	403
His	Trp	Tyr	Tyr	Ser	Arg	Thr	Glu	Glu	Gly	Lys	Ser	Tyr	Gly	Tyr	Ser	
				90					95					100		

tgc	cg	att	cca	gtg	act	gaa	ggg	tgc	gat	gca	tgg	acc	cct	cct	gtt	451
Cys	Arg	Ile	Pro	Val	Thr	Glu	Gly	Ser	Asp	Ala	Trp	Thr	Pro	Pro	Val	
			105					110					115			

atc	cct	gag	ggt	gag	cca	gcg	cag	ggt	gaa	acc	atc	atc	atg	gat	gcc	499
Ile	Pro	Glu	Gly	Glu	Pro	Ala	Gln	Gly	Glu	Thr	Ile	Ile	Met	Asp	Ala	
		120					125					130				

aac	gag	ttg	gca	gaa	ggc	cac	gaa	ttc	ttc	tcc	atg	ggt	gca	tca	tct	547
Asn	Glu	Leu	Ala	Glu	Gly	His	Glu	Phe	Phe	Ser	Met	Gly	Ala	Ser	Ser	
	135					140					145					

gtc	acc	acc	tct	ggc	cg	tac	ctt	gcg	tat	tcc	acc	gat	gtc	acg	ggc	595
Val	Thr	Thr	Ser	Gly	Arg	Tyr	Leu	Ala	Tyr	Ser	Thr	Asp	Val	Thr	Gly	
	150				155					160					165	

gaa	gag	cg	ttt	acg	ttg	cg	atc	aag	gat	cta	gaa	act	ggc	gag	ctg	643
Glu	Glu	Arg	Phe	Thr	Leu	Arg	Ile	Lys	Asp	Leu	Glu	Thr	Gly	Glu	Leu	
			170					175						180		

ctt	cct	gat	acc	ctg	act	ggc	att	ttc	tac	ggt	gct	act	tgg	gtg	ggg	691
Leu	Pro	Asp	Thr	Leu	Thr	Gly	Ile	Phe	Tyr	Gly	Ala	Thr	Trp	Val	Gly	
			185					190						195		

gag gag tac ctc ttt tac cag cgc gtt gat gat gcg tgg cgt cca gat 739
 Glu Glu Tyr Leu Phe Tyr Gln Arg Val Asp Asp Ala Trp Arg Pro Asp
 200 205 210
 act gtg tgg cgc cac aag gtg ggt acc ccg gtt gaa gaa gac gtg ttg 787
 Thr Val Trp Arg His Lys Val Gly Thr Pro Val Glu Glu Asp Val Leu
 215 220 225
 gtg tac cac gag cct gat gaa cgt tat tcc acc tgg gtg ggc acc act 835
 Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr Trp Val Gly Thr Thr
 230 235 240 245
 cgt tca gaa aaa gtt cat cct ttt tgg ttg cgc ctc caa gat cac ctc 883
 Arg Ser Glu Lys Val His Pro Phe Trp Leu Arg Leu Gln Asp His Leu
 250 255 260
 tgaagtacgc gtgcttcctt tcg 906

<210> 194
 <211> 261
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 194
 Met Ser Glu Arg Leu Asn Ala Pro Gln Ala Pro Ile His Pro Ile Thr
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 Arg Thr His His Gly Ile Asp Phe Val Asp Asn Tyr Glu Trp Leu Arg
 20 25 30
 Asp Lys Glu Ser Gln Glu Thr Leu Asp Tyr Leu Glu Ala Glu Asn Ala
 35 40 45
 Phe Thr Lys Gln Glu Thr Glu Gln Leu Ala Thr Leu Arg Asp Asn Ile
 50 55 60
 Tyr Glu Glu Ile Lys Ser Arg Val Lys Glu Thr Asp Met Ser Ile Pro
 65 70 75 80
 Val Arg Ala Gly Lys His Trp Tyr Tyr Ser Arg Thr Glu Glu Gly Lys
 85 90 95
 Ser Tyr Gly Tyr Ser Cys Arg Ile Pro Val Thr Glu Gly Ser Asp Ala
 100 105 110
 Trp Thr Pro Pro Val Ile Pro Glu Gly Glu Pro Ala Gln Gly Glu Thr
 115 120 125
 Ile Ile Met Asp Ala Asn Glu Leu Ala Glu Gly His Glu Phe Phe Ser
 130 135 140
 Met Gly Ala Ser Ser Val Thr Thr Ser Gly Arg Tyr Leu Ala Tyr Ser
 145 150 155 160
 Thr Asp Val Thr Gly Glu Glu Arg Phe Thr Leu Arg Ile Lys Asp Leu
 165 170 175
 Glu Thr Gly Glu Leu Leu Pro Asp Thr Leu Thr Gly Ile Phe Tyr Gly
 180 185 190

Ala Thr Trp Val Gly Glu Glu Tyr Leu Phe Tyr Gln Arg Val Asp Asp
 195 200 205

Ala Trp Arg Pro Asp Thr Val Trp Arg His Lys Val Gly Thr Pro Val
 210 215 220

Glu Glu Asp Val Leu Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr
 225 230 235 240

Trp Val Gly Thr Thr Arg Ser Glu Lys Val His Pro Phe Trp Leu Arg
 245 250 255

Leu Gln Asp His Leu
 260

<210> 195
 <211> 906
 <212> DNA
 <213> Corynebacterium glutamicum.

<220>
 <221> CDS
 <222> (101)..(883)
 <223> FRXA00621

<400> 195
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acgagcgtgc agaagatgtg cgtgactaag atcggggggct atg tct gaa cgc cta 115
 Met Ser Glu Arg Leu
 1 5

aac gct ccg caa gca cca atc cat ccc atc acc cga acc cac cac ggt 163
 Asn Ala Pro Gln Ala Pro Ile His Pro Ile Thr Arg Thr His His Gly
 10 15 20

att gat ttc gta gac aac tat gaa tgg ctg agg gat aaa gaa tcc caa 211
 Ile Asp Phe Val Asp Asn Tyr Glu Trp Leu Arg Asp Lys Glu Ser Gln
 25 30 35

gaa acc ttg gac tac ctg gag gcg gag aat gcg ttc acc aag cag gag 259
 Glu Thr Leu Asp Tyr Leu Glu Ala Glu Asn Ala Phe Thr Lys Gln Glu
 40 45 50

act gaa cag cta gcc aca ctg cgg gac aac atc tat gaa gag att aag 307
 Thr Glu Gln Leu Ala Thr Leu Arg Asp Asn Ile Tyr Glu Glu Ile Lys
 55 60 65

tca cgc gtt aaa gaa acc gac atg tcc atc cca gtg cgt gcc gga aag 355
 Ser Arg Val Lys Glu Thr Asp Met Ser Ile Pro Val Arg Ala Gly Lys
 70 75 80 85

cac tgg tat tac tct cgc act gaa gaa ggc aag agc tac ggc tat tcc 403
 His Trp Tyr Tyr Ser Arg Thr Glu Glu Lys Ser Tyr Gly Tyr Ser
 90 95 100

tgc cgc att cca gtg act gaa ggg tgc gat gca tgg acc cct cct gtt 451
 Cys Arg Ile Pro Val Thr Glu Gly Ser Asp Ala Trp Thr Pro Pro Val
 105 110 115

atc cct gag ggt gag cca gcg cag ggt gaa acc atc atc atg gat gcc 499
 Ile Pro Glu Gly Glu Pro Ala Gln Gly Glu Thr Ile Ile Met Asp Ala
 120 125 130

aac gag ttg gca gaa ggc cac gaa ttc ttc tcc atg ggt gca tca tct 547
 Asn Glu Leu Ala Glu Gly His Glu Phe Phe Ser Met Gly Ala Ser Ser
 135 140 145

gtc acc acc tct ggc cgc tac ctt gcg tat tcc acc gat gtc acg ggc 595
 Val Thr Thr Ser Gly Arg Tyr Leu Ala Tyr Ser Thr Asp Val Thr Gly
 150 155 160 165

gaa gag cgc ttt acg ttg cgc atc aag gat cta gaa act ggc gag ctg 643
 Glu Glu Arg Phe Thr Leu Arg Ile Lys Asp Leu Glu Thr Gly Glu Leu
 170 175 180

ctt cct gat acc ctg act ggc att ttc tac ggt gct act tgg gtg ggg 691
 Leu Pro Asp Thr Leu Thr Gly Ile Phe Tyr Gly Ala Thr Trp Val Gly
 185 190 195

gag gag tac ctc ttt tac cag cgc gtt gat gat gcg tgg cgt cca gat 739
 Glu Glu Tyr Leu Phe Tyr Gln Arg Val Asp Asp Ala Trp Arg Pro Asp
 200 205 210

act gtg tgg cgc cac aag gtg ggt acc ccg gtt gaa gaa gac gtg ttg 787
 Thr Val Trp Arg His Lys Val Gly Thr Pro Val Glu Glu Asp Val Leu
 215 220 225

gtg tac cac gag cct gat gaa cgt tat tcc acc tgg gtg ggc acc act 835
 Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr Trp Val Gly Thr Thr
 230 235 240 245

cgt tca gaa aaa gtt cat cct ttt tgg ttg cgc ctc caa gat cac ctc 883
 Arg Ser Glu Lys Val His Pro Phe Trp Leu Arg Leu Gln Asp His Leu
 250 255 260

tgaagtacgc gtgcttcctt tcg 906

<210> 196

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 196

Met Ser Glu Arg Leu Asn Ala Pro Gln Ala Pro Ile His Pro Ile Thr
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Arg Thr His His Gly Ile Asp Phe Val Asp Asn Tyr Glu Trp Leu Arg
20 25 30

Asp Lys Glu Ser Gln Glu Thr Leu Asp Tyr Leu Glu Ala Glu Asn Ala
35 40 45

Phe Thr Lys Gln Glu Thr Glu Gln Leu Ala Thr Leu Arg Asp Asn Ile
50 55 60

Tyr Glu Glu Ile Lys Ser Arg Val Lys Glu Thr Asp Met Ser Ile Pro
65 70 75 80

Val	Arg	Ala	Gly	Lys	His	Trp	Tyr	Tyr	Ser	Arg	Thr	Glu	Glu	Gly	Lys	
				85					90					95		
Ser	Tyr	Gly	Tyr	Ser	Cys	Arg	Ile	Pro	Val	Thr	Glu	Gly	Ser	Asp	Ala	
				100					105					110		
Trp	Thr	Pro	Pro	Val	Ile	Pro	Glu	Gly	Glu	Pro	Ala	Gln	Gly	Glu	Thr	
				115					120					125		
Ile	Ile	Met	Asp	Ala	Asn	Glu	Leu	Ala	Glu	Gly	His	Glu	Phe	Phe	Ser	
				130					135					140		
Met	Gly	Ala	Ser	Ser	Val	Thr	Thr	Ser	Gly	Arg	Tyr	Leu	Ala	Tyr	Ser	
				145					150					155		
Thr	Asp	Val	Thr	Gly	Glu	Glu	Arg	Phe	Thr	Leu	Arg	Ile	Lys	Asp	Leu	
				165					170					175		
Glu	Thr	Gly	Glu	Leu	Leu	Pro	Asp	Thr	Leu	Thr	Gly	Ile	Phe	Tyr	Gly	
				180					185					190		
Ala	Thr	Trp	Val	Gly	Glu	Glu	Tyr	Leu	Phe	Tyr	Gln	Arg	Val	Asp	Asp	
				195					200					205		
Ala	Trp	Arg	Pro	Asp	Thr	Val	Trp	Arg	His	Lys	Val	Gly	Thr	Pro	Val	
				210					215					220		
Glu	Glu	Asp	Val	Leu	Val	Tyr	His	Glu	Pro	Asp	Glu	Arg	Tyr	Ser	Thr	
				225					230					235		
Trp	Val	Gly	Thr	Thr	Arg	Ser	Glu	Lys	Val	His	Pro	Phe	Trp	Leu	Arg	
				245					250					255		
Leu	Gln	Asp	His	Leu												
				260												

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<210> 197
<211> 1539
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1516)
<223> RXN00622
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accccggttg aagaagacgt gttggtgtac cactgacctg atg aac gtt att cca 115
                                         Met Asn Val Ile Pro
                                          1                               5
cct ggg tgg gca cca ctg gtt cag aaa aag ttc atc ctt ttt ggt tgc 163
Pro Gly Trp Ala Pro Leu Val Gln Lys Lys Phe Ile Leu Phe Gly Cys
                        10                                15                    20
gcc tcc aag atc acc tct gaa gta cgc gtg ctt cct ttc gac cag cca 211
Ala Ser Lys Ile Thr Ser Glu Val Arg Val Leu Pro Phe Asp Gln Pro
                25                          30                      35
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gag ggc acc cct gag gtg ctg att ccg cgc gcg gag ggt gtg gaa tac	259
Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala Glu Gly Val Glu Tyr	
40 45 50	
gac gtc gat cat gca gtc gta gac ggc tcc gat att tgg ttg gtc aca	307
Asp Val Asp His Ala Val Val Asp Gly Ser Asp Ile Trp Leu Val Thr	
55 60 65	
cac aac gcc gag ggc ccg aac ttt tcg gtg ggg tgg gct ggc gtc gac	355
His Asn Ala Glu Gly Pro Asn Phe Ser Val Gly Trp Ala Gly Val Asp	
70 75 80 85	
aag ctc aat tct ttg gac gcg ctg gcg cca ctc gtc gcg cac aag gat	403
Lys Leu Asn Ser Leu Asp Ala Leu Ala Pro Leu Val Ala His Lys Asp	
90 95 100	
gac gtg cgc att gag ggt gtc gat acc tac cgc gat ttc atc atc ctg	451
Asp Val Arg Ile Glu Gly Val Asp Thr Tyr Arg Asp Phe Ile Ile Leu	
105 110 115	
ggc tac agg tcc ggc gcg atc ggc cag gtc gcg atc atg aag ctt atc	499
Gly Tyr Arg Ser Gly Ala Ile Gly Gln Val Ala Ile Met Lys Leu Ile	
120 125 130	
gac gga acc ttc ggc gat ttc caa cag ctg gaa ttt gac gag gaa atc	547
Asp Gly Thr Phe Gly Asp Phe Gln Gln Leu Glu Phe Asp Glu Glu Ile	
135 140 145	
tac acc gtc gca tcg ggc gga aac cca gaa tgg gac gcc ccc gtc att	595
Tyr Thr Val Ala Ser Gly Gly Asn Pro Glu Trp Asp Ala Pro Val Ile	
150 155 160 165	
cgc ctt tct tac gga tca ttc acc acc ccg gcg cag ctg ttt aac tac	643
Arg Leu Ser Tyr Gly Ser Phe Thr Thr Pro Ala Gln Leu Phe Asn Tyr	
170 175 180	
tgg att gaa tcc ggc gaa cgc acg ctg ctg aag cag cag gaa gtg ctc	691
Trp Ile Glu Ser Gly Glu Arg Thr Leu Leu Lys Gln Gln Glu Val Leu	
185 190 195	
ggc gga tac aag ccg tca gac tat gtg gcc tcc cga ttg tgg gtc act	739
Gly Gly Tyr Lys Pro Ser Asp Tyr Val Ala Ser Arg Leu Trp Val Thr	
200 205 210	
gcg aaa gat ggc gcg cag att cca gtg tcc ttg gtg cac cgc acc gac	787
Ala Lys Asp Gly Ala Gln Ile Pro Val Ser Leu Val His Arg Thr Asp	
215 220 225	
ctg gat gta tcc aag ccc aac ccc acg ttg ctc tac ggc tat ggt tcc	835
Leu Asp Val Ser Lys Pro Asn Pro Thr Leu Leu Tyr Gly Tyr Gly Ser	
230 235 240 245	
tac gaa tca tcc att gat cca ggc ttc tct atc gcg cgt ttg tca ctg	883
Tyr Glu Ser Ser Ile Asp Pro Gly Phe Ser Ile Ala Arg Leu Ser Leu	
250 255 260	
atg gat cgt ggc atg att ttt gcg att gcc cac gtt cgt ggc ggt ggc	931
Met Asp Arg Gly Met Ile Phe Ala Ile Ala His Val Arg Gly Gly Gly	
265 270 275	

gaa atg ggt cgt ggc tgg tac gac aac ggc aaa acc acc acg aag aaa 979
 Glu Met Gly Arg Gly Trp Tyr Asp Asn Gly Lys Thr Thr Thr Lys Lys
 280 285 290

aac acc ttc acc gac ttc att gat gtt gcc gac gcc ctc atc gag cag 1027
 Asn Thr Phe Thr Asp Phe Ile Asp Val Ala Asp Ala Leu Ile Glu Gln
 295 300 305

aag att tct gcc cct gaa atg ctg gtt gca gaa ggc ggc tca gct ggt 1075
 Lys Ile Ser Ala Pro Glu Met Leu Val Ala Glu Gly Gly Ser Ala Gly
 310 315 320 325

ggc atg ctc atg ggc gcc att gcc aac atg gcc ggt gac cgc ttc aag 1123
 Gly Met Leu Met Gly Ala Ile Ala Asn Met Ala Gly Asp Arg Phe Lys
 330 335 340

gcg atc gaa gcc aac gtg cca ttc gtc gat ccg ctg acc tct atg ctc 1171
 Ala Ile Glu Ala Asn Val Pro Phe Val Asp Pro Leu Thr Ser Met Leu
 345 350 355

atg ccg gaa ctg cca ctg acg gtt atc gaa tgg gat gag tgg ggc gat 1219
 Met Pro Glu Leu Pro Leu Thr Val Ile Glu Trp Asp Glu Trp Gly Asp
 360 365 370

cca ctc cac gat aag gac gtc tat gaa tac atg gcg tcg tat gcc cca 1267
 Pro Leu His Asp Lys Asp Val Tyr Glu Tyr Met Ala Ser Tyr Ala Pro
 375 380 385

tat gaa aac atc gag gca aag aac tac ccc aat atc ttg gcc gta aca 1315
 Tyr Glu Asn Ile Glu Ala Lys Asn Tyr Pro Asn Ile Leu Ala Val Thr
 390 395 400 405

tcg ctc aac gac acc cga gtg ttg tac gtc gaa cca gcc aaa tgg gta 1363
 Ser Leu Asn Asp Thr Arg Val Leu Tyr Val Glu Pro Ala Lys Trp Val
 410 415 420

gcg cag ctt cgg gcg act gca acc ggt gga gaa ttc ctt ctg aaa act 1411
 Ala Gln Leu Arg Ala Thr Ala Thr Gly Gly Glu Phe Leu Leu Lys Thr
 425 430 435

gaa atg gtt gcc gga cac ggc ggt gtg tca gga cgc tac gaa aag tgg 1459
 Glu Met Val Ala Gly His Gly Gly Val Ser Gly Arg Tyr Glu Lys Trp
 440 445 450

cgt gag act gca ttt gag tac ggc tgg ttg atc aac caa gca acc ggt 1507
 Arg Glu Thr Ala Phe Glu Tyr Gly Trp Leu Ile Asn Gln Ala Thr Gly
 455 460 465

gtg acc gaa taaaacttgt tcgactagcg aac 1539
 Val Thr Glu
 470

<210> 198

<211> 472

<212> PRT

<213> Corynebacterium glutamicum

<400> 198

Met Asn Val Ile Pro Pro Gly Trp Ala Pro Leu Val Gln Lys Lys Phe
 1 5 10 15

Ile Leu Phe Gly Cys Ala Ser Lys Ile Thr Ser Glu Val Arg Val Leu
 20 25 30
 Pro Phe Asp Gln Pro Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala
 35 40 45
 Glu Gly Val Glu Tyr Asp Val Asp His Ala Val Val Asp Gly Ser Asp
 50 55 60
 Ile Trp Leu Val Thr His Asn Ala Glu Gly Pro Asn Phe Ser Val Gly
 65 70 75 80
 Trp Ala Gly Val Asp Lys Leu Asn Ser Leu Asp Ala Leu Ala Pro Leu
 85 90 95
 Val Ala His Lys Asp Asp Val Arg Ile Glu Gly Val Asp Thr Tyr Arg
 100 105 110
 Asp Phe Ile Ile Leu Gly Tyr Arg Ser Gly Ala Ile Gly Gln Val Ala
 115 120 125
 Ile Met Lys Leu Ile Asp Gly Thr Phe Gly Asp Phe Gln Gln Leu Glu
 130 135 140
 Phe Asp Glu Glu Ile Tyr Thr Val Ala Ser Gly Gly Asn Pro Glu Trp
 145 150 155 160
 Asp Ala Pro Val Ile Arg Leu Ser Tyr Gly Ser Phe Thr Thr Pro Ala
 165 170 175
 Gln Leu Phe Asn Tyr Trp Ile Glu Ser Gly Glu Arg Thr Leu Leu Lys
 180 185 190
 Gln Gln Glu Val Leu Gly Gly Tyr Lys Pro Ser Asp Tyr Val Ala Ser
 195 200 205
 Arg Leu Trp Val Thr Ala Lys Asp Gly Ala Gln Ile Pro Val Ser Leu
 210 215 220
 Val His Arg Thr Asp Leu Asp Val Ser Lys Pro Asn Pro Thr Leu Leu
 225 230 235 240
 Tyr Gly Tyr Gly Ser Tyr Glu Ser Ser Ile Asp Pro Gly Phe Ser Ile
 245 250 255
 Ala Arg Leu Ser Leu Met Asp Arg Gly Met Ile Phe Ala Ile Ala His
 260 265 270
 Val Arg Gly Gly Gly Glu Met Gly Arg Gly Trp Tyr Asp Asn Gly Lys
 275 280 285
 Thr Thr Thr Lys Lys Asn Thr Phe Thr Asp Phe Ile Asp Val Ala Asp
 290 295 300
 Ala Leu Ile Glu Gln Lys Ile Ser Ala Pro Glu Met Leu Val Ala Glu
 305 310 315 320
 Gly Gly Ser Ala Gly Gly Met Leu Met Gly Ala Ile Ala Asn Met Ala
 325 330 335

<400> 199																
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accccggttg aagaagacgt gttgggtgtac cacgagcctg						atg	aac	ggt	att	cca	115					
						Met	Asn	Val	Ile	Pro						
						1	.			5						
cct	ggg	tgg	gca	cca	ctc	gtt	cag	aaa	aag	ttc	atc	ctt	ttt	ggt	tgc	163
Pro	Gly	Trp	Ala	Pro	Leu	Val	Gln	Lys	Lys	Phe	Ile	Leu	Phe	Gly	Cys	
				10					15					20		
gcc	tcc	aag	atc	acc	tct	gaa	gta	cgc	gtg	ctt	cct	ttc	gac	cag	cca	211
Ala	Ser	Lys	Ile	Thr	Ser	Glu	Val	Arg	Val	Leu	Pro	Phe	Asp	Gln	Pro	
				25					30					35		
gag	ggc	acc	cct	gag	gtg	ctg	att	ccg	cgc	gcg	gag	ggg	gtg	gaa	tac	259
Glu	Gly	Thr	Pro	Glu	Val	Leu	Ile	Pro	Arg	Ala	Glu	Gly	Val	Glu	Tyr	
				40					45					50		
gac	gtc	gat	cat	gca	gtc	gta	gac	ggc	tcc	gat	att	tgg	ttg	gtc	aca	307
Asp	Val	Asp	His	Ala	Val	Val	Asp	Gly	Ser	Asp	Ile	Trp	Leu	Val	Thr	
				55					60					65		

cac aac gcc gag ggc ccg aac ttt tgc gtg ggg tgg gct ggc gtc gac	355
His Asn Ala Glu Gly Pro Asn Phe Ser Val Gly Trp Ala Gly Val Asp	
70 75 80 85	
aag ctc aat tct ttg gac gcg ctg gcg cca ctc gtc gcg cac aag gat	403
Lys Leu Asn Ser Leu Asp Ala Leu Ala Pro Leu Val Ala His Lys Asp	
90 95 100	
gac gtg cgc att gag ggt gtc gat acc tac cgc gat ttc atc atc ctg	451
Asp Val Arg Ile Glu Gly Val Asp Thr Tyr Arg Asp Phe Ile Ile Leu	
105 110 115	
ggc tac agg tcc ggc gcg atc ggc cag gtc gcg atc atg aag ctt atc	499
Gly Tyr Arg Ser Gly Ala Ile Gly Gln Val Ala Ile Met Lys Leu Ile	
120 125 130	
gac gga acc ttc ggc gat ttc caa cag ctg gaa ttt gac gag gaa atc	547
Asp Gly Thr Phe Gly Asp Phe Gln Gln Leu Glu Phe Asp Glu Glu Ile	
135 140 145	
tac acc gtc gca tgc ggc gga aac cca gaa tgg gac gcc ccc gtc att	595
Tyr Thr Val Ala Ser Gly Gly Asn Pro Glu Trp Asp Ala Pro Val Ile	
150 155 160 165	
cgc ctt tct tac gga tca ttc acc acc ccg gcg cag ctg ttt aac tac	643
Arg Leu Ser Tyr Gly Ser Phe Thr Thr Pro Ala Gln Leu Phe Asn Tyr	
170 175 180	
tgg att gaa tcc ggc gaa cgc acg ctg ctg aag cag cag gaa gtg ctc	691
Trp Ile Glu Ser Gly Glu Arg Thr Leu Leu Lys Gln Gln Glu Val Leu	
185 190 195	
ggc gga tac aag ccg tca gac tat gtg gcc tcc cga ttg tgg gtc act	739
Gly Gly Tyr Lys Pro Ser Asp Tyr Val Ala Ser Arg Leu Trp Val Thr	
200 205 210	
gcg aaa gat ggc gcg cag att cca gtg tcc ttg gtg cac cgc acc gac	787
Ala Lys Asp Gly Ala Gln Ile Pro Val Ser Leu Val His Arg Thr Asp	
215 220 225	
ctg gat gta tcc aag ccc aac ccc acg ttg ctc tac ggc tat ggt tcc	835
Leu Asp Val Ser Lys Pro Asn Pro Thr Leu Leu Tyr Gly Tyr Gly Ser	
230 235 240 245	
tac gaa tca tcc att gat cca ggc ttc tct atc gcg cgt ttg tca ctg	883
Tyr Glu Ser Ser Ile Asp Pro Gly Phe Ser Ile Ala Arg Leu Ser Leu	
250 255 260	
atg gat cgt ggc atg att ttt gcg att gcc cac gtt cgt ggc ggt ggc	931
Met Asp Arg Gly Met Ile Phe Ala Ile Ala His Val Arg Gly Gly Gly	
265 270 275	
gaa atg ggt cgt ggc tgg tac gac aac ggc aaa acc acc acg aag aaa	979
Glu Met Gly Arg Gly Trp Tyr Asp Asn Gly Lys Thr Thr Thr Lys Lys	
280 285 290	
aac acc ttc acc gac ttc att gat gtt gcc gac gcc ctc atc gag cag	1027
Asn Thr Phe Thr Asp Phe Ile Asp Val Ala Asp Ala Leu Ile Glu Gln	
295 300 305	
aag att tct gcc cct gaa atg ctg gtt gca gaa ggc ggc tca gct ggt	1075

Lys Ile Ser Ala Pro Glu Met Leu Val Ala Glu Gly Gly Ser Ala Gly
 310 315 320 325
 ggc atg ctc atg ggc gcc att gcc aac atg gcc ggt gac cgc ttc aag 1123
 Gly Met Leu Met Gly Ala Ile Ala Asn Met Ala Gly Asp Arg Phe Lys
 330 335 340
 gcg atc gaa gcc aac gtg cca ttc gtc gat ccg ctg acc tct atg ctc 1171
 Ala Ile Glu Ala Asn Val Pro Phe Val Asp Pro Leu Thr Ser Met Leu
 345 350 355
 atg ccg gaa ctg cca ctg acg gtt atc gaa tgg gat gag tgg ggc gat 1219
 Met Pro Glu Leu Pro Leu Thr Val Ile Glu Trp Asp Glu Trp Gly Asp
 360 365 370
 cca ctc cac gat aag gac gtc tat gaa tac atg gcg tcg tat gcc cca 1267
 Pro Leu His Asp Lys Asp Val Tyr Glu Tyr Met Ala Ser Tyr Ala Pro
 375 380 385
 tat gaa aac atc gag gca aag aac tac ccc aat atc ttg gcc gta aca 1315
 Tyr Glu Asn Ile Glu Ala Lys Asn Tyr Pro Asn Ile Leu Ala Val Thr
 390 395 400 405
 tcg ctc aac gac acc cga gtg ttg tac gtc gaa cca gcc aaa tgg gta 1363
 Ser Leu Asn Asp Thr Arg Val Leu Tyr Val Glu Pro Ala Lys Trp Val
 410 415 420
 gcg cag ctt cgg gcg act gca acc ggt gga gaa ttc ctt ctg aaa act 1411
 Ala Gln Leu Arg Ala Thr Ala Thr Gly Gly Glu Phe Leu Leu Lys Thr
 425 430 435
 gaa atg gtt gcc gga cac ggc ggt gtg tca gga cgc tac gaa aag tgg 1459
 Glu Met Val Ala Gly His Gly Gly Val Ser Gly Arg Tyr Glu Lys Trp
 440 445 450
 cgt gag act gca ttt gag tac ggc tgg ttg atc aac caa gca acc ggt 1507
 Arg Glu Thr Ala Phe Glu Tyr Gly Trp Leu Ile Asn Gln Ala Thr Gly
 455 460 465
 gtg acc gaa taaaacttgt tcgactagcg aac 1539
 Val Thr Glu
 470

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<211> 472

<212> PRT

<213> Corynebacterium glutamicum

<400> 200

Met Asn Val Ile Pro Pro Gly Trp Ala Pro Leu Val Gln Lys Lys Phe
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 Ile Leu Phe Gly Cys Ala Ser Lys Ile Thr Ser Glu Val Arg Val Leu
 20 25 30
 Pro Phe Asp Gln Pro Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala
 35 40 45
 Glu Gly Val Glu Tyr Asp Val Asp His Ala Val Val Asp Gly Ser Asp
 50 55 60

Ile	Trp	Leu	Val	Thr	His	Asn	Ala	Glu	Gly	Pro	Asn	Phe	Ser	Val	Gly	65	70	75	80
Trp	Ala	Gly	Val	Asp	Lys	Leu	Asn	Ser	Leu	Asp	Ala	Leu	Ala	Pro	Leu	85	90	95	
Val	Ala	His	Lys	Asp	Asp	Val	Arg	Ile	Glu	Gly	Val	Asp	Thr	Tyr	Arg	100	105	110	
Asp	Phe	Ile	Ile	Leu	Gly	Tyr	Arg	Ser	Gly	Ala	Ile	Gly	Gln	Val	Ala	115	120	125	
Ile	Met	Lys	Leu	Ile	Asp	Gly	Thr	Phe	Gly	Asp	Phe	Gln	Gln	Leu	Glu	130	135	140	
Phe	Asp	Glu	Glu	Ile	Tyr	Thr	Val	Ala	Ser	Gly	Gly	Asn	Pro	Glu	Trp	145	150	155	160
Asp	Ala	Pro	Val	Ile	Arg	Leu	Ser	Tyr	Gly	Ser	Phe	Thr	Thr	Pro	Ala	165	170	175	
Gln	Leu	Phe	Asn	Tyr	Trp	Ile	Glu	Ser	Gly	Glu	Arg	Thr	Leu	Leu	Lys	180	185	190	
Gln	Gln	Glu	Val	Leu	Gly	Gly	Tyr	Lys	Pro	Ser	Asp	Tyr	Val	Ala	Ser	195	200	205	
Arg	Leu	Trp	Val	Thr	Ala	Lys	Asp	Gly	Ala	Gln	Ile	Pro	Val	Ser	Leu	210	215	220	
Val	His	Arg	Thr	Asp	Leu	Asp	Val	Ser	Lys	Pro	Asn	Pro	Thr	Leu	Leu	225	230	235	240
Tyr	Gly	Tyr	Gly	Ser	Tyr	Glu	Ser	Ser	Ile	Asp	Pro	Gly	Phe	Ser	Ile	245	250	255	
Ala	Arg	Leu	Ser	Leu	Met	Asp	Arg	Gly	Met	Ile	Phe	Ala	Ile	Ala	His	260	265	270	
Val	Arg	Gly	Gly	Gly	Glu	Met	Gly	Arg	Gly	Trp	Tyr	Asp	Asn	Gly	Lys	275	280	285	
Thr	Thr	Thr	Lys	Lys	Asn	Thr	Phe	Thr	Asp	Phe	Ile	Asp	Val	Ala	Asp	290	295	300	
Ala	Leu	Ile	Glu	Gln	Lys	Ile	Ser	Ala	Pro	Glu	Met	Leu	Val	Ala	Glu	305	310	315	320
Gly	Gly	Ser	Ala	Gly	Gly	Met	Leu	Met	Gly	Ala	Ile	Ala	Asn	Met	Ala	325	330	335	
Gly	Asp	Arg	Phe	Lys	Ala	Ile	Glu	Ala	Asn	Val	Pro	Phe	Val	Asp	Pro	340	345	350	
Leu	Thr	Ser	Met	Leu	Met	Pro	Glu	Leu	Pro	Leu	Thr	Val	Ile	Glu	Trp	355	360	365	
Asp	Glu	Trp	Gly	Asp	Pro	Leu	His	Asp	Lys	Asp	Val	Tyr	Glu	Tyr	Met	370	375	380	

Ala Ser Tyr Ala Pro Tyr Glu Asn Ile Glu Ala Lys Asn Tyr Pro Asn
 385 390 395 400

Ile Leu Ala Val Thr Ser Leu Asn Asp Thr Arg Val Leu Tyr Val Glu
 405 410 415

Pro Ala Lys Trp Val Ala Gln Leu Arg Ala Thr Ala Thr Gly Gly Glu
 420 425 430

Phe Leu Leu Lys Thr Glu Met Val Ala Gly His Gly Gly Val Ser Gly
 435 440 445

Arg Tyr Glu Lys Trp Arg Glu Thr Ala Phe Glu Tyr Gly Trp Leu Ile
 450 455 460

Asn Gln Ala Thr Gly Val Thr Glu
 465 470

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 <211> 750
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(727)
 <223> RXN02146

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taactcgggtc agcaaacagg aagaatttgg agtttcatca gtg ggt aag cac cgt 115
 Val Gly Lys His Arg
 1 5

cgc aac aat tca aac gca act cgc aag gct gta gca gca tct gca gtt 163
 Arg Asn Asn Ser Asn Ala Thr Arg Lys Ala Val Ala Ala Ser Ala Val
 10 15 20

gcg ctt gga gca acc gca gct atc gcc tcc cca gca cag gca gct gag 211
 Ala Leu Gly Ala Thr Ala Ala Ile Ala Ser Pro Ala Gln Ala Ala Glu
 25 30 35

gtt gtt gtt cct ggc acc gga atc agc gtt gac atc gct ggc atc gag 259
 Val Val Val Pro Gly Thr Gly Ile Ser Val Asp Ile Ala Gly Ile Glu
 40 45 50

acc act cca ggt ctt aac aac gtt cca gga atc gat cag tgg atc cct 307
 Thr Thr Pro Gly Leu Asn Asn Val Pro Gly Ile Asp Gln Trp Ile Pro
 55 60 65

tcc ctt agc agc cag gca gct cct act gct tac gca gcc gtc att gat 355
 Ser Leu Ser Ser Gln Ala Ala Pro Thr Ala Tyr Ala Ala Val Ile Asp
 70 75 80 85

gca cct gca gca cag gct gca cct gca gca agc acc ggt cag gca atc 403
 Ala Pro Ala Ala Gln Ala Ala Pro Ala Ala Ser Thr Gly Gln Ala Ile
 90 95 100

gtt gat gca gcg cgc acc aag att ggt tcc cca tac ggt tgg ggt gct 451

Val Asp Ala Ala Arg Thr Lys Ile Gly Ser Pro Tyr Gly Trp Gly Ala
 105 110 115

acc ggt cct aac gct ttc gac tgc tcc ggc ctt acc tca tgg gca tac 499
 Thr Gly Pro Asn Ala Phe Asp Cys Ser Gly Leu Thr Ser Trp Ala Tyr
 120 125 130

agc cag gtt ggc aag tcc atc cca cgt acc tcc cag gct cag gct gca 547
 Ser Gln Val Gly Lys Ser Ile Pro Arg Thr Ser Gln Ala Gln Ala Ala
 135 140 145

cag ggc acc cct gtt gct tac tct gac ctt cag gct ggc gac atc gtt 595
 Gln Gly Thr Pro Val Ala Tyr Ser Asp Leu Gln Ala Gly Asp Ile Val
 150 155 160 165

gcg ttc tac tcc ggc gct acc cac gtt ggt atc tac tcc ggc cac ggc 643
 Ala Phe Tyr Ser Gly Ala Thr His Val Gly Ile Tyr Ser Gly His Gly
 170 175 180

acc gtt atc cac gca ctg aac agc agc acc cct ctg tct gag cac tcc 691
 Thr Val Ile His Ala Leu Asn Ser Ser Thr Pro Leu Ser Glu His Ser
 185 190 195

ttg gat tac atg cca ttc cac tct gca gtt cgt ttc taatctgcat 737
 Leu Asp Tyr Met Pro Phe His Ser Ala Val Arg Phe
 200 205

aaagtcttaa gct 750

<210> 202

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

Val Gly Lys His Arg Arg Asn Asn Ser Asn Ala Thr Arg Lys Ala Val
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Ala Ala Ser Ala Val Ala Leu Gly Ala Thr Ala Ala Ile Ala Ser Pro
 20 25 30

Ala Gln Ala Ala Glu Val Val Val Pro Gly Thr Gly Ile Ser Val Asp
 35 40 45

Ile Ala Gly Ile Glu Thr Thr Pro Gly Leu Asn Asn Val Pro Gly Ile
 50 55 60

Asp Gln Trp Ile Pro Ser Leu Ser Ser Gln Ala Ala Pro Thr Ala Tyr
 65 70 75 80

Ala Ala Val Ile Asp Ala Pro Ala Ala Gln Ala Ala Pro Ala Ala Ser
 85 90 95

Thr Gly Gln Ala Ile Val Asp Ala Ala Arg Thr Lys Ile Gly Ser Pro
 100 105 110

Tyr Gly Trp Gly Ala Thr Gly Pro Asn Ala Phe Asp Cys Ser Gly Leu
 115 120 125

Thr Ser Trp Ala Tyr Ser Gln Val Gly Lys Ser Ile Pro Arg Thr Ser

130	135	140
Gln Ala Gln Ala Ala	Gln Gly Thr Pro Val	Ala Tyr Ser Asp Leu Gln
145	150	155 160
Ala Gly Asp Ile Val	Ala Phe Tyr Ser Gly	Ala Thr His Val Gly Ile
	165	170 175
Tyr Ser Gly His Gly	Thr Val Ile His Ala	Leu Asn Ser Ser Thr Pro
	180	185 190
Leu Ser Glu His Ser	Leu Asp Tyr Met Pro	Phe His Ser Ala Val Arg
	195	200 205

Phe

<210> 203
 <211> 807
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(784)
 <223> RXN03133

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 Val Thr Cys Ala Thr
 1 5
 ccc ctt acg cca cca ctg ctg tgc cac ctc aat cca cgc cac gct ccg 163
 Pro Leu Thr Pro Pro Leu Leu Cys His Leu Asn Pro Arg His Ala Pro
 10 15 20
 ctc acc gat cca cac att gac gct tcc agg cgc cac cgc ggt ccc ttc 211
 Leu Thr Asp Pro His Ile Asp Ala Ser Arg Arg His Arg Gly Pro Phe
 25 30 35
 cac gcc act ccc agc tac gca ggc ttt cac ccc tca ttt acc gac gac 259
 His Ala Thr Pro Ser Tyr Ala Gly Phe His Pro Ser Phe Thr Asp Asp
 40 45 50
 acc gcc cgc atg ctg ggc aac cta gcc aaa att ggc gcg gtt gcc acc 307
 Thr Ala Arg Met Leu Gly Asn Leu Ala Lys Ile Gly Ala Val Ala Thr
 55 60 65
 tgg gaa aag acg ctt gtc gac gcc gca agc tgg gcc gaa ctc ccc cac 355
 Trp Glu Lys Thr Leu Val Asp Ala Ala Ser Trp Ala Glu Leu Pro His
 70 75 80 85
 cca cca gtc atc gtc ggg gat acc ccg ccc tcg act gtc acg ccg gac 403
 Pro Pro Val Ile Val Gly Asp Thr Pro Pro Ser Thr Val Thr Pro Asp
 90 95 100
 aac gcc tgg tac cag ttt cgc gtc ggc aag cat ctt ggt cgc gat gcg 451
 Asn Ala Trp Tyr Gln Phe Arg Val Gly Lys His Leu Gly Arg Asp Ala

105	110	115	
ttc gcg gaa atc gtc atg tgc ctt ggc cac gtg ttt tgc cat cat gtc			499
Phe Ala Glu Ile Val Met Cys Leu Gly His Val Phe Cys His His Val			
120	125	130	
ccc cag gta tgg tcg aca acc tgc gca tct cag gac gct gat tcc acc			547
Pro Gln Val Trp Ser Thr Thr Cys Ala Ser Gln Asp Ala Asp Ser Thr			
135	140	145	
acg atg ctc att gaa gcc gag acc gcg ggg gca ttg gcc atc gct cgc			595
Thr Met Leu Ile Glu Ala Glu Thr Ala Gly Ala Leu Ala Ile Ala Arg			
150	155	160	165
gtc ggc ggc ccg acc cgt cga ggt ggt tcc ttc ttc ggc gat gcc ctt			643
Val Gly Gly Pro Thr Arg Arg Gly Gly Ser Phe Phe Gly Asp Ala Leu			
170	175	180	
ctc aaa gag ggg acg cca ctt cct gct ggt ttc cga cta gat gtt gtt			691
Leu Lys Glu Gly Thr Pro Leu Pro Ala Gly Phe Arg Leu Asp Val Val			
185	190	195	
cta cac gcc gcc tca gaa att gag gat ctg ctg cgc ggt gac acc aca			739
Leu His Ala Ala Ser Glu Ile Glu Asp Leu Leu Arg Gly Asp Thr Thr			
200	205	210	
gcc gtt gtc agc ggc gct tgg tct gtg gag gat cgc cga ggt tac			784
Ala Val Val Ser Gly Ala Trp Ser Val Glu Asp Arg Arg Gly Tyr			
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taacaaatag gcccaacaaa gag			807
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<400> 204			
Val Thr Cys Ala Thr Pro Leu Thr Pro Pro Leu Leu Cys His Leu Asn			
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Pro Arg His Ala Pro Leu Thr Asp Pro His Ile Asp Ala Ser Arg Arg			
20	25	30	
His Arg Gly Pro Phe His Ala Thr Pro Ser Tyr Ala Gly Phe His Pro			
35	40	45	
Ser Phe Thr Asp Asp Thr Ala Arg Met Leu Gly Asn Leu Ala Lys Ile			
50	55	60	
Gly Ala Val Ala Thr Trp Glu Lys Thr Leu Val Asp Ala Ala Ser Trp			
65	70	75	80
Ala Glu Leu Pro His Pro Pro Val Ile Val Gly Asp Thr Pro Pro Ser			
85	90	95	
Thr Val Thr Pro Asp Asn Ala Trp Tyr Gln Phe Arg Val Gly Lys His			
100	105	110	
Leu Gly Arg Asp Ala Phe Ala Glu Ile Val Met Cys Leu Gly His Val			

115	120	125
Phe Cys His His Val Pro Gln Val Trp Ser Thr Thr Cys Ala Ser Gln 130 135 140		
Asp Ala Asp Ser Thr Thr Met Leu Ile Glu Ala Glu Thr Ala Gly Ala 145 150 155 160		
Leu Ala Ile Ala Arg Val Gly Gly Pro Thr Arg Arg Gly Gly Ser Phe 165 170 175		
Phe Gly Asp Ala Leu Leu Lys Glu Gly Thr Pro Leu Pro Ala Gly Phe 180 185 190		
Arg Leu Asp Val Val Leu His Ala Ala Ser Glu Ile Glu Asp Leu Leu 195 200 205		
Arg Gly Asp Thr Thr Ala Val Val Ser Gly Ala Trp Ser Val Glu Asp 210 215 220		
Arg Arg Gly Tyr 225		

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1411)
 <223> RXN02820

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 aatatctccc cacataaaag ttccttgata ggctcgagag atg aaa gtg acc caa 115
 Met Lys Val Thr Gln
 1 5
 agc aca ttc ctt aaa tcg gta gct gcg ttc act gtc gca gcc tta acc 163
 Ser Thr Phe Leu Lys Ser Val Ala Ala Phe Thr Val Ala Ala Leu Thr
 10 15 20
 ctg acc atc tct tcg tgt tcc agc ggt gaa gac acc tcc gca agc tcc 211
 Leu Thr Ile Ser Ser Cys Ser Ser Gly Glu Asp Thr Ser Ala Ser Ser
 25 30 35
 acg gat act gaa aac tcc tca acc caa gca gca gcg tct ccc cca ctt 259
 Thr Asp Thr Glu Asn Ser Ser Thr Gln Ala Ala Ala Ser Pro Pro Leu
 40 45 50
 gcg cct tgt gaa ctt ccc gcc gac gct tct gct gaa gag gaa gta gaa 307
 Ala Pro Cys Glu Leu Pro Ala Asp Ala Ser Ala Glu Glu Glu Val Glu
 55 60 65
 ggc act cac aca ggt gaa gat att tct gtt gcc ccg gaa atc ggt acc 355
 Gly Thr His Thr Gly Glu Asp Ile Ser Val Ala Pro Glu Ile Gly Thr
 70 75 80 85

ggc tac cgc gag ggc atg acc cct gtt caa acc caa ggt tat gcg gtg	403
Gly Tyr Arg Glu Gly Met Thr Pro Val Gln Thr Gln Gly Tyr Ala Val	
90 95 100	
gca act gca aac ccc atc gct tct gaa gca gcc tgc gcg gtg tta aga	451
Ala Thr Ala Asn Pro Ile Ala Ser Glu Ala Ala Cys Ala Val Leu Arg	
105 110 115	
gaa ggc ggc act gca gct gat gct ctt gtc acc gcg cag ttt gtt ttg	499
Glu Gly Gly Thr Ala Ala Asp Ala Leu Val Thr Ala Gln Phe Val Leu	
120 125 130	
gga ctg acg gaa ccg cag tcg tct ggc ctt ggt ggt ggc gga tac att	547
Gly Leu Thr Glu Pro Gln Ser Ser Gly Leu Gly Gly Gly Tyr Ile	
135 140 145	
ctg tac tac gac gcc gaa gcc aat gcg gtg aca gcc att gat ggc cgt	595
Leu Tyr Tyr Asp Ala Glu Ala Asn Ala Val Thr Ala Ile Asp Gly Arg	
150 155 160 165	
gaa aca gcg cca gtt gct gct gat gaa aac tat ctc att cat gtt tct	643
Glu Thr Ala Pro Val Ala Ala Asp Glu Asn Tyr Leu Ile His Val Ser	
170 175 180	
gca gag gat caa acg gca cct gtt cct gat gcc cga cgt tcc ggc agg	691
Ala Glu Asp Gln Thr Ala Pro Val Pro Asp Ala Arg Arg Ser Gly Arg	
185 190 195	
tca att ggt gtg cca gga atc gtg gca gcc ctt gga cag ctg cat gat	739
Ser Ile Gly Val Pro Gly Ile Val Ala Ala Leu Gly Gln Leu His Asp	
200 205 210	
tca ttc gga aag acc tcc tgg cag gac gtg ctg aca act ccg cag cag	787
Ser Phe Gly Lys Thr Ser Trp Gln Asp Val Leu Thr Thr Pro Gln Gln	
215 220 225	
ctc gca act gat ggt ttt tcc atc agc cct cgc atg tca gca tca att	835
Leu Ala Thr Asp Gly Phe Ser Ile Ser Pro Arg Met Ser Ala Ser Ile	
230 235 240 245	
gct aac tcc gct gag gat ctc tcc cac gat ccg gaa gct gcc gca tat	883
Ala Asn Ser Ala Glu Asp Leu Ser His Asp Pro Glu Ala Ala Ala Tyr	
250 255 260	
ttc ctt gat gaa aac ggt gat gcg aag gca ccc ggc aca ctt tta caa	931
Phe Leu Asp Glu Asn Gly Asp Ala Lys Ala Pro Gly Thr Leu Leu Gln	
265 270 275	
aac cct gac tat gca gaa acg att cgt ctc atc tct gaa ggt ggc ccc	979
Asn Pro Asp Tyr Ala Glu Thr Ile Arg Leu Ile Ser Glu Gly Gly Pro	
280 285 290	
gat gcg ttc tac acg ggt gag att gca gca gac atc gtg gaa cgc gcc	1027
Asp Ala Phe Tyr Thr Gly Glu Ile Ala Ala Asp Ile Val Glu Arg Ala	
295 300 305	
acc cgt gag gtt gac ggt ttc aca cca tca ctg atg agc acg gca gat	1075
Thr Arg Glu Val Asp Gly Phe Thr Pro Ser Leu Met Ser Thr Ala Asp	
310 315 320 325	
ttg gct gcc tac act ccg gaa act cgt gaa gct ttg tgt gct ccc tac	1123

Leu Ala Ala Tyr Thr Pro Glu Thr Arg Glu Ala Leu Cys Ala Pro Tyr
 330 335 340
 cgc gac aag att gtt tgt ggc atg cca ccg tca tca tcg ggt ggc gtc 1171
 Arg Asp Lys Ile Val Cys Gly Met Pro Pro Ser Ser Ser Gly Gly Val
 345 350 355
 aca gtg atg gaa acc ctg ggt atc ttg aac aac ttt gat ctc gcc caa 1219
 Thr Val Met Glu Thr Leu Gly Ile Leu Asn Asn Phe Asp Leu Ala Gln
 360 365 370
 tac cca ccc act gag gtt ggt ttg gat ggc gga ttg cca aat gcg gaa 1267
 Tyr Pro Pro Thr Glu Val Gly Leu Asp Gly Gly Leu Pro Asn Ala Glu
 375 380 385
 gct gtt cac ctg att tca gag gct gag cgc ctg gct tat gct gat cgc 1315
 Ala Val His Leu Ile Ser Glu Ala Glu Arg Leu Ala Tyr Ala Asp Arg
 390 395 400 405
 gat gct tac atc ggt gat cct gct ttc gtg gaa gtt cca gca ggt ggt 1363
 Asp Ala Tyr Ile Gly Asp Pro Ala Phe Val Glu Val Pro Ala Gly Gly
 410 415 420
 gtc caa cag tgg atc aac cat gtc cac acg ggc gaa cac tcc aaa ctt 1411
 Val Gln Gln Trp Ile Asn His Val His Thr Gly Glu His Ser Lys Leu
 425 430 435

<210> 206

<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 206

Met Lys Val Thr Gln Ser Thr Phe Leu Lys Ser Val Ala Ala Phe Thr
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 Val Ala Ala Leu Thr Leu Thr Ile Ser Ser Cys Ser Ser Gly Glu Asp
 20 25 30
 Thr Ser Ala Ser Ser Thr Asp Thr Glu Asn Ser Ser Thr Gln Ala Ala
 35 40 45
 Ala Ser Pro Pro Leu Ala Pro Cys Glu Leu Pro Ala Asp Ala Ser Ala
 50 55 60
 Glu Glu Glu Val Glu Gly Thr His Thr Gly Glu Asp Ile Ser Val Ala
 65 70 75 80
 Pro Glu Ile Gly Thr Gly Tyr Arg Glu Gly Met Thr Pro Val Gln Thr
 85 90 95
 Gln Gly Tyr Ala Val Ala Thr Ala Asn Pro Ile Ala Ser Glu Ala Ala
 100 105 110
 Cys Ala Val Leu Arg Glu Gly Gly Thr Ala Ala Asp Ala Leu Val Thr
 115 120 125
 Ala Gln Phe Val Leu Gly Leu Thr Glu Pro Gln Ser Ser Gly Leu Gly
 130 135 140

Gly Gly Gly Tyr Ile Leu Tyr Tyr Asp Ala Glu Ala Asn Ala Val Thr
 145 150 155 160
 Ala Ile Asp Gly Arg Glu Thr Ala Pro Val Ala Ala Asp Glu Asn Tyr
 165 170 175
 Leu Ile His Val Ser Ala Glu Asp Gln Thr Ala Pro Val Pro Asp Ala
 180 185 190
 Arg Arg Ser Gly Arg Ser Ile Gly Val Pro Gly Ile Val Ala Ala Leu
 195 200 205
 Gly Gln Leu His Asp Ser Phe Gly Lys Thr Ser Trp Gln Asp Val Leu
 210 215 220
 Thr Thr Pro Gln Gln Leu Ala Thr Asp Gly Phe Ser Ile Ser Pro Arg
 225 230 235 240
 Met Ser Ala Ser Ile Ala Asn Ser Ala Glu Asp Leu Ser His Asp Pro
 245 250 255
 Glu Ala Ala Ala Tyr Phe Leu Asp Glu Asn Gly Asp Ala Lys Ala Pro
 260 265 270
 Gly Thr Leu Leu Gln Asn Pro Asp Tyr Ala Glu Thr Ile Arg Leu Ile
 275 280 285
 Ser Glu Gly Gly Pro Asp Ala Phe Tyr Thr Gly Glu Ile Ala Ala Asp
 290 295 300
 Ile Val Glu Arg Ala Thr Arg Glu Val Asp Gly Phe Thr Pro Ser Leu
 305 310 315 320
 Met Ser Thr Ala Asp Leu Ala Ala Tyr Thr Pro Glu Thr Arg Glu Ala
 325 330 335
 Leu Cys Ala Pro Tyr Arg Asp Lys Ile Val Cys Gly Met Pro Pro Ser
 340 345 350
 Ser Ser Gly Gly Val Thr Val Met Glu Thr Leu Gly Ile Leu Asn Asn
 355 360 365
 Phe Asp Leu Ala Gln Tyr Pro Pro Thr Glu Val Gly Leu Asp Gly Gly
 370 375 380
 Leu Pro Asn Ala Glu Ala Val His Leu Ile Ser Glu Ala Glu Arg Leu
 385 390 395 400
 Ala Tyr Ala Asp Arg Asp Ala Tyr Ile Gly Asp Pro Ala Phe Val Glu
 405 410 415
 Val Pro Ala Gly Gly Val Gln Gln Trp Ile Asn His Val His Thr Gly
 420 425 430
 Glu His Ser Lys Leu
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<211> 507

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (1)..(507)

<223> FRXA02820

<400> 207

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Ala Asn Ser Ala Glu Asp Leu Ser His Asp Pro Glu Ala Ala Ala Tyr
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ttc ctt gat gaa aac ggt gat gcg aag gca ccc ggc aca ctt tta caa 96
Phe Leu Asp Glu Asn Gly Asp Ala Lys Ala Pro Gly Thr Leu Leu Gln
             20             25             30

aac cct gac tat gca gaa acg att cgt ctc atc tct gaa ggt ggc ccc 144
Asn Pro Asp Tyr Ala Glu Thr Ile Arg Leu Ile Ser Glu Gly Gly Pro
             35             40             45

gat gcg ttc tac acg ggt gag att gca gca gac atc gtg gaa cgc gcc 192
Asp Ala Phe Tyr Thr Gly Glu Ile Ala Ala Asp Ile Val Glu Arg Ala
             50             55             60

acc cgt gag gtt gac ggt ttc aca cca tca ctg atg agc acg gca gat 240
Thr Arg Glu Val Asp Gly Phe Thr Pro Ser Leu Met Ser Thr Ala Asp
             65             70             75             80

ttg gct gcc tac act ccg gaa act cgt gaa gct ttg tgt gct ccc tac 288
Leu Ala Ala Tyr Thr Pro Glu Thr Arg Glu Ala Leu Cys Ala Pro Tyr
             85             90             95

cgc gac aag att gtt tgt ggc atg cca ccg tca tca tcg ggt ggc gtc 336
Arg Asp Lys Ile Val Cys Gly Met Pro Pro Ser Ser Ser Gly Gly Val
             100            105            110

aca gtg atg gaa acc ctg ggt atc ttg aac aac ttt gat ctc gcc caa 384
Thr Val Met Glu Thr Leu Gly Ile Leu Asn Asn Phe Asp Leu Ala Gln
             115            120            125

tac cca ccc act gag gtt ggt ttg gat ggc gga ttg cca aat gcg gaa 432
Tyr Pro Pro Thr Glu Val Gly Leu Asp Gly Gly Leu Pro Asn Ala Glu
             130            135            140

gct gtt cac ctg att tca gag gct gag cgc ctg gct tat gct gat cgc 480
Ala Val His Leu Ile Ser Glu Ala Glu Arg Leu Ala Tyr Ala Asp Arg
             145            150            155            160

gat gct tac atc ggt gat cct gct ttc 507
Asp Ala Tyr Ile Gly Asp Pro Ala Phe
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<210> 208

<211> 169

<212> PRT

<213> Corynebacterium glutamicum

<400> 208

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 Asn Pro Asp Tyr Ala Glu Thr Ile Arg Leu Ile Ser Glu Gly Gly Pro
 35 40 45
 Asp Ala Phe Tyr Thr Gly Glu Ile Ala Ala Asp Ile Val Glu Arg Ala
 50 55 60
 Thr Arg Glu Val Asp Gly Phe Thr Pro Ser Leu Met Ser Thr Ala Asp
 65 70 75 80
 Leu Ala Ala Tyr Thr Pro Glu Thr Arg Glu Ala Leu Cys Ala Pro Tyr
 85 90 95
 Arg Asp Lys Ile Val Cys Gly Met Pro Pro Ser Ser Ser Gly Gly Val
 100 105 110
 Thr Val Met Glu Thr Leu Gly Ile Leu Asn Asn Phe Asp Leu Ala Gln
 115 120 125
 Tyr Pro Pro Thr Glu Val Gly Leu Asp Gly Gly Leu Pro Asn Ala Glu
 130 135 140
 Ala Val His Leu Ile Ser Glu Ala Glu Arg Leu Ala Tyr Ala Asp Arg
 145 150 155 160
 Asp Ala Tyr Ile Gly Asp Pro Ala Phe
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<210> 209

<211> 604

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(604)

<223> FRXA02000

<400> 209

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aatatctccc cacataaaag ttccttgata ggctcgagag atg aaa gtg acc caa 115
 Met Lys Val Thr Gln
 1 5

agc aca ttc ctt aaa tcg gta gct gcg ttc act gtc gca gcc tta acc 163
 Ser Thr Phe Leu Lys Ser Val Ala Ala Phe Thr Val Ala Ala Leu Thr
 10 15 20

ctg acc atc tct tcg tgt tcc agc ggt gaa gac acc tcc gca agc tcc 211
 Leu Thr Ile Ser Ser Cys Ser Ser Gly Glu Asp Thr Ser Ala Ser Ser
 25 30 35

acg gat act gaa aac tcc tca acc caa gca gca gcg tct ccc cca ctt 259
 Thr Asp Thr Glu Asn Ser Ser Thr Gln Ala Ala Ala Ser Pro Pro Leu
 40 45 50

ggc cct tgt gaa ctt ccc gcc gac gct tct gct gaa gag gaa gta gaa 307
 Ala Pro Cys Glu Leu Pro Ala Asp Ala Ser Ala Glu Glu Glu Val Glu
 55 60 65

ggc act cac aca ggt gaa gat att tct gtt gcc ccg gaa atc ggt acc 355
 Gly Thr His Thr Gly Glu Asp Ile Ser Val Ala Pro Glu Ile Gly Thr
 70 75 80 85

ggc tac cgc gag ggc atg acc cct gtt caa acc caa ggt tat gcg gtg 403
 Gly Tyr Arg Glu Gly Met Thr Pro Val Gln Thr Gln Gly Tyr Ala Val
 90 95 100

gca act gca aac ccc atc gct tct gaa gca gcc tgc gcg gtg tta aga 451
 Ala Thr Ala Asn Pro Ile Ala Ser Glu Ala Ala Cys Ala Val Leu Arg
 105 110 115

gaa ggc ggc act gca gct gat gct ctt gtc acc gcg cag ttt gtt ttg 499
 Glu Gly Gly Thr Ala Ala Asp Ala Leu Val Thr Ala Gln Phe Val Leu
 120 125 130

gga ctg acg gaa ccg cag tcg tct ggc ctt ggt ggt ggc gga tac att 547
 Gly Leu Thr Glu Pro Gln Ser Ser Gly Leu Gly Gly Gly Tyr Ile
 135 140 145

ctg tac tac gac gcc gaa gcc aat gcg gtg aca gcc att gat ggc cgt 595
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gaa aca gcg 604
 Glu Thr Ala

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<212> PRT

<213> Corynebacterium glutamicum

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 20 25 30

Thr Ser Ala Ser Ser Thr Asp Thr Glu Asn Ser Ser Thr Gln Ala Ala
 35 40 45

Ala Ser Pro Pro Leu Ala Pro Cys Glu Leu Pro Ala Asp Ala Ser Ala
 50 55 60

Glu Glu Glu Val Glu Gly Thr His Thr Gly Glu Asp Ile Ser Val Ala
 65 70 75 80

Pro Glu Ile Gly Thr Gly Tyr Arg Glu Gly Met Thr Pro Val Gln Thr
 85 90 95

Gln Gly Tyr Ala Val Ala Thr Ala Asn Pro Ile Ala Ser Glu Ala Ala
 100 105 110

Cys Ala Val Leu Arg Glu Gly Gly Thr Ala Ala Asp Ala Leu Val Thr


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115              120              125
Ala Gln Phe Val Leu Gly Leu Thr Glu Pro Gln Ser Ser Gly Leu Gly
130              135              140

Gly Gly Gly Tyr Ile Leu Tyr Tyr Asp Ala Glu Ala Asn Ala Val Thr
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Ala Ile Asp Gly Arg Glu Thr Ala
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<212> DNA
<213> Corynebacterium glutamicum

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<222> (53)..(730)
<223> RXN02944

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Ala Gln Asn Leu Ile Asp Pro Glu His Ser Met Gly Gln Ala Thr Ala
5              10              15

ggt gtg agc cag aac cca gtc atg gct gcc ctg ccg gaa agt ggc acc 154
Gly Val Ser Gln Asn Pro Val Met Ala Ala Leu Pro Glu Ser Gly Thr
20              25              30

agc cat att tcc atc atc gat tcc tat ggc aac gca gca tcg ttg acc 202
Ser His Ile Ser Ile Ile Asp Ser Tyr Gly Asn Ala Ala Ser Leu Thr
35              40              45              50

acc agt gtg gaa gct gct ttc ggt tcc ttc cac ttc acc cgt ggt ttc 250
Thr Ser Val Glu Ala Ala Phe Gly Ser Phe His Phe Thr Arg Gly Phe
55              60              65

att ttg aat aat cag ctg aca gat ttc tcc gct gaa cca ctt gat gag 298
Ile Leu Asn Asn Gln Leu Thr Asp Phe Ser Ala Glu Pro Leu Asp Glu
70              75              80

gac ggc gag ccc gtg gcc aat cgt gtc gag tca gca aag cgc cca cgg 346
Asp Gly Glu Pro Val Ala Asn Arg Val Glu Ser Ala Lys Arg Pro Arg
85              90              95

tct tcc atg tcg cca atg cta gtg ttc aac gcc agt ggc gat ggt gaa 394
Ser Ser Met Ser Pro Met Leu Val Phe Asn Ala Ser Gly Asp Gly Glu
100             105             110

atc gcg gat ctg aat atg gtg ctg ggc tcc cct ggc gga tcc ttg att 442
Ile Ala Asp Leu Asn Met Val Leu Gly Ser Pro Gly Gly Ser Leu Ile
115             120             125             130

att cag tac gtg gtg aaa acc ctg gtc aac atc atc gac tgg gat atg 490
Ile Gln Tyr Val Val Lys Thr Leu Val Asn Ile Ile Asp Trp Asp Met

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135										140					145					
gat	cca	cag	cag	gca	gtg	tct	gcg	ccc	aac	ttt	ggt	gcg	atg	aac	cag	538				
Asp	Pro	Gln	Gln	Ala	Val	Ser	Ala	Pro	Asn	Phe	Gly	Ala	Met	Asn	Gln					
150										155					160					
cct	aag	act	gga	ctg	gga	agc	gag	cat	ccg	ctg	atc	gcc	aat	gat	tca	586				
Pro	Lys	Thr	Gly	Leu	Gly	Ser	Glu	His	Pro	Leu	Ile	Ala	Asn	Asp	Ser					
165										170					175					
gca	gag	ctt	gta	tct	gaa	ctg	gaa	agc	aaa	ggc	cac	gaa	gtt	aat	gtg	634				
Ala	Glu	Leu	Val	Ser	Glu	Leu	Glu	Ser	Lys	Gly	His	Glu	Val	Asn	Val					
180										185					190					
ggc	gag	caa	tcc	agt	ggc	cta	tcg	gcg	ttg	gtg	aaa	aac	ggc	gac	acc	682				
Gly	Glu	Gln	Ser	Ser	Gly	Leu	Ser	Ala	Leu	Val	Lys	Asn	Gly	Asp	Thr					
195										200					205					210
att	gtc	ggt	ggc	gcc	gat	cca	cgt	aga	gaa	ggc	gtg	gtc	ttg	ggt	ggc	730				
Ile	Val	Gly	Gly	Ala	Asp	Pro	Arg	Arg	Glu	Gly	Val	Val	Leu	Gly	Gly					
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<210> 212

<211> 226

<212> PRT

<213> Corynebacterium glutamicum

<400> 212

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Thr	Ala	Gly	Val	Ser	Gln	Asn	Pro	Val	Met	Ala	Ala	Leu	Pro	Glu	Ser
			20					25					30		
Gly	Thr	Ser	His	Ile	Ser	Ile	Ile	Asp	Ser	Tyr	Gly	Asn	Ala	Ala	Ser
		35					40					45			
Leu	Thr	Thr	Ser	Val	Glu	Ala	Ala	Phe	Gly	Ser	Phe	His	Phe	Thr	Arg
	50					55					60				
Gly	Phe	Ile	Leu	Asn	Asn	Gln	Leu	Thr	Asp	Phe	Ser	Ala	Glu	Pro	Leu
65					70				75					80	
Asp	Glu	Asp	Gly	Glu	Pro	Val	Ala	Asn	Arg	Val	Glu	Ser	Ala	Lys	Arg
				85					90					95	
Pro	Arg	Ser	Ser	Met	Ser	Pro	Met	Leu	Val	Phe	Asn	Ala	Ser	Gly	Asp
			100					105					110		
Gly	Glu	Ile	Ala	Asp	Leu	Asn	Met	Val	Leu	Gly	Ser	Pro	Gly	Gly	Ser
		115					120					125			
Leu	Ile	Ile	Gln	Tyr	Val	Val	Lys	Thr	Leu	Val	Asn	Ile	Ile	Asp	Trp
	130					135					140				
Asp	Met	Asp	Pro	Gln	Gln	Ala	Val	Ser	Ala	Pro	Asn	Phe	Gly	Ala	Met
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Gly Gly
225

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<223> RXS00197
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Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly Phe Leu Val Leu Tyr
      105                      110                      115
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ggc	gtg	gcg	gtg	agc	tcc	gga	atc	ccg	aat	ccg	gat	gtg	gat	acc	acc	499
Gly	Val	Ala	Val	Ser	Ser	Gly	Ile	Pro	Asn	Pro	Asp	Val	Asp	Thr	Thr	
		120					125					130				
gcg	aca	gtc	gac	acc	gtt	cag	tgc	gtg	ccg	gaa	acc	caa	att	tcc	gca	547
Ala	Thr	Val	Asp	Thr	Val	Gln	Cys	Val	Pro	Glu	Thr	Gln	Ile	Ser	Ala	
	135					140					145					
act	gaa	ctg	tcc	tcc	tgc	gta	ggc	tca	ggc	cca	gcg	ggc	gac	gcc	ggc	595
Thr	Glu	Leu	Ser	Ser	Cys	Val	Gly	Ser	Gly	Pro	Ala	Gly	Asp	Ala	Gly	
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att	gag	cac	ggc	gat	aag	att	ttg	gcc	gtc	aac	ggc	caa	gag	atg	gca	643
Ile	Glu	His	Gly	Asp	Lys	Ile	Leu	Ala	Val	Asn	Gly	Gln	Glu	Met	Ala	
			170						175					180		
agc	ttc	acc	gcc	atc	cgc	gat	gcg	atc	ctc	gag	ctc	cca	ggc	gaa	acg	691
Ser	Phe	Thr	Ala	Ile	Arg	Asp	Ala	Ile	Leu	Glu	Leu	Pro	Gly	Glu	Thr	
			185					190					195			
gca	acg	ctg	acg	att	gaa	cgg	gag	gga	acg	ctt	ttc	gac	gtc	gac	ctc	739
Ala	Thr	Leu	Thr	Ile	Glu	Arg	Glu	Gly	Thr	Leu	Phe	Asp	Val	Asp	Leu	
		200					205					210				
cag	gtt	gcc	tct	gtc	acc	cgt	ctc	gcc	tct	gac	ggc	tca	gaa	att	acc	787
Gln	Val	Ala	Ser	Val	Thr	Arg	Leu	Ala	Ser	Asp	Gly	Ser	Glu	Ile	Thr	
	215					220					225					
gtc	ggc	gcg	gtg	ggc	atg	tcg	agc	ctt	cca	ccg	acc	gat	gtg	tac	aaa	835
Val	Gly	Ala	Val	Gly	Met	Ser	Ser	Leu	Pro	Pro	Thr	Asp	Val	Tyr	Lys	
230					235					240					245	
aaa	tac	ggc	cca	atc	gag	ggc	gtg	gga	gca	act	gca	cgt	ttc	acc	ggc	883
Lys	Tyr	Gly	Pro	Ile	Glu	Gly	Val	Gly	Ala	Thr	Ala	Arg	Phe	Thr	Gly	
			250					255					260			
gac	atg	atc	agc	gcc	acg	tgg	gat	ggc	ctc	aaa	gcc	ttc	ccg	gcg	aaa	931
Asp	Met	Ile	Ser	Ala	Thr	Trp	Asp	Gly	Leu	Lys	Ala	Phe	Pro	Ala	Lys	
			265				270					275				
atc	cca	ggg	gtc	gtc	gca	tcc	atc	ttc	ggc	gca	gaa	cga	gat	gta	gaa	979
Ile	Pro	Gly	Val	Val	Ala	Ser	Ile	Phe	Gly	Ala	Glu	Arg	Asp	Val	Glu	
		280					285				290					
agc	ccc	atg	agt	gtg	gtg	ggc	gcc	gta	cgc	atc	ggc	ggc	gaa	ttt	gtc	1027
Ser	Pro	Met	Ser	Val	Val	Gly	Ala	Val	Arg	Ile	Gly	Gly	Glu	Phe	Val	
	295					300					305					
gaa	cgt	tcc	atg	tgg	gac	atg	ttc	atg	atg	atg	ctg	gcc	agc	ctg	aac	1075
Glu	Arg	Ser	Met	Trp	Asp	Met	Phe	Met	Met	Met	Leu	Ala	Ser	Leu	Asn	
310					315					320					325	
ttc	ttc	ctc	gcg	ctg	ttt	aac	ctc	gtg	ccg	ctg	cca	cca	ctt	gat	ggc	1123
Phe	Phe	Leu	Ala	Leu	Phe	Asn	Leu	Val	Pro	Leu	Pro	Pro	Leu	Asp	Gly	
			330						335					340		
gga	cac	att	gcc	gtg	gtg	atc	tat	gaa	aaa	atc	cgc	gac	ttc	ttc	cgc	1171
Gly	His	Ile	Ala	Val	Val	Ile	Tyr	Glu	Lys	Ile	Arg	Asp	Phe	Phe	Arg	
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<210> 214
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<212> PRT
<213> Corynebacterium glutamicum
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Phe	Gly	Met	Lys	Val	Arg	Arg	Phe	Phe	Ile	Gly	Phe	Gly	Pro	Thr	Val
		35					40					45			
Phe	Ala	Lys	Arg	Arg	Gly	Glu	Thr	Val	Tyr	Gly	Leu	Lys	Ala	Ile	Pro
	50					55					60				
Val	Gly	Gly	Phe	Cys	Asp	Ile	Ala	Gly	Met	Thr	Ala	Gln	Asp	Glu	Leu
65					70					75					80
Asp	Pro	Glu	Asp	Leu	Pro	Arg	Ala	Met	Tyr	Leu	Lys	Pro	Trp	Trp	Gln
				85					90					95	
Arg	Ile	Ile	Val	Leu	Ser	Gly	Gly	Val	Ile	Met	Asn	Leu	Ile	Val	Gly
			100					105					110		
Phe	Leu	Val	Leu	Tyr	Gly	Val	Ala	Val	Ser	Ser	Gly	Ile	Pro	Asn	Pro
		115					120					125			
Asp	Val	Asp	Thr	Thr	Ala	Thr	Val	Asp	Thr	Val	Gln	Cys	Val	Pro	Glu
	130					135					140				
Thr	Gln	Ile	Ser	Ala	Thr	Glu	Leu	Ser	Ser	Cys	Val	Gly	Ser	Gly	Pro
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Ala	Gly	Asp	Ala	Gly	Ile	Glu	His	Gly	Asp	Lys	Ile	Leu	Ala	Val	Asn
				165					170					175	
Gly	Gln	Glu	Met	Ala	Ser	Phe	Thr	Ala	Ile	Arg	Asp	Ala	Ile	Leu	Glu
			180					185					190		
Leu	Pro	Gly	Glu	Thr	Ala	Thr	Leu	Thr	Ile	Glu	Arg	Glu	Gly	Thr	Leu
		195					200					205			
Phe	Asp	Val	Asp	Leu	Gln	Val	Ala	Ser	Val	Thr	Arg	Leu	Ala	Ser	Asp
	210					215					220				

Gly Ser Glu Ile Thr Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro
 225 230 235 240
 Thr Asp Val Tyr Lys Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr
 245 250 255
 Ala Arg Phe Thr Gly Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys
 260 265 270
 Ala Phe Pro Ala Lys Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala
 275 280 285
 Glu Arg Asp Val Glu Ser Pro Met Ser Val Val Gly Ala Val Arg Ile
 290 295 300
 Gly Gly Glu Phe Val Glu Arg Ser Met Trp Asp Met Phe Met Met Met
 305 310 315 320
 Leu Ala Ser Leu Asn Phe Phe Leu Ala Leu Phe Asn Leu Val Pro Leu
 325 330 335
 Pro Pro Leu Asp Gly Gly His Ile Ala Val Val Ile Tyr Glu Lys Ile
 340 345 350
 Arg Asp Phe Phe Arg Lys Leu Arg Gly Lys Pro Ala Gly Gly Pro Ala
 355 360 365
 Asp Tyr Thr Lys Leu Met Pro Val Thr Val Ala Val Ala Ala Leu Leu
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 385 390 395 400
 Arg Leu Phe Gly

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 <213> Corynebacterium glutamicum

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 <223> RXS01223

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 Met Thr Ser Val Ser
 1 5
 ttt ttg tct aaa atc caa gca ctg ttt gcc ccc aag cct gaa ctt ccc 163
 Phe Leu Ser Lys Ile Gln Ala Leu Phe Ala Pro Lys Pro Glu Leu Pro
 10 15 20
 gcc gcc aaa tgg ctg gtc gtg ggc ctg ggc aac ccc ggc gcc aag tac 211
 Ala Ala Lys Trp Leu Val Val Gly Leu Gly Asn Pro Gly Ala Lys Tyr

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Glu	Ser	Thr	Arg	His	Asn	Val	Gly	Tyr	Met	Cys	Gln	Asp	Met	Leu	Ile					
40						45			50											
gac	gcc	cac	cag	cag	cag	ccc	ctc	acc	ccc	gcc	acg	ggc	tac	aag	gcc	307				
Asp	Ala	His	Gln	Gln	Gln	Pro	Leu	Thr	Pro	Ala	Thr	Gly	Tyr	Lys	Ala					
55			60			65														
ctc	aca	acg	cag	ctc	gca	cca	ggg	gtg	ctc	gcc	gtt	cga	tcc	acc	act	355				
Leu	Thr	Thr	Gln	Leu	Ala	Pro	Gly	Val	Leu	Ala	Val	Arg	Ser	Thr	Thr					
70				75		80								85						
ttt	atg	aac	cac	tcc	ggc	caa	ggg	gtc	gca	ccg	atc	gcc	gca	gcg	ttg	403				
Phe	Met	Asn	His	Ser	Gly	Gln	Gly	Val	Ala	Pro	Ile	Ala	Ala	Ala	Leu					
90				95				100												
ggg	atc	cca	gca	gag	cgc	atc	atc	gtg	atc	cac	gac	gag	ctc	gat	ctg	451				
Gly	Ile	Pro	Ala	Glu	Arg	Ile	Ile	Val	Ile	His	Asp	Glu	Leu	Asp	Leu					
105			110			115														
ccc	gct	gga	aaa	gta	cgc	ctg	aaa	aag	ggc	gga	aac	gaa	aac	ggg	cac	499				
Pro	Ala	Gly	Lys	Val	Arg	Leu	Lys	Lys	Gly	Gly	Asn	Glu	Asn	Gly	His					
120			125			130														
aac	ggc	ctg	aaa	tcc	ctc	acg	gaa	gag	ctc	ggc	acc	aga	gac	tac	ctg	547				
Asn	Gly	Leu	Lys	Ser	Leu	Thr	Glu	Glu	Leu	Gly	Thr	Arg	Asp	Tyr	Leu					
135			140			145														
cgc	gtc	cgc	atc	ggc	att	tca	cga	cca	cca	gca	gga	atg	gcc	gtg	ccc	595				
Arg	Val	Arg	Ile	Gly	Ile	Ser	Arg	Pro	Pro	Ala	Gly	Met	Ala	Val	Pro					
150				155		160								165						
gac	tac	gtt	ttg	gaa	cca	gtc	gat	cac	gac	caa	cca	ggc	att	gaa	ctt	643				
Asp	Tyr	Val	Leu	Glu	Pro	Val	Asp	His	Asp	Gln	Pro	Gly	Ile	Glu	Leu					
170				175				180												
gcc	gcc	gag	gca	gtg	gat	ttg	ctg	ctg	gcc	cag	gga	tta	tct	gct	gcg	691				
Ala	Ala	Glu	Ala	Val	Asp	Leu	Leu	Leu	Ala	Gln	Gly	Leu	Ser	Ala	Ala					
185			190			195														
caa	aac	gct	atc	cac	agc	cgc	tagattgcta	gagattcccg							cac	735				
Gln	Asn	Ala	Ile	His	Ser	Arg														
200																				

<210> 216

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

Met	Thr	Ser	Val	Ser	Phe	Leu	Ser	Lys	Ile	Gln	Ala	Leu	Phe	Ala	Pro
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Lys	Pro	Glu	Leu	Pro	Ala	Ala	Lys	Trp	Leu	Val	Val	Gly	Leu	Gly	Asn
			20					25					30		

Pro	Gly	Ala	Lys	Tyr	Glu	Ser	Thr	Arg	His	Asn	Val	Gly	Tyr	Met	Cys
		35					40					45			

Gln Asp Met Leu Ile Asp Ala His Gln Gln Gln Pro Leu Thr Pro Ala
 50 55 60
 Thr Gly Tyr Lys Ala Leu Thr Thr Gln Leu Ala Pro Gly Val Leu Ala
 65 70 75 80
 Val Arg Ser Thr Thr Phe Met Asn His Ser Gly Gln Gly Val Ala Pro
 85 90 95
 Ile Ala Ala Ala Leu Gly Ile Pro Ala Glu Arg Ile Ile Val Ile His
 100 105 110
 Asp Glu Leu Asp Leu Pro Ala Gly Lys Val Arg Leu Lys Lys Gly Gly
 115 120 125
 Asn Glu Asn Gly His Asn Gly Leu Lys Ser Leu Thr Glu Glu Leu Gly
 130 135 140
 Thr Arg Asp Tyr Leu Arg Val Arg Ile Gly Ile Ser Arg Pro Pro Ala
 145 150 155 160
 Gly Met Ala Val Pro Asp Tyr Val Leu Glu Pro Val Asp His Asp Gln
 165 170 175
 Pro Gly Ile Glu Leu Ala Ala Glu Ala Val Asp Leu Leu Leu Ala Gln
 180 185 190
 Gly Leu Ser Ala Ala Gln Asn Ala Ile His Ser Arg-
 195 200

<210> 217
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1342)
 <223> RXS01642

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 Met Arg Arg Leu Ile
 1 5
 gcg gtt agc ttg gcc gct ctg ttt atg ttg gct tcc act cca gcg acg 163
 Ala Val Ser Leu Ala Ala Leu Phe Met Leu Ala Ser Thr Pro Ala Thr
 10 15 20
 agg gca cag gaa gta gaa gct ctc gct tgc ccc gag gta gcg atc gcc 211
 Arg Ala Gln Glu Val Glu Ala Leu Ala Cys Pro Glu Val Ala Ile Ala
 25 30 35
 gat cct tcc tcc gca gtt tta gat gaa cac ctt tcg cag tca tta tcc 259
 Asp Pro Ser Ser Ala Val Leu Asp Glu His Leu Ser Gln Ser Leu Ser
 40 45 50

caa gct cac caa cta gca act ggc gcc ggt gtg atg gtg gca gtc atc	307
Gln Ala His Gln Leu Ala Thr Gly Ala Gly Val Met Val Ala Val Ile	
55 60 65	
gac acc gga gta tcc ctg cat cca cgt ctg ccc cac tta att ccc ggc	355
Asp Thr Gly Val Ser Leu His Pro Arg Leu Pro His Leu Ile Pro Gly	
70 75 80 85	
ggg gat ttc gtg ggc gcc cac caa agc ccc gat gtg cca ggt gaa ctt	403
Gly Asp Phe Val Gly Ala His Gln Ser Pro Asp Val Pro Gly Glu Leu	
90 95 100	
atc gat tgc gac ggc cac ggc acc atc gtc gcc gga atc atc gcc tcc	451
Ile Asp Cys Asp Gly His Gly Thr Ile Val Ala Gly Ile Ile Ala Ser	
105 110 115	
caa gga aac ccc ggc acc ggc tgg cca tat gac ggc agc tcc gat cct	499
Gln Gly Asn Pro Gly Thr Gly Trp Pro Tyr Asp Gly Ser Ser Asp Pro	
120 125 130	
tat atc ggt gtc gcc cca gat tcc gga atc atc tcc att aaa caa acc	547
Tyr Ile Gly Val Ala Pro Asp Ser Gly Ile Ile Ser Ile Lys Gln Thr	
135 140 145	
agc tca tat gtg cgt act cgt gaa gat tcc aac gtc gga acg ctg agc	595
Ser Ser Tyr Val Arg Thr Arg Glu Asp Ser Asn Val Gly Thr Leu Ser	
150 155 160 165	
acc ctg gcg gaa tcc atc cac cga gct ctc gat tcc ggt gcc cac gtg	643
Thr Leu Ala Glu Ser Ile His Arg Ala Leu Asp Ser Gly Ala His Val	
170 175 180	
atc aat att tcc gtg gtg tcc tgt ttg ccc caa tca ccc gac gag gcc	691
Ile Asn Ile Ser Val Val Ser Cys Leu Pro Gln Ser Pro Asp Glu Ala	
185 190 195	
gca tcg ttc cag cct ctg acg gat gct ctt aac aga gca gaa ctt caa	739
Ala Ser Phe Gln Pro Leu Thr Asp Ala Leu Asn Arg Ala Glu Leu Gln	
200 205 210	
ggg gtg ata gtg gtg gca gca gca gga aac ctc ggg cag gat tgt cca	787
Gly Val Ile Val Val Ala Ala Ala Gly Asn Leu Gly Gln Asp Cys Pro	
215 220 225	
gtt gga tct acc gtt tat cct gca cat tca gac act gtg ctc tct gtg	835
Val Gly Ser Thr Val Tyr Pro Ala His Ser Asp Thr Val Leu Ser Val	
230 235 240 245	
tcg gca cgt ttt gat tct cac acg ctt gca gaa tat tcc atg cct ggc	883
Ser Ala Arg Phe Asp Ser His Thr Leu Ala Glu Tyr Ser Met Pro Gly	
250 255 260	
aac caa caa atc ctc tct gca cca agc cac att cag gct ggt cta tca	931
Asn Gln Gln Ile Leu Ser Ala Pro Ser His Ile Gln Ala Gly Leu Ser	
265 270 275	
ccg cgt ggc gac ggc ttc gcc agc cac atg atc acc acc gct ggc gaa	979
Pro Arg Gly Asp Gly Phe Ala Ser His Met Ile Thr Thr Ala Gly Glu	
280 285 290	
agc ccc ttc gag ggc acc agt ttt gcc gct cca gtt gtc agc gcc aca	1027

Ser Pro Phe Glu Gly Thr Ser Phe Ala Ala Pro Val Val Ser Ala Thr
 295 300 305
 gct gca ctg ctt cgc cag cat ttt ccc ttt gcc aca ccc tat gaa att 1075
 Ala Ala Leu Leu Arg Gln His Phe Pro Phe Ala Thr Pro Tyr Glu Ile
 310 315 320 325
 cgt gca cga atc ttc aac agc atc gac cct gca aga ggc gct att gat 1123
 Arg Ala Arg Ile Phe Asn Ser Ile Asp Pro Ala Arg Gly Ala Ile Asp
 330 335 340
 ccc tac ctg gca ctt act caa gaa atc tat ccc acc act ccc ctg gtt 1171
 Pro Tyr Leu Ala Leu Thr Gln Glu Ile Tyr Pro Thr Thr Pro Leu Val
 345 350 355
 cat gag atc gca cta agt gtt ccc acg ccg ccg gat gat tct cca cgg 1219
 His Glu Ile Ala Leu Ser Val Pro Thr Pro Pro Asp Asp Ser Pro Arg
 360 365 370
 gag cgg ggc atc cta gtt acc gca atc att gtt ggg ttg ctc gca gtg 1267
 Glu Arg Gly Ile Leu Val Thr Ala Ile Ile Val Gly Leu Leu Ala Val
 375 380 385
 tta gct gtg ctg atg gga cta cgc cga att cat cat cac tcg gcc ttt 1315
 Leu Ala Val Leu Met Gly Leu Arg Arg Ile His His His Ser Ala Phe
 390 395 400 405
 caa aaa gct agc tca agt gtt atc act. taatctatga ggcaccgttc aga 1365
 Gln Lys Ala Ser Ser Ser Val Ile Thr
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 <213> *Corynebacterium glutamicum*
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 20 25 30
 Glu Val Ala Ile Ala Asp Pro Ser Ser Ala Val Leu Asp Glu His Leu
 35 40 45
 Ser Gln Ser Leu Ser Gln Ala His Gln Leu Ala Thr Gly Ala Gly Val
 50 55 60
 Met Val Ala Val Ile Asp Thr Gly Val Ser Leu His Pro Arg Leu Pro
 65 70 75 80
 His Leu Ile Pro Gly Gly Asp Phe Val Gly Ala His Gln Ser Pro Asp
 85 90 95
 Val Pro Gly Glu Leu Ile Asp Cys Asp Gly His Gly Thr Ile Val Ala
 100 105 110
 Gly Ile Ile Ala Ser Gln Gly Asn Pro Gly Thr Gly Trp Pro Tyr Asp
 115 120 125

Gly Ser Ser Asp Pro Tyr Ile Gly Val Ala Pro Asp Ser Gly Ile Ile
 130 135 140
 Ser Ile Lys Gln Thr Ser Ser Tyr Val Arg Thr Arg Glu Asp Ser Asn
 145 150 155 160
 Val Gly Thr Leu Ser Thr Leu Ala Glu Ser Ile His Arg Ala Leu Asp
 165 170 175
 Ser Gly Ala His Val Ile Asn Ile Ser Val Val Ser Cys Leu Pro Gln
 180 185 190
 Ser Pro Asp Glu Ala Ala Ser Phe Gln Pro Leu Thr Asp Ala Leu Asn
 195 200 205
 Arg Ala Glu Leu Gln Gly Val Ile Val Val Ala Ala Ala Gly Asn Leu
 210 215 220
 Gly Gln Asp Cys Pro Val Gly Ser Thr Val Tyr Pro Ala His Ser Asp
 225 230 235 240
 Thr Val Leu Ser Val Ser Ala Arg Phe Asp Ser His Thr Leu Ala Glu
 245 250 255
 Tyr Ser Met Pro Gly Asn Gln Gln Ile Leu Ser Ala Pro Ser His Ile
 260 265 270
 Gln Ala Gly Leu Ser Pro Arg Gly Asp Gly Phe Ala Ser His Met Ile
 275 280 285
 Thr Thr Ala Gly Glu Ser Pro Phe Glu Gly Thr Ser Phe Ala Ala Pro
 290 295 300
 Val Val Ser Ala Thr Ala Ala Leu Leu Arg Gln His Phe Pro Phe Ala
 305 310 315 320
 Thr Pro Tyr Glu Ile Arg Ala Arg Ile Phe Asn Ser Ile Asp Pro Ala
 325 330 335
 Arg Gly Ala Ile Asp Pro Tyr Leu Ala Leu Thr Gln Glu Ile Tyr Pro
 340 345 350
 Thr Thr Pro Leu Val His Glu Ile Ala Leu Ser Val Pro Thr Pro Pro
 355 360 365
 Asp Asp Ser Pro Arg Glu Arg Gly Ile Leu Val Thr Ala Ile Ile Val
 370 375 380
 Gly Leu Leu Ala Val Leu Ala Val Leu Met Gly Leu Arg Arg Ile His
 385 390 395 400
 His His Ser Ala Phe Gln Lys Ala Ser Ser Ser Val Ile Thr
 405 410

<210> 219

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1075)

<223> RXA01728

<400> 219

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ggaaagtgat tttggcacct gcccgcagtt gaaggaagct atg gca gat gcc gtt 115
                                         Met Ala Asp Ala Val
                                         1 5

gag cgc gag gtc ttc gga tac cca cca gat gct act ggg ttg aat gat 163
Glu Arg Glu Val Phe Gly Tyr Pro Pro Asp Ala Thr Gly Leu Asn Asp
                        10 15 20

gcg ttg act gga ttc tac gag cgt cgc tat ggg ttt ggc cca aat ccg 211
Ala Leu Thr Gly Phe Tyr Glu Arg Arg Tyr Gly Phe Gly Pro Asn Pro
                        25 30 35

gaa agt gtt ttc gcc att ccg gat gtg gtt cgt ggc ctg aag ctt gcc 259
Glu Ser Val Phe Ala Ile Pro Asp Val Val Arg Gly Leu Lys Leu Ala
                        40 45 50

att gag cat ttc act aag cct ggt tcg gcg atc att gtg ccg ttg cct 307
Ile Glu His Phe Thr Lys Pro Gly Ser Ala Ile Ile Val Pro Leu Pro
                        55 60 65

gca tac cct cct ttc att gag ttg cct aag gtg act ggt cgt cag gcg 355
Ala Tyr Pro Pro Phe Ile Glu Leu Pro Lys Val Thr Gly Arg Gln Ala
                        70 75 80 85

atc tac att gat gcg cat gag tac gat ttg aag gaa att gag aag gcc 403
Ile Tyr Ile Asp Ala His Glu Tyr Asp Leu Lys Glu Ile Glu Lys Ala
                        90 95 100

ttc gct gac ggt gcg gga tca ctg ttg ttc tgc aat cca cac aac cca 451
Phe Ala Asp Gly Ala Gly Ser Leu Leu Phe Cys Asn Pro His Asn Pro
                        105 110 115

ctg ggc acg gtc ttt tct gaa gag tac atc cgc gag ctg acc gat att 499
Leu Gly Thr Val Phe Ser Glu Glu Tyr Ile Arg Glu Leu Thr Asp Ile
                        120 125 130

gcg gcg aag tac gat gcc cgc atc atc gtc gat gag atc cac gcg cca 547
Ala Ala Lys Tyr Asp Ala Arg Ile Ile Val Asp Glu Ile His Ala Pro
                        135 140 145

ctg gtt tat gaa ggc acc cat gtg gtt gct gct ggt gtt tct gag aac 595
Leu Val Tyr Glu Gly Thr His Val Val Ala Ala Gly Val Ser Glu Asn
                        150 155 160 165

gct gca aac act tgc atc acc atc acc gca act tct aag gcg tgg aac 643
Ala Ala Asn Thr Cys Ile Thr Ile Thr Ala Thr Ser Lys Ala Trp Asn
                        170 175 180

act gct ggt ttg aag tgt gct cag atc ttc ttc agt aat gaa gcc gat 691
Thr Ala Gly Leu Lys Cys Ala Gln Ile Phe Phe Ser Asn Glu Ala Asp
                        185 190 195

gtg aag gcc tgg aag aat ttg tcg gat att acc cgt gac ggt gtg tcc 739

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Val	Lys	Ala	Trp	Lys	Asn	Leu	Ser	Asp	Ile	Thr	Arg	Asp	Gly	Val	Ser		
		200					205					210					
atc	ctt	gga	ttg	atc	gct	gcg	gag	aca	gtg	tac	aac	gag	ggc	gaa	gaa	787	
Ile	Leu	Gly	Leu	Ile	Ala	Ala	Glu	Thr	Val	Tyr	Asn	Glu	Gly	Glu	Glu		
	215					220					225						
ttc	ctt	gat	gag	tca	att	cag	att	ctc	aag	gac	aac	cgt	gac	ttt	gcg	835	
Phe	Leu	Asp	Glu	Ser	Ile	Gln	Ile	Leu	Lys	Asp	Asn	Arg	Asp	Phe	Ala		
230					235					240					245		
gct	gct	gaa	ctg	gaa	aag	ctt	ggc	gtg	aag	gtc	tac	gca	ccg	gac	tcc	883	
Ala	Ala	Glu	Leu	Glu	Lys	Leu	Gly	Val	Lys	Val	Tyr	Ala	Pro	Asp	Ser		
				250					255					260			
act	tat	ttg	atg	tgg	ttg	gac	ttc	gct	ggc	acc	aag	atc	gaa	gag	gcg	931	
Thr	Tyr	Leu	Met	Trp	Leu	Asp	Phe	Ala	Gly	Thr	Lys	Ile	Glu	Glu	Ala		
			265					270					275				
cct	tct	aaa	att	ctt	cgt	gag	gag	ggg	aag	gtc	atg	ctg	aat	gat	ggc	979	
Pro	Ser	Lys	Ile	Leu	Arg	Glu	Glu	Gly	Lys	Val	Met	Leu	Asn	Asp	Gly		
		280					285					290					
gca	gct	ttt	ggt	ggt	ttc	acc	acc	tgc	gct	cgt	ctt	aat	ttt	gcg	tgt	1027	
Ala	Ala	Phe	Gly	Gly	Phe	Thr	Thr	Cys	Ala	Arg	Leu	Asn	Phe	Ala	Cys		
		295				300					305						
tcc	aga	gag	acc	ctt	gag	gag	ggg	ctg	cgc	cgt	atc	gcc	agc	gtg	ttg	1075	
Ser	Arg	Glu	Thr	Leu	Glu	Glu	Gly	Leu	Arg	Arg	Ile	Ala	Ser	Val	Leu		
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<210> 220

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 220

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Thr	Gly	Leu	Asn	Asp	Ala	Leu	Thr	Gly	Phe	Tyr	Glu	Arg	Arg	Tyr	Gly
			20					25					30		

Phe	Gly	Pro	Asn	Pro	Glu	Ser	Val	Phe	Ala	Ile	Pro	Asp	Val	Val	Arg
		35					40					45			

Gly	Leu	Lys	Leu	Ala	Ile	Glu	His	Phe	Thr	Lys	Pro	Gly	Ser	Ala	Ile
	50					55					60				

Ile	Val	Pro	Leu	Pro	Ala	Tyr	Pro	Pro	Phe	Ile	Glu	Leu	Pro	Lys	Val
	65				70					75					80

Thr	Gly	Arg	Gln	Ala	Ile	Tyr	Ile	Asp	Ala	His	Glu	Tyr	Asp	Leu	Lys
				85					90					95	

Glu	Ile	Glu	Lys	Ala	Phe	Ala	Asp	Gly	Ala	Gly	Ser	Leu	Leu	Phe	Cys
			100					105					110		

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Asn Pro His Asn Pro Leu Gly Thr Val Phe Ser Glu Glu Tyr Ile Arg
   115                               120               125

Glu Leu Thr Asp Ile Ala Ala Lys Tyr Asp Ala Arg Ile Ile Val Asp
   130                               135               140

Glu Ile His Ala Pro Leu Val Tyr Glu Gly Thr His Val Val Ala Ala
  145                               150               155               160

Gly Val Ser Glu Asn Ala Ala Asn Thr Cys Ile Thr Ile Thr Ala Thr
                165                               170               175

Ser Lys Ala Trp Asn Thr Ala Gly Leu Lys Cys Ala Gln Ile Phe Phe
                180                               185               190

Ser Asn Glu Ala Asp Val Lys Ala Trp Lys Asn Leu Ser Asp Ile Thr
   195                               200               205

Arg Asp Gly Val Ser Ile Leu Gly Leu Ile Ala Ala Glu Thr Val Tyr
  210                               215               220

Asn Glu Gly Glu Glu Phe Leu Asp Glu Ser Ile Gln Ile Leu Lys Asp
  225                               230               235               240

Asn Arg Asp Phe Ala Ala Ala Glu Leu Glu Lys Leu Gly Val Lys Val
                245                               250               255

Tyr Ala Pro Asp Ser Thr Tyr Leu Met Trp Leu Asp Phe Ala Gly Thr
   260                               265               270

Lys Ile Glu Glu Ala Pro Ser Lys Ile Leu Arg Glu Glu Gly Lys Val
   275                               280               285

Met Leu Asn Asp Gly Ala Ala Phe Gly Gly Phe Thr Thr Cys Ala Arg
  290                               295               300

Leu Asn Phe Ala Cys Ser Arg Glu Thr Leu Glu Glu Gly Leu Arg Arg
  305                               310               315               320

Ile Ala Ser Val Leu
                325

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<210> 221

<211> 732

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(709)

<223> RXA02214

<400> 221

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                Met Ser Pro Thr Val
                1                5

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ttg cct gct aca caa gct gac ttc cct aag atc gtc gat gtt ctg gtt    163

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Leu Pro Ala Thr Gln Ala Asp Phe Pro Lys Ile Val Asp Val Leu Val
          10          15          20

gaa gca ttc gcc aac gat cca gca ttt tta cga tgg atc ccg cag ccg 211
Glu Ala Phe Ala Asn Asp Pro Ala Phe Leu Arg Trp Ile Pro Gln Pro
          25          30          35

gac ccc ggt tca gca aag ctt cga gca ctt ttc gaa ctg cag att gag 259
Asp Pro Gly Ser Ala Lys Leu Arg Ala Leu Phe Glu Leu Gln Ile Glu
          40          45          50

aag cag tat gca gtg gcg gga aat att gat gtc gcg cgt gat tct gag 307
Lys Gln Tyr Ala Val Ala Gly Asn Ile Asp Val Ala Arg Asp Ser Glu
          55          60          65

gga gaa atc gtc ggc gtc gcg tta tgg gat cgg cca gat ggt aat cac 355
Gly Glu Ile Val Gly Val Ala Leu Trp Asp Arg Pro Asp Gly Asn His
          70          75          80          85

agt gcc aaa gat caa gca gcg atg ctc ccc cgg ctc gtc tcc att ttc 403
Ser Ala Lys Asp Gln Ala Ala Met Leu Pro Arg Leu Val Ser Ile Phe
          90          95          100

ggg atc aag gct gca cac gtg gcg tgg acg gat ttg agt tcg gct cgt 451
Gly Ile Lys Ala Ala His Val Ala Trp Thr Asp Leu Ser Ser Ala Arg
          105          110          115

ttc cac ccc aaa ttc ccc cat tgg tac ctc tac acc gtg gca aca tct 499
Phe His Pro Lys Phe Pro His Trp Tyr Leu Tyr Thr Val Ala Thr Ser
          120          125          130

agc tct gcc cgt gga acg gat gtt ggc agt gcg ctt ctt aat cac gga 547
Ser Ser Ala Arg Gly Thr Asp Val Gly Ser Ala Leu Leu Asn His Gly
          135          140          145

atc gct cgc gcg gct gat gaa gct atc tat ttg gag gcg acg ccg act 595
Ile Ala Arg Ala Ala Asp Glu Ala Ile Tyr Leu Glu Ala Thr Pro Thr
          150          155          160          165

cgt gcg gct caa cta tat aac cgt ctg gga ttc gtg ccc ttg ggt tat 643
Arg Ala Ala Gln Leu Tyr Asn Arg Leu Gly Phe Val Pro Leu Gly Tyr
          170          175          180

atc ccc tca gat gat gat ggc act cct gaa ctg gcg atg tgg aaa ccg 691
Ile Pro Ser Asp Asp Asp Gly Thr Pro Glu Leu Ala Met Trp Lys Pro
          185          190          195

cca gcg atg cca act gtt taaccctgaa ggcgatttaa ggg 732
Pro Ala Met Pro Thr Val
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<210> 222

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 222

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Met Ser Pro Thr Val Leu Pro Ala Thr Gln Ala Asp Phe Pro Lys Ile
  1           5           10          15

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<212> DNA
<213> Corynebacterium glutamicum
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<223> RXA02716
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                                         Val Ser Pro Ile Ile
                                         1                               5

cgt aaa ttg agt atc ccc gag ttc acc acc aac acc cca gtg ttg gtg 163
Arg Lys Leu Ser Ile Pro Glu Phe Thr Thr Asn Thr Pro Val Leu Val
                        10                        15                        20

gat atc tac atc gca gcg atg aac tat gac aaa gca atc agg gat acc 211
Asp Ile Tyr Ile Ala Ala Met Asn Tyr Asp Lys Ala Ile Arg Asp Thr
                        25                        30                        35

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cgg atc gaa gtc tgg cgg aga aac tcc cag aac ccc gga ttc aca gca 259
 Arg Ile Glu Val Trp Arg Arg Asn Ser Gln Asn Pro Gly Phe Thr Ala
 40 45 50

gtg gca gcg ctg atg gat gat cag gtc gtg ggc gtg gcc tat ggc ttc 307
 Val Ala Ala Leu Met Asp Asp Gln Val Val Gly Val Ala Tyr Gly Phe
 55 60 65

aat ggc agc cca gat cat tgg tgg caa cac caa tta cgc cgg gga ctc 355
 Asn Gly Ser Pro Asp His Trp Trp Gln His Gln Leu Arg Arg Gly Leu
 70 75 80 85

cga caa caa gga ggc ccg acg gaa gag gaa atc cat atc atc cac aac 403
 Arg Gln Gln Gly Gly Pro Thr Glu Glu Glu Ile His Ile Ile His Asn
 90 95 100

tac ttt gag gtt gcg gaa gtt cat gtt cag cct ggc ttc caa ggt cac 451
 Tyr Phe Glu Val Ala Glu Val His Val Gln Pro Gly Phe Gln Gly His
 105 110 115

ggc att ggc cga aag ctg atg cat gaa ctg tta aaa gac aaa caa aac 499
 Gly Ile Gly Arg Lys Leu Met His Glu Leu Leu Lys Asp Lys Gln Asn
 120 125 130

act ttt gcc att ttg tct aca ccc gag gtc gac gat gag gcg aac cat 547
 Thr Phe Ala Ile Leu Ser Thr Pro Glu Val Asp Asp Glu Ala Asn His
 135 140 145

gcg ttt agc ctg tat cgc tct ctc ggc ttc act gac ttg ctc agg cag 595
 Ala Phe Ser Leu Tyr Arg Ser Leu Gly Phe Thr Asp Leu Leu Arg Gln
 150 155 160 165

ttt agg ttt gac ggg gat caa cgg ccg ttt gcc gta ttg atc acc gcc 643
 Phe Arg Phe Asp Gly Asp Gln Arg Pro Phe Ala Val Leu Ile Thr Ala
 170 175 180

ctc ccc ctt cat gat tcc taagagggct taacgcaccg cgt 684
 Leu Pro Leu His Asp Ser
 185

<210> 224

<211> 187

<212> PRT

<213> Corynebacterium glutamicum

<400> 224

Val Ser Pro Ile Ile Arg Lys Leu Ser Ile Pro Glu Phe Thr Thr Asn
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Thr Pro Val Leu Val Asp Ile Tyr Ile Ala Ala Met Asn Tyr Asp Lys
 20 25 30

Ala Ile Arg Asp Thr Arg Ile Glu Val Trp Arg Arg Asn Ser Gln Asn
 35 40 45

Pro Gly Phe Thr Ala Val Ala Ala Leu Met Asp Asp Gln Val Val Gly
 50 55 60

Val Ala Tyr Gly Phe Asn Gly Ser Pro Asp His Trp Trp Gln His Gln

65		70		75		80
Leu Arg Arg Gly	Leu Arg Gln Gln Gly	Gly Pro Thr Glu Glu Glu Ile				
	85	90			95	
His Ile Ile His	Asn Tyr Phe Glu Val Ala Glu Val His Val Gln Pro					
	100	105			110	
Gly Phe Gln Gly	His Gly Ile Gly Arg Lys Leu Met His Glu Leu Leu					
	115	120			125	
Lys Asp Lys Gln	Asn Thr Phe Ala Ile Leu Ser Thr Pro Glu Val Asp					
	130	135			140	
Asp Glu Ala Asn	His Ala Phe Ser Leu Tyr Arg Ser Leu Gly Phe Thr					
	145	150			155	160
Asp Leu Leu Arg	Gln Phe Arg Phe Asp Gly Asp Gln Arg Pro Phe Ala					
	165	170			175	
Val Leu Ile Thr	Ala Leu Pro Leu His Asp Ser					
	180	185				

<210> 225

<211> 3945

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(3922)

<223> RXN01499

<400> 225

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                                         Leu Trp Asp Val Leu
                                         1           5

gaa tcc gtc gcc tct act tat cct gag gca gca gct att gac gat ggc 163
Glu Ser Val Ala Ser Thr Tyr Pro Glu Ala Ala Ala Ile Asp Asp Gly
                        10                        15                        20

cag gtg ttg acc tac gca gag ttg atg gaa gaa gtc acc gcg ttg gct 211
Gln Val Leu Thr Tyr Ala Glu Leu Met Glu Glu Val Thr Ala Leu Ala
                        25                        30                        35

gat tcc att cat gca cag ggc att cgc cgt ggt gat cgc atc ggt att 259
Asp Ser Ile His Ala Gln Gly Ile Arg Arg Gly Asp Arg Ile Gly Ile
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Arg Met Pro Ser Gly Thr Arg Asp Leu Tyr Ile Ala Ile Leu Ala Thr
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Leu Ala Ala Gly Ala Ala Tyr Val Pro Val Asp Ala Asp Asp Pro Glu
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Asp Ala Thr Gly Phe His Met Leu Arg Pro Thr Ala Gly Gly Asp Thr	
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Arg Arg Pro Arg Leu Asp Asp Thr Ala Trp Ile Ile Phe Thr Ser Gly	
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Ser Thr Gly Lys Pro Lys Gly Val Ala Val Ser His Arg Ser Ala Ala	
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gct ttc gtg gat gcc gaa gca caa atg ttc ctt gtc gat cac cct tcc	595
Ala Phe Val Asp Ala Glu Ala Gln Met Phe Leu Val Asp His Pro Ser	
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Gly Pro Leu Gly Pro Glu Asp Arg Val Leu Ala Gly Leu Ser Val Ala	
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Phe Asp Ala Ser Cys Glu Glu Met Trp Leu Ala Trp Gly His Gly Ala	
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Cys Leu Val Pro Ala Pro Arg Ser Leu Val Arg Ser Gly Met Asp Leu	
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Gly Pro Trp Leu Ile Arg Arg Asp Ile Ser Val Val Ser Thr Val Pro	
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Thr Leu Ala Gly Leu Trp Pro Ala Glu Ala Leu Ser Gln Val Arg Leu	
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Gly Glu Pro Val Gly Ile Gly Glu Val Gly Glu Leu Val Ile Gly Gly	
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Ala	Pro	Leu	Lys	Ser	Val	Gly	Trp	Thr	Arg	Ala	Tyr	Arg	Ser	Gly	Asp	
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cac	gtt	cgt	ctg	gaa	gaa	gat	ggc	ctc	tac	ttt	gtg	ggc	cgc	gtt	gat	1219
His	Val	Arg	Leu	Glu	Glu	Asp	Gly	Leu	Tyr	Phe	Val	Gly	Arg	Val	Asp	
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gat	cag	gtg	aaa	atc	ggc	ggc	cga	cgc	atc	gag	ctc	ggc	gaa	gtt	gat	1267
Asp	Gln	Val	Lys	Ile	Gly	Gly	Arg	Arg	Ile	Glu	Leu	Gly	Glu	Val	Asp	
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gcc	aat	gtg	gca	gcg	ctt	tcc	aac	gtt	cgt	tcc	tcc	gca	gtg	gtt	gtt	1315
Ala	Asn	Val	Ala	Ala	Leu	Ser	Asn	Val	Arg	Ser	Ser	Ala	Val	Val	Val	
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cag	acc	act	ggc	gca	gat	caa	aaa	gtt	ctg	gtt	gca	tac	gtt	tct	ttg	1363
Gln	Thr	Thr	Gly	Ala	Asp	Gln	Lys	Val	Leu	Val	Ala	Tyr	Val	Ser	Leu	
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Glu	Asp	Ala	Ala	Ala	Gly	Phe	Asp	His	Asn	Val	Ala	Thr	Ala	Arg	Leu	
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Thr	Glu	Thr	Met	Pro	Ala	Ala	Leu	Val	Pro	Arg	Ile	His	Val	Met	Asp	
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Asp	Leu	Pro	Val	Thr	Thr	Ser	Gly	Lys	Val	Asp	Lys	Lys	Ser	Leu	Pro	
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Ser	Ser	Lys	Asp	Ala	Asp	Phe	Phe	Ser	Leu	Gly	Gly	Thr	Ser	Leu	Ala	
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Ala	Ala	Thr	Leu	Val	Gly	Arg	Val	Arg	Ala	Lys	Val	Pro	Thr	Ala	Ala	
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Trp	Ile	Ala	Trp	Leu	Leu	Leu	Gly	Asn	Asn	Ile	Met	Ala	Ala	Leu	Asp	
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Phe	Asp	Trp	Ala	Val	His	Val	Ser	Trp	Trp	Leu	Val	Ile	Gly	Met	Ile	
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Leu	Val	Phe	Ala	Thr	Pro	Ile	Gly	Arg	Leu	Pro	Ile	Gly	Gly	Trp	Gly	
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gcc	cgc	atc	atc	acc	cgt	ggc	ata	act	cct	ggc	tcc	tac	cct	cgt	ggc	2083
Ala	Arg	Ile	Ile	Thr	Arg	Gly	Ile	Thr	Pro	Gly	Ser	Tyr	Pro	Arg	Gly	
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Ser	Gly	Ser	Arg	Asn	Ile	Ser	Gly	Ala	Thr	Trp	Val	Asn	Tyr	Phe	Ala	
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Thr	Leu	Leu	Pro	Gly	Thr	Val	Val	Gly	Thr	Gly	Ala	His	Leu	Leu	Pro	
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Trp Ala Val Gln Arg Leu Met Asp Asp Ala Arg Thr Tyr Leu Phe Pro	
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Leu Tyr Ala Ser Gln Leu Thr Pro Leu Trp Phe Arg Ser Leu Gly Ala	
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Lys Ile Gly Lys Asp Val Glu Ile Ser Thr Ala Val Met Val Pro Lys	
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 35 40 45
 Asp Arg Ile Gly Ile Arg Met Pro Ser Gly Thr Arg Asp Leu Tyr Ile
 50 55 60
 Ala Ile Leu Ala Thr Leu Ala Ala Gly Ala Ala Tyr Val Pro Val Asp
 65 70 75 80
 Ala Asp Asp Pro Glu Glu Arg Ala Glu Met Val Phe Gly Glu Ala Asn
 85 90 95
 Ile Asn Ala Leu Phe Asp Ala Thr Gly Phe His Met Leu Arg Pro Thr
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 Ala Gly Gly Asp Thr Arg Arg Pro Arg Leu Asp Asp Thr Ala Trp Ile
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 Ile Phe Thr Ser Gly Ser Thr Gly Lys Pro Lys Gly Val Ala Val Ser
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 His Arg Ser Ala Ala Ala Phe Val Asp Ala Glu Ala Gln Met Phe Leu
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 690 695 700
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 Leu Trp Asp Val Leu
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 Glu Ser Val Ala Ser Thr Tyr Pro Glu Ala Ala Ala Ile Asp Asp Gly
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 Gln Val Leu Thr Tyr Ala Glu Leu Met Glu Glu Val Thr Ala Leu Ala
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 Asp Ser Ile His Ala Gln Gly Ile Arg Arg Gly Asp Arg Ile Gly Ile
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 Arg Met Pro Ser Gly Thr Arg Asp Leu Tyr Ile Ala Ile Leu Ala Thr
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 Arg Arg Pro Arg Leu Asp Asp Thr Ala Trp Ile Ile Phe Thr Ser Gly
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Cys	Leu	Val	Pro	Ala	Pro	Arg	Ser	Leu	Val	Arg	Ser	Gly	Met	Asp	Leu	
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Thr	Leu	Ala	Gly	Leu	Trp	Pro	Ala	Glu	Ala	Leu	Ser	Gln	Val	Arg	Leu	
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Ser	Thr	Pro	Asp	Arg	Glu	Val	Trp	Asn	Thr	Tyr	Gly	Pro	Thr	Glu	Ala	
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Gly	Glu	Pro	Val	Gly	Ile	Gly	Glu	Val	Gly	Glu	Leu	Val	Ile	Gly	Gly	
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Val	Gly	Leu	Ala	Arg	Tyr	Leu	Asp	Pro	Glu	Lys	Asp	Arg	Glu	Lys	Tyr	
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Ala	Pro	Leu	Lys	Ser	Val	Gly	Trp	Thr	Arg	Ala	Tyr	Arg	Ser	Gly	Asp	
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His	Val	Arg	Leu	Glu	Glu	Asp	Gly	Leu	Tyr	Phe	Val	Gly	Arg	Val	Asp	
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Asp	Gln	Val	Lys	Ile	Gly	Gly	Arg	Arg	Ile	Glu	Leu	Gly	Glu	Val	Asp	
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gcc	aat	gtg	gca	gcg	ctt	tcc	aac	gtt	cgt	tcc	tcc	gca	gtg	gtt	gtt	1315
Ala	Asn	Val	Ala	Ala	Leu	Ser	Asn	Val	Arg	Ser	Ser	Ala	Val	Val	Val	
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cag	acc	act	ggg	gcg	gat	caa	aaa	gtt	ctg	gtt	gca	tac	gtt	tct	ttg	1363
Gln	Thr	Thr	Gly	Ala	Asp	Gln	Lys	Val	Leu	Val	Ala	Tyr	Val	Ser	Leu	
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gaa	gat	gct	gca	gct	gga	ttt	gat	cac	aac	gtc	gcg	act	gcc	cga	ctc	1411
Glu	Asp	Ala	Ala	Ala	Gly	Phe	Asp	His	Asn	Val	Ala	Thr	Ala	Arg	Leu	

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Thr	Glu	Thr	Met	Pro	Ala	Ala	Leu	Val	Pro	Arg	Ile	His	Val	Met	Asp	
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Asp	Leu	Pro	Val	Thr	Thr	Ser	Gly	Lys	Val	Asp	Lys	Lys	Ser	Leu	Pro	
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Trp	Pro	Leu	Pro	Gly	Thr	Val	Val	Glu	Ala	Asn	Asp	Leu	Ser	Ala	Thr	
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Ser	Ser	Lys	Asp	Ala	Asp	Phe	Phe	Ser	Leu	Gly	Gly	Thr	Ser	Leu	Ala	
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Ala	Ala	Thr	Leu	Val	Gly	Arg	Val	Arg	Ala	Lys	Val	Pro	Thr	Ala	Ala	
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Val	Arg	Asp	Leu	Tyr	Asp	His	Pro	Arg	Leu	Glu	Lys	Phe	Ala	Glu	Arg	
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Gln	Val	Glu	Glu	Arg	Val	Val	Lys	Pro	Val	Ser	Phe	Gly	Thr	Arg	Val	
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Met	Gln	Thr	Leu	Ile	Gln	Ile	Pro	Ile	Met	Thr	Leu	Gln	Ala	Ala	Gln	
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tgg	att	gca	tgg	ttg	ctg	ttg	ggc	aac	aac	atc	atg	gca	gcg	ctt	gat	1939
Trp	Ile	Ala	Trp	Leu	Leu	Leu	Gly	Asn	Asn	Ile	Met	Ala	Ala	Leu	Asp	
		600					605					610				
ttc	gat	tgg	gct	gtt	cat	gtc	tcc	tgg	tgg	ctt	gtc	atc	ggc	atg	att	1987
Phe	Asp	Trp	Ala	Val	His	Val	Ser	Trp	Trp	Leu	Val	Ile	Gly	Met	Ile	
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Leu	Val	Phe	Ala	Thr	Pro	Ile	Gly	Arg	Leu	Pro	Ile	Gly	Gly	Trp	Gly	
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gcc	cgc	atc	atc	acc	cgt	ggc	ata	act	cct	ggc	tcc	tac	cct	cgt	ggc	2083
Ala	Arg	Ile	Ile	Thr	Arg	Gly	Ile	Thr	Pro	Gly	Ser	Tyr	Pro	Arg	Gly	
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ggt	tcc	act	cac	ctg	cgc	att	tgg	tcc	gcc	gag	cgc	ctt	gct	gat	gcc	2131
Gly	Ser	Thr	His	Leu	Arg	Ile	Trp	Ser	Ala	Glu	Arg	Leu	Ala	Asp	Ala	
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Ser Gly Ser Arg Asn Ile Ser Gly Ala Thr Trp Val Asn Tyr Phe Ala	
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Arg Ser Leu Gly Val Lys Met Gly Lys Gly Val Asp Leu His Ser Leu	
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cca cca atc act ggc ctt ttg acc ttg ggc aac aat gtt tcc atc gag	2275
Pro Pro Ile Thr Gly Leu Thr Leu Gly Asn Asn Val Ser Ile Glu	
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caa gaa gtt gac ctt cgt ggc tac tgg ctc gac ggc gat atc ctg cgt	2323
Gln Glu Val Asp Leu Arg Gly Tyr Trp Leu Asp Gly Asp Ile Leu Arg	
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Val Gly Thr Ile Glu Val His Asp Asn Ala Arg Ile Gly Ala Arg Ser	
745 750 755	
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Thr Leu Leu Pro Gly Thr Val Val Gly Thr Gly Ala His Leu Leu Pro	
760 765 770	
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Gly Ser Thr Val Thr Gly Asp Lys Thr Ile Lys Pro Gly Ser Arg Trp	
775 780 785	
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Ala Gly Ser Pro Ala Gln Lys Val Gly Arg Ala Lys His Arg Phe Pro	
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Thr Ser His Pro Pro Arg Arg Ser Arg Trp Val Pro Val Phe Gly Ala	
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Thr Ser Ile Val Leu Ser Leu Leu Pro Leu Gln Ala Leu Ala Ile Gly	
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Ala Ala Ile Thr Leu Trp Leu Ala Thr Ile Ser Pro Leu Pro Leu Ile	
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Ile Lys Gly Gly Thr Ala Pro Val Arg Ser Arg Leu Gly Trp Gln Val	
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Trp Ala Val Gln Arg Leu Met Asp Asp Ala Arg Thr Tyr Leu Phe Pro	
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Lys Ile Gly Lys Asp Val Glu Ile Ser Thr Ala Val Met Val Pro Lys	
935 940 945	
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Leu	Gly	Glu	Val	Asp	Ala	Asn	Val	Ala	Ala	Leu	Ser	Asn	Val	Arg	Ser		
385					390					395					400		
Ser	Ala	Val	Val	Val	Gln	Thr	Thr	Gly	Ala	Asp	Gln	Lys	Val	Leu	Val		
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Ala	Tyr	Val	Ser	Leu	Glu	Asp	Ala	Ala	Ala	Gly	Phe	Asp	His	Asn	Val		
			420					425					430				
Ala	Thr	Ala	Arg	Leu	Thr	Glu	Thr	Met	Pro	Ala	Ala	Leu	Val	Pro	Arg		
		435					440					445					

Ile His Val Met Asp Asp Leu Pro Val Thr Thr Ser Gly Lys Val Asp
 450 455 460
 Lys Lys Ser Leu Pro Trp Pro Leu Pro Gly Thr Val Val Glu Ala Asn
 465 470 475 480
 Asp Leu Ser Ala Thr Glu Ala Trp Ile Ala Gln Glu Trp Val Asp Ile
 485 490 495
 Leu Gly Thr Ser Val Ser Ser Lys Asp Ala Asp Phe Phe Ser Leu Gly
 500 505 510
 Gly Thr Ser Leu Ala Ala Ala Thr Leu Val Gly Arg Val Arg Ala Lys
 515 520 525
 Val Pro Thr Ala Ala Val Arg Asp Leu Tyr Asp His Pro Arg Leu Glu
 530 535 540
 Lys Phe Ala Glu Arg Val Glu Ala Ile Ala Ala Asp Thr Gly Ile Ser
 545 550 555 560
 Leu Glu Ala Pro Asn Gln Val Glu Glu Arg Val Val Lys Pro Val Ser
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 Phe Gly Thr Arg Val Met Gln Thr Leu Ile Gln Ile Pro Ile Met Thr
 580 585 590
 Leu Gln Ala Ala Gln Trp Ile Ala Trp Leu Leu Leu Gly Asn Asn Ile
 595 600 605
 Met Ala Ala Leu Asp Phe Asp Trp Ala Val His Val Ser Trp Trp Leu
 610 615 620
 Val Ile Gly Met Ile Leu Val Phe Ala Thr Pro Ile Gly Arg Leu Pro
 625 630 635 640
 Ile Gly Gly Trp Gly Ala Arg Ile Ile Thr Arg Gly Ile Thr Pro Gly
 645 650 655
 Ser Tyr Pro Arg Gly Gly Ser Thr His Leu Arg Ile Trp Ser Ala Glu
 660 665 670
 Arg Leu Ala Asp Ala Ser Gly Ser Arg Asn Ile Ser Gly Ala Thr Trp
 675 680 685
 Val Asn Tyr Phe Ala Arg Ser Leu Gly Val Lys Met Gly Lys Gly Val
 690 695 700
 Asp Leu His Ser Leu Pro Pro Ile Thr Gly Leu Leu Thr Leu Gly Asn
 705 710 715 720
 Asn Val Ser Ile Glu Gln Glu Val Asp Leu Arg Gly Tyr Trp Leu Asp
 725 730 735
 Gly Asp Ile Leu Arg Val Gly Thr Ile Glu Val His Asp Asn Ala Arg
 740 745 750
 Ile Gly Ala Arg Ser Thr Leu Leu Pro Gly Thr Val Val Gly Thr Gly
 755 760 765
 Ala His Leu Leu Pro Gly Ser Thr Val Thr Gly Asp Lys Thr Ile Lys

770	775	780
Pro Gly Ser Arg Trp Ala Gly Ser Pro Ala Gln Lys Val Gly Arg Ala 785 790 795 800		
Lys His Arg Phe Pro Thr Ser His Pro Pro Arg Arg Ser Arg Trp Val 805 810 815		
Pro Val Phe Gly Ala Thr Ser Ile Val Leu Ser Leu Leu Pro Leu Gln 820 825 830		
Ala Leu Ala Ile Gly Ala Ala Ile Thr Leu Trp Leu Ala Thr Ile Ser 835 840 845		
Pro Leu Pro Leu Ile Trp Gly Val Leu Val Phe Ala Thr Val Gly Ala 850 855 860		
Leu Ala Ala Phe Phe Ala Tyr Thr Val Thr Ile Trp Val Leu Val Arg 865 870 875 880		
Leu Ile Gln Ile Gly Ile Lys Gly Gly Thr Ala Pro Val Arg Ser Arg 885 890 895		
Leu Gly Trp Gln Val Trp Ala Val Gln Arg Leu Met Asp Asp Ala Arg 900 905 910		
Thr Tyr Leu Phe Pro Leu Tyr Ala Ser Gln Leu Thr Pro Leu Trp Phe 915 920 925		
Arg Ser Leu Gly Ala Lys Ile Gly Lys Asp Val Glu Ile Ser Thr Ala 930 935 940		
Val Met Val Pro Lys Leu Ala Asp Ile Arg Glu Gly Ala Phe Leu Ala 945 950 955 960		
Asp Asp Thr Leu Ile Gly Gly Tyr Glu Leu Gly Asn Gly Trp Leu Leu 965 970 975		
Ser Gly Glu Thr Arg Val Gly Lys Arg Ser Phe Ile Gly Asn Ser Gly 980 985 990		
Ile Ala Gly Pro Glu Arg Lys Leu Ala Lys Asn Ser Leu Val Ala Val 995 1000 1005		
Leu Ser Ser Thr Pro Lys Lys Ala Lys Ala Asn Ser Asn Trp Trp Gly 1010 1015 1020		
Ser Pro Pro Glu Arg Met Arg Arg Val Thr Val Glu Val Asp Glu Gly 1025 1030 1035 1040		
Glu Ala Lys Thr Tyr Ser Pro Gly Phe Gly Val Lys Phe Ala Arg Gly 1045 1050 1055		
Ala Val Glu Thr Ala Arg Leu Leu Ala Pro Ile Thr Ser Gly Val Leu 1060 1065 1070		
Ala Ala Leu Ser Leu Leu Leu Met Gln Tyr Leu Leu Thr Glu Phe Asn 1075 1080 1085		
Met Trp Ile Thr Trp Leu Leu Gly Gly Leu Ile Leu Met Thr Val Gly 1090 1095 1100		

Val Leu Ala Met Gly Ile Thr Val Val Met Lys Trp Val Cys Val Gly
 1105 1110 1115 1120
 Lys His Lys Pro Ser Glu His Pro Leu Phe Ser Arg Phe Val Trp Leu
 1125 1130 1135
 Asn Glu Leu Gln Asp Ala Phe Val Glu Ser Val Ala Gly Pro Trp Phe
 1140 1145 1150
 Leu Val Pro Asn Leu Gly Thr Gly Ala Leu Asn Ala Gly Met Ser Ala
 1155 1160 1165
 Leu Gly Ala His Ile Gly Arg Gly Ala Trp Ile Glu Ser Tyr Trp Leu
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 Pro Glu Thr Asp Leu Cys Tyr Ile Gly Lys Gly Ala Thr Val Gly Pro
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 Gly Val Val Val Gln Thr His Leu Phe Gln Asp Arg Val Met Ser Leu
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 Asp Thr Val Thr Val Ala Asp Gly Ala Thr Leu Ala Asp His Ser Val
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 Ala Leu Pro Ala Ser Leu Ile Asp Ala Ser Ala Thr Ile Gly Pro Gly
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 Gly Asn Pro Ile Glu Pro Trp Ser Asn Ser
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 <223> RXN00787

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 Val Ser Gln Pro Leu
 1 5
 agc aag cgt ctc agc ata cga aaa gca ctc gcc agc gcc ttc ata gtt 163
 Ser Lys Arg Leu Ser Ile Arg Lys Ala Leu Ala Ser Ala Phe Ile Val
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 gcg ctg gcg ttt tcg ctt tcc cca gta gcc aaa gcc caa gcc aat gaa 211
 Ala Leu Ala Phe Ser Leu Ser Pro Val Ala Lys Ala Gln Ala Asn Glu
 25 30 35
 act ccg acg atg atc gtg ttg gac aat tca ggc tcc atg aca gct caa 259

Thr	Pro	Thr	Met	Ile	Val	Leu	Asp	Asn	Ser	Gly	Ser	Met	Thr	Ala	Gln	
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gat	gcc	ggc	gga	cag	acc	cgt	atc	gat	gca	gca	aaa	caa	gcc	tcc	act	307
Asp	Ala	Gly	Gly	Gln	Thr	Arg	Ile	Asp	Ala	Ala	Lys	Gln	Ala	Ser	Thr	
	55					60					65					
cag	tta	att	aat	gac	atc	tcc	gac	cgc	acc	gac	gta	ggc	ctg	acc	tac	355
Gln	Leu	Ile	Asn	Asp	Ile	Ser	Asp	Arg	Thr	Asp	Val	Gly	Leu	Thr	Tyr	
70					75					80					85	
tac	ggc	gga	aac	acc	ggc	gaa	aca	gaa	gca	gac	gtt	gag	atg	gga	tgc	403
Tyr	Gly	Gly	Asn	Thr	Gly	Glu	Thr	Glu	Ala	Asp	Val	Glu	Met	Gly	Cys	
				90					95					100		
caa	gac	gtc	acc	atc	ctt	ggc	ggc	ccc	tcc	cga	gga	aat	gca	gac	acc	451
Gln	Asp	Val	Thr	Ile	Leu	Gly	Gly	Pro	Ser	Arg	Gly	Asn	Ala	Asp	Thr	
			105					110					115			
tta	att	gac	acg	atc	aac	agc	ctg	cag	cct	cga	ggc	ttc	acc	ccc	atc	499
Leu	Ile	Asp	Thr	Ile	Asn	Ser	Leu	Gln	Pro	Arg	Gly	Phe	Thr	Pro	Ile	
		120					125					130				
ggc	aaa	gca	ctc	acc	gat	acc	gcc	gcc	gag	ctc	ccc	gaa	ggc	gga	aac	547
Gly	Lys	Ala	Leu	Thr	Asp	Thr	Ala	Ala	Glu	Leu	Pro	Glu	Gly	Gly	Asn	
	135					140					145					
att	gtg	ttg	gtc	tcc	gat	ggc	atc	gcc	aac	tgc	acc	cca	ccg	gat	gtc	595
Ile	Val	Leu	Val	Ser	Asp	Gly	Ile	Ala	Asn	Cys	Thr	Pro	Pro	Asp	Val	
150					155					160					165	
tgc	gaa	gta	gcc	caa	gaa	ctg	gct	caa	agt	gga	atc	aac	ctg	gtt	atc	643
Cys	Glu	Val	Ala	Gln	Glu	Leu	Ala	Gln	Ser	Gly	Ile	Asn	Leu	Val	Ile	
				170					175					180		
aac	acc	atc	gga	cta	aat	gtt	gat	cca	gca	gcg	cgc	gaa	gaa	ctg	gag	691
Asn	Thr	Ile	Gly	Leu	Asn	Val	Asp	Pro	Ala	Ala	Arg	Glu	Glu	Leu	Glu	
			185					190					195			
tgc	atc	gct	gga	gtc	ggc	ggc	ggc	act	tac	gcg	gat	gct	tcc	gac	gcg	739
Cys	Ile	Ala	Gly	Val	Gly	Gly	Gly	Thr	Tyr	Ala	Asp	Ala	Ser	Asp	Ala	
		200				205						210				
cag	agc	ctt	acc	gat	gcg	ctg	aca	cga	gcc	gcc	agt	agg	caa	tac	aac	787
Gln	Ser	Leu	Thr	Asp	Ala	Leu	Thr	Arg	Ala	Ala	Ser	Arg	Gln	Tyr	Asn	
	215					220					225					
tct	tac	acc	tcc	gat	gtg	aca	aaa	att	gat	ggg	gca	tcg	gaa	caa	agc	835
Ser	Tyr	Thr	Ser	Asp	Val	Thr	Lys	Ile	Asp	Gly	Ala	Ser	Glu	Gln	Ser	
230					235					240					245	
gca	gcc	gta	gaa	att	gat	gag	gat	aca	gaa	cta	ttc	ctc	acc	gac	ctg	883
Ala	Ala	Val	Glu	Ile	Asp	Glu	Asp	Thr	Glu	Leu	Phe	Leu	Thr	Asp	Leu	
				250					255					260		
cca	caa	gaa	tcc	cgc	ttt	tgg	aaa	atc	cct	gta	gag	cca	ggc	gaa	acc	931
Pro	Gln	Glu	Ser	Arg	Phe	Trp	Lys	Ile	Pro	Val	Glu	Pro	Gly	Glu	Thr	
			265					270					275			
atc	tca	gtt	tct	gcc	aac	aca	gtt	acc	gac	cca	aca	gta	ctc	acc	atg	979
Ile	Ser	Val	Ser	Ala	Asn	Thr	Val	Thr	Asp	Pro	Thr	Val	Leu	Thr	Met	

280	285	290	
ggg caa ggc gga atc aag ctt gaa gcc caa ctc cat act gaa gag gct Gly Gln Gly Gly Ile Lys Leu Glu Ala Gln Leu His Thr Glu Glu Ala 295 300 305			1027
cca caa tac ggc ctg cgt ggt cgg tgc act cgg gtc tca ttt gat aat Pro Gln Tyr Gly Leu Arg Gly Arg Cys Thr Arg Val Ser Phe Asp Asn 310 315 320 325			1075
ttc aag ccc ggc ctt ggt gta cgc gga atc caa aac gcg tcc gtt gca Phe Lys Pro Gly Leu Gly Val Arg Gly Ile Gln Asn Ala Ser Val Ala 330 335 340			1123
tca aaa gaa gtg ggc acc aac aac tgt gac acc gat gcc atc tac ctc Ser Lys Glu Val Gly Thr Asn Asn Cys Asp Thr Asp Ala Ile Tyr Leu 345 350 355			1171
gaa att tct aga agc gga gat tac ctc aac ggg cag gac att cca acg Glu Ile Ser Arg Ser Gly Asp Tyr Leu Asn Gly Gln Asp Ile Pro Thr 360 365 370			1219
gaa atc acc atc gag cgc ttc gga aaa gta gat gaa tca aca atc gga Glu Ile Thr Ile Glu Arg Phe Gly Lys Val Asp Glu Ser Thr Ile Gly 375 380 385			1267
aat gtc aca gag gaa cat agc tcc gtc gat ctt acc gag gct gca gca Asn Val Thr Glu Glu His Ser Ser Val Asp Leu Thr Glu Ala Ala Ala 390 395 400 405			1315
tca gag gca cac cct gtc aca cct ggc cag tgg ttc aca tcg gcc gct Ser Glu Ala His Pro Val Thr Pro Gly Gln Trp Phe Thr Ser Ala Ala 410 415 420			1363
gat cta gat ccc gca ggt gag aaa gtc tcc tcc atc atc gtt cca gga Asp Leu Asp Pro Ala Gly Glu Lys Val Ser Ser Ile Ile Val Pro Gly 425 430 435			1411
gaa acc cac ttc tat gcg ctg cct gtc gac tac ggc caa gaa ctg cgc Glu Thr His Phe Tyr Ala Leu Pro Val Asp Tyr Gly Gln Glu Leu Arg 440 445 450			1459
gca gct gta gaa aca act ttt gac caa atc gac agt tcc gcg ctt ggc Ala Ala Val Glu Thr Thr Phe Asp Gln Ile Asp Ser Ser Ala Leu Gly 455 460 465			1507
acg cat ctt tat atc caa gcg ttc agc cca aac cgg gca gag ata gag Thr His Leu Tyr Ile Gln Ala Phe Ser Pro Asn Arg Ala Glu Ile Glu 470 475 480 485			1555
ctc acc aat aga gat acg tca tat gcg gac gac aac ggg ctc aaa act Leu Thr Asn Arg Asp Thr Ser Tyr Ala Asp Asp Asn Gly Leu Lys Thr 490 495 500			1603
ttt gga ttc ttc acc cca gtg agt gca gca aat ttg ttc gag aaa agt Phe Gly Phe Phe Thr Pro Val Ser Ala Ala Asn Leu Phe Glu Lys Ser 505 510 515			1651
tct caa ggc ata tcg cta agg agc cca tgg caa ggt ggc acc caa tac Ser Gln Gly Ile Ser Leu Arg Ser Pro Trp Gln Gly Gly Thr Gln Tyr 520 525 530			1699

ctc gca gtg aca tac cta cca agt ggt caa gat gaa gat gta tcc gca 1747
 Leu Ala Val Thr Tyr Leu Pro Ser Gly Gln Asp Glu Asp Val Ser Ala
 535 540 545

act gat cag ctg ccc aca ttg gaa tat gaa ctc gtg gca gaa gcg ttt 1795
 Thr Asp Gln Leu Pro Thr Leu Glu Tyr Glu Leu Val Ala Glu Ala Phe
 550 555 560 565

gga gac cct gtt gac cca ccg gtt ttc gct tca ttg acg gga gca acc 1843
 Gly Asp Pro Val Asp Pro Pro Val Phe Ala Ser Leu Thr Gly Ala Thr
 570 575 580

cca agc acc tcc acc ccc cca tca gat gtt gcg gaa gat gaa caa atc 1891
 Pro Ser Thr Ser Thr Pro Pro Ser Asp Val Ala Glu Asp Glu Gln Ile
 585 590 595

tcc gag gca aca gaa gaa gac tca agc agt ttc ccc atc gtg tgg att 1939
 Ser Glu Ala Thr Glu Glu Asp Ser Ser Ser Phe Pro Ile Val Trp Ile
 600 605 610

ggg ctg ggt gtc att ggc tta ggc ata atc att ggt ttg atc ttt gcg 1987
 Gly Leu Gly Val Ile Gly Leu Gly Ile Ile Ile Gly Leu Ile Phe Ala
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 Leu Arg Arg Lys Asn
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<212> PRT

<213> Corynebacterium glutamicum

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Ser Ala Phe Ile Val Ala Leu Ala Phe Ser Leu Ser Pro Val Ala Lys
 20 25 30

Ala Gln Ala Asn Glu Thr Pro Thr Met Ile Val Leu Asp Asn Ser Gly
 35 40 45

Ser Met Thr Ala Gln Asp Ala Gly Gly Gln Thr Arg Ile Asp Ala Ala
 50 55 60

Lys Gln Ala Ser Thr Gln Leu Ile Asn Asp Ile Ser Asp Arg Thr Asp
 65 70 75 80

Val Gly Leu Thr Tyr Tyr Gly Gly Asn Thr Gly Glu Thr Glu Ala Asp
 85 90 95

Val Glu Met Gly Cys Gln Asp Val Thr Ile Leu Gly Gly Pro Ser Arg
 100 105 110

Gly Asn Ala Asp Thr Leu Ile Asp Thr Ile Asn Ser Leu Gln Pro Arg
 115 120 125

Gly Phe Thr Pro Ile Gly Lys Ala Leu Thr Asp Thr Ala Ala Glu Leu

130					135					140					
Pro	Glu	Gly	Gly	Asn	Ile	Val	Leu	Val	Ser	Asp	Gly	Ile	Ala	Asn	Cys
145					150					155					160
Thr	Pro	Pro	Asp	Val	Cys	Glu	Val	Ala	Gln	Glu	Leu	Ala	Gln	Ser	Gly
				165					170					175	
Ile	Asn	Leu	Val	Ile	Asn	Thr	Ile	Gly	Leu	Asn	Val	Asp	Pro	Ala	Ala
			180					185					190		
Arg	Glu	Glu	Leu	Glu	Cys	Ile	Ala	Gly	Val	Gly	Gly	Gly	Thr	Tyr	Ala
		195					200					205			
Asp	Ala	Ser	Asp	Ala	Gln	Ser	Leu	Thr	Asp	Ala	Leu	Thr	Arg	Ala	Ala
	210					215					220				
Ser	Arg	Gln	Tyr	Asn	Ser	Tyr	Thr	Ser	Asp	Val	Thr	Lys	Ile	Asp	Gly
225					230					235					240
Ala	Ser	Glu	Gln	Ser	Ala	Ala	Val	Glu	Ile	Asp	Glu	Asp	Thr	Glu	Leu
				245					250					255	
Phe	Leu	Thr	Asp	Leu	Pro	Gln	Glu	Ser	Arg	Phe	Trp	Lys	Ile	Pro	Val
			260					265					270		
Glu	Pro	Gly	Glu	Thr	Ile	Ser	Val	Ser	Ala	Asn	Thr	Val	Thr	Asp	Pro
		275					280					285			
Thr	Val	Leu	Thr	Met	Gly	Gln	Gly	Gly	Ile	Lys	Leu	Glu	Ala	Gln	Leu
	290					295					300				
His	Thr	Glu	Glu	Ala	Pro	Gln	Tyr	Gly	Leu	Arg	Gly	Arg	Cys	Thr	Arg
305					310					315					320
Val	Ser	Phe	Asp	Asn	Phe	Lys	Pro	Gly	Leu	Gly	Val	Arg	Gly	Ile	Gln
				325					330					335	
Asn	Ala	Ser	Val	Ala	Ser	Lys	Glu	Val	Gly	Thr	Asn	Asn	Cys	Asp	Thr
			340					345					350		
Asp	Ala	Ile	Tyr	Leu	Glu	Ile	Ser	Arg	Ser	Gly	Asp	Tyr	Leu	Asn	Gly
		355					360					365			
Gln	Asp	Ile	Pro	Thr	Glu	Ile	Thr	Ile	Glu	Arg	Phe	Gly	Lys	Val	Asp
	370					375					380				
Glu	Ser	Thr	Ile	Gly	Asn	Val	Thr	Glu	Glu	His	Ser	Ser	Val	Asp	Leu
385					390					395					400
Thr	Glu	Ala	Ala	Ala	Ser	Glu	Ala	His	Pro	Val	Thr	Pro	Gly	Gln	Trp
				405					410					415	
Phe	Thr	Ser	Ala	Ala	Asp	Leu	Asp	Pro	Ala	Gly	Glu	Lys	Val	Ser	Ser
			420					425					430		
Ile	Ile	Val	Pro	Gly	Glu	Thr	His	Phe	Tyr	Ala	Leu	Pro	Val	Asp	Tyr
		435					440					445			
Gly	Gln	Glu	Leu	Arg	Ala	Ala	Val	Glu	Thr	Thr	Phe	Asp	Gln	Ile	Asp
	450					455					460				

Ser Ser Ala Leu Gly Thr His Leu Tyr Ile Gln Ala Phe Ser Pro Asn
 465 470 475 480
 Arg Ala Glu Ile Glu Leu Thr Asn Arg Asp Thr Ser Tyr Ala Asp Asp
 485 490 495
 Asn Gly Leu Lys Thr Phe Gly Phe Phe Thr Pro Val Ser Ala Ala Asn
 500 505 510
 Leu Phe Glu Lys Ser Ser Gln Gly Ile Ser Leu Arg Ser Pro Trp Gln
 515 520 525
 Gly Gly Thr Gln Tyr Leu Ala Val Thr Tyr Leu Pro Ser Gly Gln Asp
 530 535 540
 Glu Asp Val Ser Ala Thr Asp Gln Leu Pro Thr Leu Glu Tyr Glu Leu
 545 550 555 560
 Val Ala Glu Ala Phe Gly Asp Pro Val Asp Pro Pro Val Phe Ala Ser
 565 570 575
 Leu Thr Gly Ala Thr Pro Ser Thr Ser Thr Pro Pro Ser Asp Val Ala
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 Glu Asp Glu Gln Ile Ser Glu Ala Thr Glu Glu Asp Ser Ser Ser Phe
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 Val Ser Gln Pro Leu
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 Ser Lys Arg Leu Ser Ile Arg Lys Ala Leu Ala Ser Ala Phe Ile Val
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 Ala Leu Ala Phe Ser Leu Ser Pro Val Ala Lys Ala Gln Ala Asn Glu
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		40					45					50					
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Asp	Ala	Gly	Gly	Gln	Thr	Arg	Ile	Asp	Ala	Ala	Lys	Gln	Ala	Ser	Thr		
	55					60					65						
cag	tta	att	aat	gac	atc	tcc	gac	cgc	acc	gac	gta	ggc	ctg	acc	tac	355	
Gln	Leu	Ile	Asn	Asp	Ile	Ser	Asp	Arg	Thr	Asp	Val	Gly	Leu	Thr	Tyr		
	70				75					80					85		
tac	ggc	gga	aac	acc	ggc	gaa	aca	gaa	gca	gac	gtt	gag	atg	gga	tgc	403	
Tyr	Gly	Gly	Asn	Thr	Gly	Glu	Thr	Glu	Ala	Asp	Val	Glu	Met	Gly	Cys		
				90					95					100			
caa	gac	gtc	acc	atc	ctt	ggc	ggc	ccc	tcc	cga	gga	aat	gca	gac	acc	451	
Gln	Asp	Val	Thr	Ile	Leu	Gly	Gly	Pro	Ser	Arg	Gly	Asn	Ala	Asp	Thr		
			105					110					115				
tta	att	gac	acg	atc	aac	agc	ctg	cag	cct	cga	ggc	ttc	acc	ccc	atc	499	
Leu	Ile	Asp	Thr	Ile	Asn	Ser	Leu	Gln	Pro	Arg	Gly	Phe	Thr	Pro	Ile		
	120						125					130					
ggc	aaa	gca	ctc	acc	gat	acc	gcc	gcc	gag	ctc	ccc	gaa	ggc	gga	aac	547	
Gly	Lys	Ala	Leu	Thr	Asp	Thr	Ala	Ala	Glu	Leu	Pro	Glu	Gly	Gly	Asn		
	135					140					145						
att	gtg	ttg	gtc	tcc	gat	ggc	atc	gcc	aac	tgc	acc	cca	ccg	gat	gtc	595	
Ile	Val	Leu	Val	Ser	Asp	Gly	Ile	Ala	Asn	Cys	Thr	Pro	Pro	Asp	Val		
	150				155					160					165		
tgc	gaa	gta	gcc	caa	gaa	ctg	gct	caa	agt	gga	atc	aac	ctg	gtt	atc	643	
Cys	Glu	Val	Ala	Gln	Glu	Leu	Ala	Gln	Ser	Gly	Ile	Asn	Leu	Val	Ile		
				170				175						180			
aac	acc	atc	gga	cta	aat	gtt	gat	cca	gca	gcg	cgc	gaa	gaa	ctg	gag	691	
Asn	Thr	Ile	Gly	Leu	Asn	Val	Asp	Pro	Ala	Ala	Arg	Glu	Glu	Leu	Glu		
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tgc																694	
Cys																	

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<211> 198

<212> PRT

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<400> 232

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			20					25					30				
Ala	Gln	Ala	Asn	Glu	Thr	Pro	Thr	Met	Ile	Val	Leu	Asp	Asn	Ser	Gly		
		35					40					45					
Ser	Met	Thr	Ala	Gln	Asp	Ala	Gly	Gly	Gln	Thr	Arg	Ile	Asp	Ala	Ala		
	50					55					60						

Lys Gln Ala Ser Thr Gln Leu Ile Asn Asp Ile Ser Asp Arg Thr Asp
 65 70 75 80
 Val Gly Leu Thr Tyr Tyr Gly Gly Asn Thr Gly Glu Thr Glu Ala Asp
 85 90 95
 Val Glu Met Gly Cys Gln Asp Val Thr Ile Leu Gly Gly Pro Ser Arg
 100 105 110
 Gly Asn Ala Asp Thr Leu Ile Asp Thr Ile Asn Ser Leu Gln Pro Arg
 115 120 125
 Gly Phe Thr Pro Ile Gly Lys Ala Leu Thr Asp Thr Ala Ala Glu Leu
 130 135 140
 Pro Glu Gly Gly Asn Ile Val Leu Val Ser Asp Gly Ile Ala Asn Cys
 145 150 155 160
 Thr Pro Pro Asp Val Cys Glu Val Ala Gln Glu Leu Ala Gln Ser Gly
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 Arg Glu Glu Leu Glu Cys
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 <223> FRXA00791

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 Leu Phe Leu Thr Asp Leu Pro Gln Glu Ser Arg Phe Trp Lys Ile Pro
 1 5 10 15
 gta gag cca ggt gaa acc atc tca gtt tct gcc aac aca gtt acc gac 96
 Val Glu Pro Gly Glu Thr Ile Ser Val Ser Ala Asn Thr Val Thr Asp
 20 25 30
 cca aca gta ctc acc atg ggg caa ggc gga atc aag ctt gaa gcc caa 144
 Pro Thr Val Leu Thr Met Gly Gln Gly Gly Ile Lys Leu Glu Ala Gln
 35 40 45
 ctc cat act gaa gag gct cca caa tac ggc ctg cgt ggt cgg tgc act 192
 Leu His Thr Glu Glu Ala Pro Gln Tyr Gly Leu Arg Gly Arg Cys Thr
 50 55 60
 cgg gtc tca ttt gat aat ttc aag ccc ggc ctt ggt gta cgc gga atc 240
 Arg Val Ser Phe Asp Asn Phe Lys Pro Gly Leu Gly Val Arg Gly Ile
 65 70 75 80
 caa aac gcg tcc gtt gca tca aaa gaa gtg ggc acc aac aac tgt gac 288

Gln	Asn	Ala	Ser	Val	Ala	Ser	Lys	Glu	Val	Gly	Thr	Asn	Asn	Cys	Asp		
				85					90					95			
acc	gat	gcc	atc	tac	ctc	gaa	att	tct	aga	agc	gga	gat	tac	ctc	aac	336	
Thr	Asp	Ala	Ile	Tyr	Leu	Glu	Ile	Ser	Arg	Ser	Gly	Asp	Tyr	Leu	Asn		
			100					105					110				
ggg	cag	gac	att	cca	acg	gaa	atc	acc	atc	gag	cgc	ttc	gga	aaa	gta	384	
Gly	Gln	Asp	Ile	Pro	Thr	Glu	Ile	Thr	Ile	Glu	Arg	Phe	Gly	Lys	Val		
		115					120					125					
gat	gaa	tca	aca	atc	gga	aat	gtc	aca	gag	gaa	cat	agc	tcc	gtc	gat	432	
Asp	Glu	Ser	Thr	Ile	Gly	Asn	Val	Thr	Glu	Glu	His	Ser	Ser	Val	Asp		
	130					135					140						
ctt	acc	gag	gct	gca	gca	tca	gag	gca	cac	cct	gtc	aca	cct	ggc	cag	480	
Leu	Thr	Glu	Ala	Ala	Ala	Ser	Glu	Ala	His	Pro	Val	Thr	Pro	Gly	Gln		
145					150					155					160		
tgg	ttc	aca	tcg	gcc	gct	gat	cta	gat	ccc	gca	ggt	gag	aaa	gtc	tcc	528	
Trp	Phe	Thr	Ser	Ala	Ala	Asp	Leu	Asp	Pro	Ala	Gly	Glu	Lys	Val	Ser		
				165					170					175			
tcc	atc	atc	gtt	cca	gga	gaa	acc	cac	ttc	tat	gcg	ctg	cct	gtc	gac	576	
Ser	Ile	Ile	Val	Pro	Gly	Glu	Thr	His	Phe	Tyr	Ala	Leu	Pro	Val	Asp		
			180					185					190				
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Tyr	Gly	Gln	Glu	Leu	Arg	Ala	Ala	Val	Glu	Thr	Thr	Phe	Asp	Gln	Ile		
		195					200					205					
gac	agt	tcc	gcg	ctt	ggc	acg	cat	ctt	tat	atc	caa	gcg	ttc	agc	cca	672	
Asp	Ser	Ser	Ala	Leu	Gly	Thr	His	Leu	Tyr	Ile	Gln	Ala	Phe	Ser	Pro		
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Asn	Arg	Ala	Glu	Ile	Glu	Leu	Thr	Asn	Arg	Asp	Thr	Ser	Tyr	Ala	Asp		
225					230					235					240		
gac	aac	ggg	ctc	aaa	act	ttt	gga	ttc	ttc	acc	cca	gtg	agt	gca	gca	768	
Asp	Asn	Gly	Leu	Lys	Thr	Phe	Gly	Phe	Phe	Thr	Pro	Val	Ser	Ala	Ala		
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Asn	Leu	Phe	Glu	Lys	Ser	Ser	Gln	Gly	Ile	Ser	Leu	Arg	Ser	Pro	Trp		
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caa	ggt	ggc	acc													828	
Gln	Gly	Gly	Thr														
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<211> 276

<212> PRT

<213> Corynebacterium glutamicum

<400> 234

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 20 25 30
 Pro Thr Val Leu Thr Met Gly Gln Gly Gly Ile Lys Leu Glu Ala Gln
 35 40 45
 Leu His Thr Glu Glu Ala Pro Gln Tyr Gly Leu Arg Gly Arg Cys Thr
 50 55 60
 Arg Val Ser Phe Asp Asn Phe Lys Pro Gly Leu Gly Val Arg Gly Ile
 65 70 75 80
 Gln Asn Ala Ser Val Ala Ser Lys Glu Val Gly Thr Asn Asn Cys Asp
 85 90 95
 Thr Asp Ala Ile Tyr Leu Glu Ile Ser Arg Ser Gly Asp Tyr Leu Asn
 100 105 110
 Gly Gln Asp Ile Pro Thr Glu Ile Thr Ile Glu Arg Phe Gly Lys Val
 115 120 125
 Asp Glu Ser Thr Ile Gly Asn Val Thr Glu Glu His Ser Ser Val Asp
 130 135 140
 Leu Thr Glu Ala Ala Ala Ser Glu Ala His Pro Val Thr Pro Gly Gln
 145 150 155 160
 Trp Phe Thr Ser Ala Ala Asp Leu Asp Pro Ala Gly Glu Lys Val Ser
 165 170 175
 Ser Ile Ile Val Pro Gly Glu Thr His Phe Tyr Ala Leu Pro Val Asp
 180 185 190
 Tyr Gly Gln Glu Leu Arg Ala Ala Val Glu Thr Thr Phe Asp Gln Ile
 195 200 205
 Asp Ser Ser Ala Leu Gly Thr His Leu Tyr Ile Gln Ala Phe Ser Pro
 210 215 220
 Asn Arg Ala Glu Ile Glu Leu Thr Asn Arg Asp Thr Ser Tyr Ala Asp
 225 230 235 240
 Asp Asn Gly Leu Lys Thr Phe Gly Phe Phe Thr Pro Val Ser Ala Ala
 245 250 255
 Asn Leu Phe Glu Lys Ser Ser Gln Gly Ile Ser Leu Arg Ser Pro Trp
 260 265 270
 Gln Gly Gly Thr
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<210> 235
 <211> 1626
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1603)
 <223> RXA01057

<400> 235

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tacgccgatt ggtgaatccc tgcgcaaggc tgcagcagaa ttg cct gaa ggc caa 115
                                   Leu Pro Glu Gly Gln
                                   1 5

tct ggc acc atc gta ttg gtc tct gat ggc att gca acg tgt acg ccc 163
Ser Gly Thr Ile Val Leu Val Ser Asp Gly Ile Ala Thr Cys Thr Pro
              10              15              20

cct cca gtg tgt gag gtt gct gca gaa cta gcc gac cag ggt gtt gat 211
Pro Pro Val Cys Glu Val Ala Ala Glu Leu Ala Asp Gln Gly Val Asp
              25              30              35

ctg gtg att aac act gtt gga ttc aac gtc gat gag tct gct cgc gcg 259
Leu Val Ile Asn Thr Val Gly Phe Asn Val Asp Glu Ser Ala Arg Ala
              40              45              50

gaa ctg gag tgc att gcg cag gct gga aac ggt act tat gca gat gcg 307
Glu Leu Glu Cys Ile Ala Gln Ala Gly Asn Gly Thr Tyr Ala Asp Ala
              55              60              65

agc gat gcg gat tcg ctt gtg gca gaa ctg aag cga gct gcc acc cgc 355
Ser Asp Ala Asp Ser Leu Val Ala Glu Leu Lys Arg Ala Ala Thr Arg
              70              75              80              85

acg gca gtg ggc tat gaa tca gac ctg gaa caa atc gat ggc aac agc 403
Thr Ala Val Gly Tyr Glu Ser Asp Leu Glu Gln Ile Asp Gly Asn Ser
              90              95              100

agc caa aca agc ctg acc cca att cca gat gat gtg gaa ttg ttc aaa 451
Ser Gln Thr Ser Leu Thr Pro Ile Pro Asp Asp Val Glu Leu Phe Lys
              105              110              115

gcc gat ctt cca gca cta gat aat aaa gac ggc gaa gta act cag tac 499
Ala Asp Leu Pro Ala Leu Asp Asn Lys Asp Gly Glu Val Thr Gln Tyr
              120              125              130

tgg tcc att ccc gtt gaa gat tat gaa cgt gtg cag gta acc acc tcg 547
Trp Ser Ile Pro Val Glu Asp Tyr Glu Arg Val Gln Val Thr Thr Ser
              135              140              145

tat gtt gcg cca gtg act ttt gga ctc ggg aac gac tac ctg agc att 595
Tyr Val Ala Pro Val Thr Phe Gly Leu Gly Asn Asp Tyr Leu Ser Ile
              150              155              160              165

agg aat gaa ctg ctt ttc gga gat gaa caa gat caa acc tgt cat cgt 643
Arg Asn Glu Leu Leu Phe Gly Asp Glu Gln Asp Gln Thr Cys His Arg
              170              175              180

tcg atc agc aat gat caa att ctt gat aat tac ggt gcg cgg cct ttg 691
Ser Ile Ser Asn Asp Gln Ile Leu Asp Asn Tyr Gly Ala Arg Pro Leu
              185              190              195

gtt gcc agt gtg gag tca gat gtg att gga gat aag tgc gat acc gat 739
Val Ala Ser Val Glu Ser Asp Val Ile Gly Asp Lys Cys Asp Thr Asp
              200              205              210

gaa ctg gtt ctc gca atc acc aga agc cag cct ttc aat tgg gaa gaa 787

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Glu 215	Leu	Val	Leu	Ala	Ile	Thr 220	Arg	Ser	Gln	Pro	Phe 225	Asn	Trp	Glu	Glu	
gaa	tta	cct	gtt	gag	atc	gtg	gta	aag	cgc	ctt	aat	cac	gcg	gat	acg	835
Glu	Leu	Pro	Val	Glu	Ile	Val	Val	Lys	Arg	Leu	Asn	His	Ala	Asp	Thr	
230					235					240					245	
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Ser	Gly	Leu	Pro	Leu	Gly	Asp	Gln	Gln	Arg	Glu	Ile	Pro	Asp	Leu	Asp	
				250					255					260		
gtg	gcc	gca	gta	caa	aca	tgg	gca	ccc	acc	act	ggc	gga	tct	tgg	ttt	931
Val	Ala	Ala	Val	Gln	Thr	Trp	Ala	Pro	Thr	Thr	Gly	Gly	Ser	Trp	Phe	
				265				270					275			
acc	aac	gct	acg	gag	cta	act	cca	ggt	gaa	ggt	gtt	gaa	gca	gag	atc	979
Thr	Asn	Ala	Thr	Glu	Leu	Thr	Pro	Gly	Glu	Gly	Val	Glu	Ala	Glu	Ile	
		280					285					290				
gta	cct	ggt	gaa	aat	cac	gtt	tat	cgc	ctg	cct	atg	gca	act	ggt	cag	1027
Val	Pro	Gly	Glu	Asn	His	Val	Tyr	Arg	Leu	Pro	Met	Ala	Thr	Gly	Gln	
	295					300					305					
cag	ctg	cat	ggc	ttt	gtg	gaa	gtt	gta	gaa	aac	acg	gca	cca	gat	gat	1075
Gln	Leu	His	Gly	Phe	Val	Glu	Val	Val	Glu	Asn	Thr	Ala	Pro	Asp	Asp	
310					315					320					325	
cct	ggc	gtg	acg	gac	aaa	ttg	ggt	gtt	gca	gtg	tat	tcg	cca	aca	cga	1123
Pro	Gly	Val	Thr	Asp	Lys	Leu	Gly	Val	Ala	Val	Tyr	Ser	Pro	Thr	Arg	
				330					335					340		
cag	gac	gcc	gga	gtt	gat	atg	tgg	acg	gat	atc	gct	cca	cgt	gag	ggc	1171
Gln	Asp	Ala	Gly	Val	Asp	Met	Trp	Thr	Asp	Ile	Ala	Pro	Arg	Glu	Gly	
			345					350					355			
acc	agt	gag	tat	ttt	gca	gcg	cca	gtt	gca	ctg	act	tat	ctg	aat	atg	1219
Thr	Ser	Glu	Tyr	Phe	Ala	Ala	Pro	Val	Ala	Leu	Thr	Tyr	Leu	Asn	Met	
		360					365					370				
ttc	cct	gct	gaa	ggc	gga	ttt	ggc	act	act	tct	aag	gcc	acc	agc	acg	1267
Phe	Pro	Ala	Glu	Gly	Gly	Phe	Gly	Thr	Thr	Ser	Lys	Ala	Thr	Ser	Thr	
	375					380					385					
ttt	acg	ttt	gaa	ggc	gat	tac	tac	ctc	gtt	gtg	cac	tat	gac	gat	ctc	1315
Phe	Thr	Phe	Glu	Gly	Asp	Tyr	Tyr	Leu	Val	Val	His	Tyr	Asp	Asp	Leu	
390					395					400					405	
agt	ggc	agt	aca	atc	aga	gat	gcc	agc	aac	cag	cag	tct	ttt	ccc	ctt	1363
Ser	Gly	Ser	Thr	Ile	Arg	Asp	Ala	Ser	Asn	Gln	Gln	Ser	Phe	Pro	Leu	
				410					415					420		
cgt	tat	cgc	tta	gca	gcg	gat	gct	ttt	ggt	gat	gca	gag	cca	ggc	cca	1411
Arg	Tyr	Arg	Leu	Ala	Ala	Asp	Ala	Phe	Gly	Asp	Ala	Glu	Pro	Gly	Pro	
			425					430					435			
gtg	ttt	gaa	aag	gtt	tct	gca	acc	acc	tca	gaa	tcc	tct	agc	cca	agc	1459
Val	Phe	Glu	Lys	Val	Ser	Ala	Thr	Thr	Ser	Glu	Ser	Ser	Ser	Pro	Ser	
		440					445					450				
act	caa	cca	gat	gag	cca	gct	caa	aat	acc	gca	act	gag	gaa	agc	agc	1507
Thr	Gln	Pro	Asp	Glu	Pro	Ala	Gln	Asn	Thr	Ala	Thr	Glu	Glu	Ser	Ser	

455	460	465	
act gga atc tcc ccg ctc att gtt ggc gct atc gtc gca ctc att ttg			1555
Thr Gly Ile Ser Pro Leu Ile Val Gly Ala Ile Val Ala Leu Ile Leu			
470	475	480	485
gcg ttc gct gcg ttt gcc agc tgg cta gtt ttg aaa ggc cgc aag aaa			1603
Ala Phe Ala Ala Phe Ala Ser Trp Leu Val Leu Lys Gly Arg Lys Lys			
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<211> 501

<212> PRT

<213> Corynebacterium glutamicum

<400> 236

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	20	25	30
Asp Gln Gly Val Asp Leu Val Ile Asn Thr Val Gly Phe Asn Val Asp			
	35	40	45
Glu Ser Ala Arg Ala Glu Leu Glu Cys Ile Ala Gln Ala Gly Asn Gly			
	50	55	60
Thr Tyr Ala Asp Ala Ser Asp Ala Asp Ser Leu Val Ala Glu Leu Lys			
	65	70	75
Arg Ala Ala Thr Arg Thr Ala Val Gly Tyr Glu Ser Asp Leu Glu Gln			
	85	90	95
Ile Asp Gly Asn Ser Ser Gln Thr Ser Leu Thr Pro Ile Pro Asp Asp			
	100	105	110
Val Glu Leu Phe Lys Ala Asp Leu Pro Ala Leu Asp Asn Lys Asp Gly			
	115	120	125
Glu Val Thr Gln Tyr Trp Ser Ile Pro Val Glu Asp Tyr Glu Arg Val			
	130	135	140
Gln Val Thr Thr Ser Tyr Val Ala Pro Val Thr Phe Gly Leu Gly Asn			
	145	150	155
Asp Tyr Leu Ser Ile Arg Asn Glu Leu Leu Phe Gly Asp Glu Gln Asp			
	165	170	175
Gln Thr Cys His Arg Ser Ile Ser Asn Asp Gln Ile Leu Asp Asn Tyr			
	180	185	190
Gly Ala Arg Pro Leu Val Ala Ser Val Glu Ser Asp Val Ile Gly Asp			
	195	200	205
Lys Cys Asp Thr Asp Glu Leu Val Leu Ala Ile Thr Arg Ser Gln Pro			
	210	215	220

Phe Asn Trp Glu Glu Glu Leu Pro Val Glu Ile Val Val Lys Arg Leu
 225 230 235 240
 Asn His Ala Asp Thr Ser Gly Leu Pro Leu Gly Asp Gln Gln Arg Glu
 245 250 255
 Ile Pro Asp Leu Asp Val Ala Ala Val Gln Thr Trp Ala Pro Thr Thr
 260 265 270
 Gly Gly Ser Trp Phe Thr Asn Ala Thr Glu Leu Thr Pro Gly Glu Gly
 275 280 285
 Val Glu Ala Glu Ile Val Pro Gly Glu Asn His Val Tyr Arg Leu Pro
 290 295 300
 Met Ala Thr Gly Gln Gln Leu His Gly Phe Val Glu Val Val Glu Asn
 305 310 315 320
 Thr Ala Pro Asp Asp Pro Gly Val Thr Asp Lys Leu Gly Val Ala Val
 325 330 335
 Tyr Ser Pro Thr Arg Gln Asp Ala Gly Val Asp Met Trp Thr Asp Ile
 340 345 350
 Ala Pro Arg Glu Gly Thr Ser Glu Tyr Phe Ala Ala Pro Val Ala Leu
 355 360 365
 Thr Tyr Leu Asn Met Phe Pro Ala Glu Gly Gly Phe Gly Thr Thr Ser
 370 375 380
 Lys Ala Thr Ser Thr Phe Thr Phe Glu Gly Asp Tyr Tyr Leu Val Val
 385 390 395 400
 His Tyr Asp Asp Leu Ser Gly Ser Thr Ile Arg Asp Ala Ser Asn Gln
 405 410 415
 Gln Ser Phe Pro Leu Arg Tyr Arg Leu Ala Ala Asp Ala Phe Gly Asp
 420 425 430
 Ala Glu Pro Gly Pro Val Phe Glu Lys Val Ser Ala Thr Thr Ser Glu
 435 440 445
 Ser Ser Ser Pro Ser Thr Gln Pro Asp Glu Pro Ala Gln Asn Thr Ala
 450 455 460
 Thr Glu Glu Ser Ser Thr Gly Ile Ser Pro Leu Ile Val Gly Ala Ile
 465 470 475 480
 Val Ala Leu Ile Leu Ala Phe Ala Ala Phe Ala Ser Trp Leu Val Leu
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 Lys Gly Arg Lys Lys
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<220>

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 <223> RXA01055

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 Met Trp Gly Val Val
 1 5
 ctg ggc cct gcc acc ggt aag tat ttg gcg gag ctg atg gct acg ggc 163
 Leu Gly Pro Ala Thr Gly Lys Tyr Leu Ala Glu Leu Met Ala Thr Gly
 10 15 20
 aac acc aac ccg atc atc aag ccg ttc gat ccg ctg cgt taactgcca 212
 Asn Thr Asn Pro Ile Ile Lys Pro Phe Asp Pro Leu Arg
 25 30
 ataattgggtt gaa 225

<210> 238
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 238
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 1 5 10 15
 Leu Met Ala Thr Gly Asn Thr Asn Pro Ile Ile Lys Pro Phe Asp Pro
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 Leu Arg

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1000)
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 Met Ser Ser Ser Gly
 1 5
 aaa gtc att gtt gtt gga gcc ggc ata gtg ggt ctt gcc acc gcc tgg 163
 Lys Val Ile Val Val Gly Ala Gly Ile Val Gly Leu Ala Thr Ala Trp
 10 15 20
 cat tta cag gag cac ggg ttc gag gtg agc gtc ctt gat cgg gat ggt 211
 His Leu Gln Glu His Gly Phe Glu Val Ser Val Leu Asp Arg Asp Gly

25								30				35				
gtc	gct	gca	ggt	tct	tcg	tgg	ggt	aat	gct	ggt	tgg	tta	gcg	ccg	gcg	259
Val	Ala	Ala	Gly	Ser	Ser	Trp	Gly	Asn	Ala	Gly	Trp	Leu	Ala	Pro	Ala	
		40					45					50				
aaa	act	att	ccg	ttg	tcg	gag	ccg	ggg	ctg	tgg	acg	tat	ggt	ccg	aaa	307
Lys	Thr	Ile	Pro	Leu	Ser	Glu	Pro	Gly	Leu	Trp	Thr	Tyr	Gly	Pro	Lys	
	55					60					65					
gag	ctg	ttc	aat	ccg	gtg	tcg	ccg	atg	cat	atg	cca	ctt	cgt	gtg	gat	355
Glu	Leu	Phe	Asn	Pro	Val	Ser	Pro	Met	His	Met	Pro	Leu	Arg	Val	Asp	
	70				75					80					85	
ccc	aaa	ctg	tgg	ctt	ttc	ttg	gcg	caa	ttt	atg	gcg	cag	gct	ttt	caa	403
Pro	Lys	Leu	Trp	Leu	Phe	Leu	Ala	Gln	Phe	Met	Ala	Gln	Ala	Phe	Gln	
				90					95					100		
cgc	aag	tgg	gat	tcc	acg	atg	gcg	gac	ctc	acg	gag	atc	gat	aag	gtc	451
Arg	Lys	Trp	Asp	Ser	Thr	Met	Ala	Asp	Leu	Thr	Glu	Ile	Asp	Lys	Val	
			105					110					115			
gcg	ctc	gaa	gct	ttt	gat	gaa	ctg	tcg	atc	ggt	ggc	gtg	gaa	ggc	ctc	499
Ala	Leu	Glu	Ala	Phe	Asp	Glu	Leu	Ser	Ile	Gly	Gly	Val	Glu	Gly	Leu	
		120					125					130				
acc	cat	gaa	ggt	cca	ttt	gtt	att	ggt	ttt	gag	gaa	gag	cgc	caa	tcg	547
Thr	His	Glu	Gly	Pro	Phe	Val	Ile	Gly	Phe	Glu	Glu	Glu	Arg	Gln	Ser	
	135					140					145					
gcg	ggt	ttc	cgt	aag	gaa	att	gat	ggc	gtg	agc	agg	cac	ggc	cag	aaa	595
Ala	Gly	Phe	Arg	Lys	Glu	Ile	Asp	Gly	Val	Ser	Arg	His	Gly	Gln	Lys	
	150				155					160					165	
gtg	gag	atg	tct	cga	ctg	gag	aat	cca	caa	gag	ttg	gcg	ccg	atg	ctg	643
Val	Glu	Met	Ser	Arg	Leu	Glu	Asn	Pro	Gln	Glu	Leu	Ala	Pro	Met	Leu	
				170					175					180		
aat	gag	caa	att	cag	gtg	gct	tac	cgt	ttg	gaa	ggc	cag	cgt	ttc	atc	691
Asn	Glu	Gln	Ile	Gln	Val	Ala	Tyr	Arg	Leu	Glu	Gly	Gln	Arg	Phe	Ile	
			185					190					195			
gag	ccg	ggt	cca	tac	gtg	cag	tca	ttg	gcg	gat	gct	gtg	gtg	aag	cgt	739
Glu	Pro	Gly	Pro	Tyr	Val	Gln	Ser	Leu	Ala	Asp	Ala	Val	Val	Lys	Arg	
		200					205					210				
ggt	ggc	gtg	atc	cgc	gcc	ggg	gca	gaa	gtt	gtg	cat	gtg	gcg	aag	ggt	787
Gly	Gly	Val	Ile	Arg	Ala	Gly	Ala	Glu	Val	Val	His	Val	Ala	Lys	Gly	
		215				220					225					
gat	cgt	ccc	gcg	gtc	att	ttg	gcg	gat	ggt	agc	cgt	gaa	gaa	gcg	gac	835
Asp	Arg	Pro	Ala	Val	Ile	Leu	Ala	Asp	Gly	Ser	Arg	Glu	Glu	Ala	Asp	
	230				235					240					245	
aag	gtg	gtt	gtg	gca	acg	ggt	gcc	tgg	ctg	ccg	ggt	cta	acg	cgt	gaa	883
Lys	Val	Val	Val	Ala	Thr	Gly	Ala	Trp	Leu	Pro	Gly	Leu	Thr	Arg	Glu	
				250					255					260		
tac	ggt	gtg	aaa	act	ctt	gtt	cag	gct	ggt	cgt	ggc	tat	tcc	ttc	tct	931
Tyr	Gly	Val	Lys	Thr	Leu	Val	Gln	Ala	Gly	Arg	Gly	Tyr	Ser	Phe	Ser	
			265					270					275			

gtg gca acg gat att cct gcc aag cat tct gtg tac ctt ccc cac cac 979
 Val Ala Thr Asp Ile Pro Ala Lys His Ser Val Tyr Leu Pro His His
 280 285 290

cgg cat ggc ctg cac gcc gta tgagggccgt ttccgcattg cgg 1023
 Arg His Gly Leu His Ala Val
 295 300

<210> 240

<211> 300

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 240

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Leu Ala Thr Ala Trp His Leu Gln Glu His Gly Phe Glu Val Ser Val
 20 25 30

Leu Asp Arg Asp Gly Val Ala Ala Gly Ser Ser Trp Gly Asn Ala Gly
 35 40 45

Trp Leu Ala Pro Ala Lys Thr Ile Pro Leu Ser Glu Pro Gly Leu Trp
 50 55 60

Thr Tyr Gly Pro Lys Glu Leu Phe Asn Pro Val Ser Pro Met His Met
 65 70 75 80

Pro Leu Arg Val Asp Pro Lys Leu Trp Leu Phe Leu Ala Gln Phe Met
 85 90 95

Ala Gln Ala Phe Gln Arg Lys Trp Asp Ser Thr Met Ala Asp Leu Thr
 100 105 110

Glu Ile Asp Lys Val Ala Leu Glu Ala Phe Asp Glu Leu Ser Ile Gly
 115 120 125

Gly Val Glu Gly Leu Thr His Glu Gly Pro Phe Val Ile Gly Phe Glu
 130 135 140

Glu Glu Arg Gln Ser Ala Gly Phe Arg Lys Glu Ile Asp Gly Val Ser
 145 150 155 160

Arg His Gly Gln Lys Val Glu Met Ser Arg Leu Glu Asn Pro Gln Glu
 165 170 175

Leu Ala Pro Met Leu Asn Glu Gln Ile Gln Val Ala Tyr Arg Leu Glu
 180 185 190

Gly Gln Arg Phe Ile Glu Pro Gly Pro Tyr Val Gln Ser Leu Ala Asp
 195 200 205

Ala Val Val Lys Arg Gly Gly Val Ile Arg Ala Gly Ala Glu Val Val
 210 215 220

His Val Ala Lys Gly Asp Arg Pro Ala Val Ile Leu Ala Asp Gly Ser
 225 230 235 240

gag ctg ctg tcc gac gtg gtg tgg aca aac aag ggc cct tgc ctt cct 499
Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro
120 125 130

gaa aac ttt gag tgg gtg cgt ggt gct ctg cgg tcc cgc gga ctc atc 547
 Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile
 135 140 145

cac gtc tac tgt gtg gac cgt ctt ccc cgc atg gtc gac tat gtg gtt 595
 His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val
 150 155 160 165

ccc cct gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt gca 643
 Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala
 170 175 180

tac ctt gct ccg ggt acc tct gtg ctg cgt gaa ggt ttc gtg tct ttc 691
 Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe
 185 190 195

aac tcc ggc acc ttg ggt gcc gca aag gtg gaa ggc cgc ctg agt tcc 739
 Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser
 200 205 210

ggt gtg gtc atc ggt gaa ggt tcc gag att gga ctg tct tct act att 787
 Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile
 215 220 225

cag tcc ccg aga gat gaa cag cgc cgc cgt ttg ccg ttg agc atc ggc 835
 Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly
 230 235 240 245

caa aac tgc aac ttt ggt gtc agc tcc gga atc atc gga gtc agt ctg 883
 Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu
 250 255 260

gga gac aat tgc gac atc gga aat aac att gtc ttg gat gga gat acc 931
 Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr
 265 270 275

ccc att tgg ttc gca gcc gat gag gag tta cgc act atc gac tcc atc 979
 Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile
 280 285 290

gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag 1027
 Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu
 295 300 305

cca gtt gcc cgc ctc aaa gct tgacccattt tcataaccag tgc 1071
 Pro Val Ala Arg Leu Lys Ala
 310 315

<210> 242

<211> 316

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

Met Ser Glu Asn Ile Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile
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Ala Met Asp Gly Thr Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile
 20 25 30

Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr
 35 40 45
 Thr Arg Leu Gly Ala Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val
 50 55 60
 Lys Leu Asp Gln Asp Arg Leu Val Glu Gln Val Ala Val Arg Thr Val
 65 70 75 80
 Ile Pro Asp Leu Ser Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu
 85 90 95
 Arg Leu His Leu Leu Ser His Arg Leu Val Arg Pro His Glu Met His
 100 105 110
 Met Gln Asn Thr Leu Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys
 115 120 125
 Gly Pro Cys Leu Pro Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg
 130 135 140
 Ser Arg Gly Leu Ile His Val Tyr Cys Val Asp Arg Leu Pro Arg Met
 145 150 155 160
 Val Asp Tyr Val Val Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg
 165 170 175
 Val Arg Leu Gly Ala Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu
 180 185 190
 Gly Phe Val Ser Phe Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu
 195 200 205
 Gly Arg Leu Ser Ser Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly
 210 215 220
 Leu Ser Ser Thr Ile Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu
 225 230 235 240
 Pro Leu Ser Ile Gly Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile
 245 250 255
 Ile Gly Val Ser Leu Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val
 260 265 270
 Leu Asp Gly Asp Thr Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg
 275 280 285
 Thr Ile Asp Ser Ile Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu
 290 295 300
 Ser Gly Phe His Glu Pro Val Ala Arg Leu Lys Ala
 305 310 315

<210> 243

<211> 771

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(748)

<223> RXS00949

<400> 243

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tggttcaccaa tacgactacg tacttttaaag gagagttgac atg aag gtt ttc atc 115
                                         Met Lys Val Phe Ile
                                         1             5

atc ggc gct gcg ggt ggc atc ggc aat cga ctt tcc agc ctg ctt cac 163
Ile Gly Ala Ala Gly Gly Ile Gly Asn Arg Leu Ser Ser Leu Leu His
                        10                        15                        20

gcc agg gga gat gca gtt agc ggc atg cac cgc aat ctt gag cag gcc 211
Ala Arg Gly Asp Ala Val Ser Gly Met His Arg Asn Leu Glu Gln Ala
                        25                        30                        35

tca aaa atc aca gac act ggg gca act gcc gta ctc ggg gat ctc atc 259
Ser Lys Ile Thr Asp Thr Gly Ala Thr Ala Val Leu Gly Asp Leu Ile
                        40                        45                        50

cac aac agc acg gag gag ctt gcg gag ctt ttc cgc ggt cac gat gcc 307
His Asn Ser Thr Glu Glu Leu Ala Glu Leu Phe Arg Gly His Asp Ala
                        55                        60                        65

atc gta ttt tct gca ggc gcc cac gga aca ggg caa gaa aat acc acg 355
Ile Val Phe Ser Ala Gly Ala His Gly Thr Gly Gln Glu Asn Thr Thr
                        70                        75                        80                        85

ctt atc gac ggc gcc ggc ctc cgt aaa gcc gcc gac gct gcc agc gcg 403
Leu Ile Asp Gly Ala Gly Leu Arg Lys Ala Ala Asp Ala Ala Ser Ala
                        90                        95                        100

gcc aac gtt tca cgc ttc atc ttg gtc tct gcg ttt ccg gaa tcc tcc 451
Ala Asn Val Ser Arg Phe Ile Leu Val Ser Ala Phe Pro Glu Ser Ser
                        105                        110                        115

cgc ggg gag aac acc acc gag aac ttt gag cac tat atg aag gtg aag 499
Arg Gly Glu Asn Thr Thr Glu Asn Phe Glu His Tyr Met Lys Val Lys
                        120                        125                        130

aag tcc gcc gat gtc tac ctc agt cac act gac cta gac tgg gtt att 547
Lys Ser Ala Asp Val Tyr Leu Ser His Thr Asp Leu Asp Trp Val Ile
                        135                        140                        145

gtc cga cca ggc gtg ctt caa gat gag gca ggg gat ggt tta gtc act 595
Val Arg Pro Gly Val Leu Gln Asp Glu Ala Gly Asp Gly Leu Val Thr
                        150                        155                        160                        165

gct ggc tta gcg att aat tac ggc aat gtt gct cgc gat aat gtc gca 643
Ala Gly Leu Ala Ile Asn Tyr Gly Asn Val Ala Arg Asp Asn Val Ala
                        170                        175                        180

gcg ttc att gat gaa gct ctg cat caa ccg cag ttg tca aag atc att 691
Ala Phe Ile Asp Glu Ala Leu His Gln Pro Gln Leu Ser Lys Ile Ile
                        185                        190                        195

gtt gaa ctc acc gac ggt tca act ccg gtg gcg gaa gcc gta gaa cgc 739

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Val Glu Leu Thr Asp Gly Ser Thr Pro Val Ala Glu Ala Val Glu Arg
 200 205 210

ctc atc aag taaagacgaa aagagggaga atg
 Leu Ile Lys
 215

771

<210> 244
 <211> 216
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 244
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 Ser Ser Leu Leu His Ala Arg Gly Asp Ala Val Ser Gly Met His Arg
 20 25 30
 Asn Leu Glu Gln Ala Ser Lys Ile Thr Asp Thr Gly Ala Thr Ala Val
 35 40 45
 Leu Gly Asp Leu Ile His Asn Ser Thr Glu Glu Leu Ala Glu Leu Phe
 50 55 60
 Arg Gly His Asp Ala Ile Val Phe Ser Ala Gly Ala His Gly Thr Gly
 65 70 75 80
 Gln Glu Asn Thr Thr Leu Ile Asp Gly Ala Gly Leu Arg Lys Ala Ala
 85 90 95
 Asp Ala Ala Ser Ala Ala Asn Val Ser Arg Phe Ile Leu Val Ser Ala
 100 105 110
 Phe Pro Glu Ser Ser Arg Gly Glu Asn Thr Thr Glu Asn Phe Glu His
 115 120 125
 Tyr Met Lys Val Lys Lys Ser Ala Asp Val Tyr Leu Ser His Thr Asp
 130 135 140
 Leu Asp Trp Val Ile Val Arg Pro Gly Val Leu Gln Asp Glu Ala Gly
 145 150 155 160
 Asp Gly Leu Val Thr Ala Gly Leu Ala Ile Asn Tyr Gly Asn Val Ala
 165 170 175
 Arg Asp Asn Val Ala Ala Phe Ile Asp Glu Ala Leu His Gln Pro Gln
 180 185 190
 Leu Ser Lys Ile Ile Val Glu Leu Thr Asp Gly Ser Thr Pro Val Ala
 195 200 205
 Glu Ala Val Glu Arg Leu Ile Lys
 210 215

<210> 245
 <211> 594
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(571)

<223> RXS00004

<400> 245

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tgccttccgg aagtattttc caattcccga tgtaggggtca gtg ctg act caa ttg 115
 Val Leu Thr Gln Leu
 1 5

att gaa tca tcg att ttc gac aac gtt gcg agc agg gag tcc tct gaa 163
 Ile Glu Ser Ser Ile Phe Asp Asn Val Ala Ser Arg Glu Ser Ser Glu
 10 15 20

ttt ctc ggc cat gct gcc atc gat cta ctt gct ggc ctt gtc tat gaa 211
 Phe Leu Gly His Ala Ala Ile Asp Leu Leu Ala Gly Leu Val Tyr Glu
 25 30 35

aaa gcc act ccc tat gct cca gat gaa gca ctt aga gtg gca gtt tat 259
 Lys Ala Thr Pro Tyr Ala Pro Asp Glu Ala Leu Arg Val Ala Val Tyr
 40 45 50

ggc tat att cgg gag aac ctt gga tcc tca caa ctt acg gtc gca gct 307
 Gly Tyr Ile Arg Glu Asn Leu Gly Ser Ser Gln Leu Thr Val Ala Ala
 55 60 65

gta gcc ggg gcg cat aga atc gcg gtt cgt acg ttg cat cga tta ttt 355
 Val Ala Gly Ala His Arg Ile Ala Val Arg Thr Leu His Arg Leu Phe
 70 75 80 85

gaa ggc gaa gca tac gga gta gcg gaa tta atc cga cac ctc cga tta 403
 Glu Gly Glu Ala Tyr Gly Val Ala Glu Leu Ile Arg His Leu Arg Leu
 90 95 100

gag gca gta tat gaa gac ctt cgg gat cct cgc ctc cag aac ctg acc 451
 Glu Ala Val Tyr Glu Asp Leu Arg Asp Pro Arg Leu Gln Asn Leu Thr
 105 110 115

att ttg gct atc ggc atg cgc cac ggc att tcc agc caa gct cat tta 499
 Ile Leu Ala Ile Gly Met Arg His Gly Ile Ser Ser Gln Ala His Leu
 120 125 130

aca aga ctg ttt cgc gct aaa tat ggg gta ccg ccg gca gag ttt cgc 547
 Thr Arg Leu Phe Arg Ala Lys Tyr Gly Val Pro Pro Ala Glu Phe Arg
 135 140 145

cga ggg tat att aat agc gct gct tgagggcacc gcaagcgtgg cgc 594
 Arg Gly Tyr Ile Asn Ser Ala Ala
 150 155

<210> 246

<211> 157

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 246

Val Leu Thr Gln Leu Ile Glu Ser Ser Ile Phe Asp Asn Val Ala Ser

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Arg Glu Ser Ser Glu Phe Leu Gly His Ala Ala Ile Asp Leu Leu Ala	20	25	30
Gly Leu Val Tyr Glu Lys Ala Thr Pro Tyr Ala Pro Asp Glu Ala Leu	35	40	45
Arg Val Ala Val Tyr Gly Tyr Ile Arg Glu Asn Leu Gly Ser Ser Gln	50	55	60
Leu Thr Val Ala Ala Val Ala Gly Ala His Arg Ile Ala Val Arg Thr	65	70	75
Leu His Arg Leu Phe Glu Gly Glu Ala Tyr Gly Val Ala Glu Leu Ile	85	90	95
Arg His Leu Arg Leu Glu Ala Val Tyr Glu Asp Leu Arg Asp Pro Arg	100	105	110
Leu Gln Asn Leu Thr Ile Leu Ala Ile Gly Met Arg His Gly Ile Ser	115	120	125
Ser Gln Ala His Leu Thr Arg Leu Phe Arg Ala Lys Tyr Gly Val Pro	130	135	140
Pro Ala Glu Phe Arg Arg Gly Tyr Ile Asn Ser Ala Ala	145	150	155

<210> 247

<211> 783

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(760)

<223> RXS00166

<400> 247

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gacttatcac gatgtccgac ctggatatcc ggctgaggcc	gtg gag tta gcc cgt	115
	Val Glu Leu Ala Arg	
	1 5	

ggg ttt ggc cga gtc ctg gat gtc ggt gca ggt acc gga aaa cta acc	163
Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly Thr Gly Lys Leu Thr	
10 15 20	

agt gag cta aca gct gat cag gtc cta gcc ctt gat cca agc atg gac	211
Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu Asp Pro Ser Met Asp	
25 30 35	

atg ttg cgg gtg ttt cgc tcc gcg ctt ccg gcg gtt ccc tgc tgg caa	259
Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala Val Pro Cys Trp Gln	
40 45 50	

gcg aca gca gaa cac aca gga ata cgt gac aac gcg gtt gat ctg att	307
Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn Ala Val Asp Leu Ile	

55	60	65	
acg tgc gca caa acg tgg cat tgg gtt gac gtg acg gct gcc tca gcg			355
Thr Cys Ala Gln Thr Trp His Trp Val Asp Val Thr Ala Ala Ser Ala			
70	75	80	85
gaa ttt gat cgg gtg att gca cct gag ggt gca gtc ctg ctc gtg tgg			403
Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala Val Leu Leu Val Trp			
	90	95	100
aat aac ctg gac acc tcc atc gcg tgg gta cac cga ctc agt cgc att			451
Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His Arg Leu Ser Arg Ile			
	105	110	115
atg cat gcc ggc gat gta ctc aag ccg gga ttc acc cca gaa acc gca			499
Met His Ala Gly Asp Val Leu Lys Pro Gly Phe Thr Pro Glu Thr Ala			
	120	125	130
gct ccc tgg ata att gat cga gaa att cgc acc acg tgg aat cag cac			547
Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr Thr Trp Asn Gln His			
	135	140	145
ctc acc cct gaa gaa atc atc cag ctc gct cac acg agg tcc tac tgg			595
Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His Thr Arg Ser Tyr Trp			
	150	155	160
tta aac gcg tca gag aaa atc aaa gag cgt gtt gat cag aac ctt cag			643
Leu Asn Ala Ser Glu Lys Ile Lys Glu Arg Val Asp Gln Asn Leu Gln			
	170	175	180
tgg tat ctc tac gag cat ttg ggt ttc agt ccc gac aat cca gtg gaa			691
Trp Tyr Leu Tyr Glu His Leu Gly Phe Ser Pro Asp Asn Pro Val Glu			
	185	190	195
ctt ccc tat cgc tgt gat gca ttt tta ctt tca cgt tcc ggt acc ctg			739
Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser Arg Ser Gly Thr Leu			
	200	205	210
gca ggc aga tct tcc aat ctt taggagccct cgccatgtac ctg			783
Ala Gly Arg Ser Ser Asn Leu			
	215	220	
<210> 248			
<211> 220			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 248			
Val Glu Leu Ala Arg Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly			
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Thr Gly Lys Leu Thr Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu			
	20	25	30
Asp Pro Ser Met Asp Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala			
	35	40	45
Val Pro Cys Trp Gln Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn			
	50	55	60

Ala Val Asp Leu Ile Thr Cys Ala Gln Thr Trp His Trp Val Asp Val
65 70 75 80

Thr Ala Ala Ser Ala Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala
85 90 95

Val Leu Leu Val Trp Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His
100 105 110

Arg Leu Ser Arg Ile Met His Ala Gly Asp Val Leu Lys Pro Gly Phe
115 120 125

Thr Pro Glu Thr Ala Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr
130 135 140

Thr Trp Asn Gln His Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His
145 150 155 160

Thr Arg Ser Tyr Trp Leu Asn Ala Ser Glu Lys Ile Lys Glu Arg Val
165 170 175

Asp Gln Asn Leu Gln Trp Tyr Leu Tyr Glu His Leu Gly Phe Ser Pro
180 185 190

Asp Asn Pro Val Glu Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser
195 200 205

Arg Ser Gly Thr Leu Ala Gly Arg Ser Ser Asn Leu
210 215 220

<210> 249

<211> 1134

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1111)

<223> RXS00288

<400> 249

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acacgggcat gaaacgtacc caagggctaa catcgggggc atg agc gcg caa atg 115
Met Ser Ala Gln Met
1 5

gat acc cct gat ccc act atg tct gct gtt gca atg tta gat tcc atc 163
Asp Thr Pro Asp Pro Thr Met Ser Ala Val Ala Met Leu Asp Ser Ile
10 15 20

cct tct gat caa cca gat ttc ctg atc gat gta gaa gta gat cga cca 211
Pro Ser Asp Gln Pro Asp Phe Leu Ile Asp Val Glu Val Asp Arg Pro
25 30 35

act ccc gga cca cat gat ctg cta gtc cac att gag gcg gtc tca att 259
Thr Pro Gly Pro His Asp Leu Leu Val His Ile Glu Ala Val Ser Ile
40 45 50

aac cct gtt gat acc aag gta cgc atg cgg gcc ggg aag caa aag cat 307

Asn	Pro	Val	Asp	Thr	Lys	Val	Arg	Met	Arg	Ala	Gly	Lys	Gln	Lys	His	
	55					60					65					
cct	aaa	att	tta	ggg	ttt	gat	gct	gca	ggg	gag	gtg	gtg	gct	gtt	gga	355
Pro	Lys	Ile	Leu	Gly	Phe	Asp	Ala	Ala	Gly	Glu	Val	Val	Ala	Val	Gly	
70					75					80					85	
tcg	cag	gtc	acg	ctc	ttc	aat	gtt	ggg	gac	aaa	gtg	ttc	tac	gca	gga	403
Ser	Gln	Val	Thr	Leu	Phe	Asn	Val	Gly	Asp	Lys	Val	Phe	Tyr	Ala	Gly	
				90					95					100		
tcc	aat	cag	cgt	cca	gga	agt	aac	gca	gag	tac	cag	gtg	gtg	gat	gaa	451
Ser	Asn	Gln	Arg	Pro	Gly	Ser	Asn	Ala	Glu	Tyr	Gln	Val	Val	Asp	Glu	
			105					110						115		
cgg	ctg	gtg	ggg	cac	gca	cca	caa	agc	ttg	ggg	gca	cac	gac	gcc	gct	499
Arg	Leu	Val	Gly	His	Ala	Pro	Gln	Ser	Leu	Gly	Ala	His	Asp	Ala	Ala	
		120					125						130			
gct	ctc	cca	ctt	gtc	gcg	ctc	act	gca	tgg	gag	tca	ctt	ttt	gac	cga	547
Ala	Leu	Pro	Leu	Val	Ala	Leu	Thr	Ala	Trp	Glu	Ser	Leu	Phe	Asp	Arg	
	135					140					145					
ttg	gga	gta	act	cag	tca	act	act	gga	aca	ctg	ttg	gtc	ttg	ggc	ggg	595
Leu	Gly	Val	Thr	Gln	Ser	Thr	Thr	Gly	Thr	Leu	Leu	Val	Leu	Gly	Gly	
150					155					160					165	
tca	gga	ggg	gtg	cct	tca	gct	ctt	att	caa	ctt	gct	cga	gct	ctc	act	643
Ser	Gly	Gly	Val	Pro	Ser	Ala	Leu	Ile	Gln	Leu	Ala	Arg	Ala	Leu	Thr	
				170					175						180	
ggg	ctg	aaa	gta	gtg	gca	aca	gct	tct	cgc	cct	gaa	tca	caa	gaa	tgg	691
Gly	Leu	Lys	Val	Val	Ala	Thr	Ala	Ser	Arg	Pro	Glu	Ser	Gln	Glu	Trp	
			185					190						195		
gtg	aca	aag	ctc	ggg	gct	cat	gag	gtg	att	gat	cac	tcc	aag	gat	ttg	739
Val	Thr	Lys	Leu	Gly	Ala	His	Glu	Val	Ile	Asp	His	Ser	Lys	Asp	Leu	
		200					205					210				
agt	gag	caa	atc	tcc	gac	gtg	gat	ttt	gtt	ttc	agc	tcg	tgg	act	act	787
Ser	Glu	Gln	Ile	Ser	Asp	Val	Asp	Phe	Val	Phe	Ser	Ser	Trp	Thr	Thr	
	215					220					225					
ggg	cgt	gaa	gta	gag	ctc	gcc	acg	ttg	atg	aaa	ccc	cag	tcc	cac	cta	835
Gly	Arg	Glu	Val	Glu	Leu	Ala	Thr	Leu	Met	Lys	Pro	Gln	Ser	His	Leu	
230					235					240					245	
gtg	ctc	atc	gat	gat	cca	gtg	gat	ccc	aat	ttg	ggc	gct	ttt	aag	caa	883
Val	Leu	Ile	Asp	Asp	Pro	Val	Asp	Pro	Asn	Leu	Gly	Ala	Phe	Lys	Gln	
				250					255					260		
aaa	gcg	atc	gct	ttg	cac	tgg	gag	ttc	atg	ttt	acc	cgc	gct	atg	ttc	931
Lys	Ala	Ile	Ala	Leu	His	Trp	Glu	Phe	Met	Phe	Thr	Arg	Ala	Met	Phe	
			265					270					275			
aac	act	cct	gat	atg	ggg	gaa	caa	ggg	aaa	att	ctg	aat	aag	atc	gcc	979
Asn	Thr	Pro	Asp	Met	Gly	Glu	Gln	Gly	Lys	Ile	Leu	Asn	Lys	Ile	Ala	
		280					285					290				
gac	atg	gtt	gat	cgg	ggg	cag	ttt	gag	tcc	gtg	aca	gca	acg	gtg	ctg	1027
Asp	Met	Val	Asp	Arg	Gly	Gln	Phe	Glu	Ser	Val	Thr	Ala	Thr	Val	Leu	

295	300	305	
gat ggg ctc aac gct gca aac atc atg gag ggg cac cgg ctc gtt gag			1075
Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly His Arg Leu Val Glu			
310	315	320	325
cag ggt aaa acc tca gga aaa att gtt gtg agg gta taaagaggac			1121
Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg Val			
	330	335	
ttgaaaaatg cac			1134

<210> 250

<211> 337

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 250

Met Ser Ala Gln Met Asp Thr Pro Asp Pro Thr Met Ser Ala Val Ala			
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Met Leu Asp Ser Ile Pro Ser Asp Gln Pro Asp Phe Leu Ile Asp Val			
	20	25	30
Glu Val Asp Arg Pro Thr Pro Gly Pro His Asp Leu Leu Val His Ile			
	35	40	45
Glu Ala Val Ser Ile Asn Pro Val Asp Thr Lys Val Arg Met Arg Ala			
	50	55	60
Gly Lys Gln Lys His Pro Lys Ile Leu Gly Phe Asp Ala Ala Gly Glu			
	65	70	75
Val Val Ala Val Gly Ser Gln Val Thr Leu Phe Asn Val Gly Asp Lys			
	85	90	95
Val Phe Tyr Ala Gly Ser Asn Gln Arg Pro Gly Ser Asn Ala Glu Tyr			
	100	105	110
Gln Val Val Asp Glu Arg Leu Val Gly His Ala Pro Gln Ser Leu Gly			
	115	120	125
Ala His Asp Ala Ala Ala Leu Pro Leu Val Ala Leu Thr Ala Trp Glu			
	130	135	140
Ser Leu Phe Asp Arg Leu Gly Val Thr Gln Ser Thr Thr Gly Thr Leu			
	145	150	155
Leu Val Leu Gly Gly Ser Gly Gly Val Pro Ser Ala Leu Ile Gln Leu			
	165	170	175
Ala Arg Ala Leu Thr Gly Leu Lys Val Val Ala Thr Ala Ser Arg Pro			
	180	185	190
Glu Ser Gln Glu Trp Val Thr Lys Leu Gly Ala His Glu Val Ile Asp			
	195	200	205
His Ser Lys Asp Leu Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe			
	210	215	220

Ser Ser Trp Thr Thr Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys
 225 230 235 240

Pro Gln Ser His Leu Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu
 245 250 255

Gly Ala Phe Lys Gln Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe
 260 265 270

Thr Arg Ala Met Phe Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile
 275 280 285

Leu Asn Lys Ile Ala Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val
 290 295 300

Thr Ala Thr Val Leu Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly
 305 310 315 320

His Arg Leu Val Glu Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg
 325 330 335

Val

<210> 251
 <211> 1347
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1324)
 <223> RXS01114

<400> 251
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ttcgacagat ctctctgcac tctaaattaa ggatcaaaaa atg aac cct caa gat 115
 Met Asn Pro Gln Asp
 1 5

att gtc atc tgt tcc cca ttg cgc acc cca gtt ggt gct tac ggc gga 163
 Ile Val Ile Cys Ser Pro Leu Arg Thr Pro Val Gly Ala Tyr Gly Gly
 10 15 20

tcc ttc acc ggc gtc cct gtt gaa gaa ttg gcc acc acc gtg atc aac 211
 Ser Phe Thr Gly Val Pro Val Glu Glu Leu Ala Thr Thr Val Ile Asn
 25 30 35

gcg atc gtt gag gca acc ggc atc acc ggc gac gat gtg gac gat ctg 259
 Ala Ile Val Glu Ala Thr Gly Ile Thr Gly Asp Asp Val Asp Asp Leu
 40 45 50

atc ctc ggc cag gca tcc ccc aac ggt gcg gct cca gca ctg ggc cgt 307
 Ile Leu Gly Gln Ala Ser Pro Asn Gly Ala Ala Pro Ala Leu Gly Arg
 55 60 65

gtt gtt gct cta gat tcc aag ctt ggc caa aac gtt cca ggc atg cag 355
 Val Val Ala Leu Asp Ser Lys Leu Gly Gln Asn Val Pro Gly Met Gln
 70 75 80 85

ctt gat cgc cgc tgt ggt tcc ggc ctg cag gca atc gtc acc gct gct	403
Leu Asp Arg Arg Cys Gly Ser Gly Leu Gln Ala Ile Val Thr Ala Ala	
90 95 100	
gca cac gtt gca tcc ggc gct gct gat ctg atc atc gca ggt ggc gca	451
Ala His Val Ala Ser Gly Ala Ala Asp Leu Ile Ile Ala Gly Gly Ala	
105 110 115	
gaa tcc atg agc cgc gtt gag tac acc gtg tcc ggc gat atc cgt tgg	499
Glu Ser Met Ser Arg Val Glu Tyr Thr Val Ser Gly Asp Ile Arg Trp	
120 125 130	
ggt gtc aag ggc ggc gac atg cag ctt cgt gac cgc ctt gca gaa gca	547
Gly Val Lys Gly Gly Asp Met Gln Leu Arg Asp Arg Leu Ala Glu Ala	
135 140 145	
cgc gaa acc gct ggc gga cgc aac cac ccg atc cct ggt ggc atg atc	595
Arg Glu Thr Ala Gly Gly Arg Asn His Pro Ile Pro Gly Gly Met Ile	
150 155 160 165	
gag acc gct gag aac ctg cgt cgc gaa tac ggc atc tcc cgc gag gag	643
Glu Thr Ala Glu Asn Leu Arg Arg Glu Tyr Gly Ile Ser Arg Glu Glu	
170 175 180	
cag gac aag atc tcc gca gcg tcc cag cag cgt tgg ggc aag gct gct	691
Gln Asp Lys Ile Ser Ala Ala Ser Gln Gln Arg Trp Gly Lys Ala Ala	
185 190 195	
gat gcg ggg ctt ttc gac gac gag atc gtg cca gtc acc gtc cct gcc	739
Asp Ala Gly Leu Phe Asp Asp Glu Ile Val Pro Val Thr Val Pro Ala	
200 205 210	
aag aag cgc ggc cag gag cca acc atc gtt tct cga gac gag cat ggt	787
Lys Lys Arg Gly Gln Glu Pro Thr Ile Val Ser Arg Asp Glu His Gly	
215 220 225	
cga cca gga aca acc gtc gaa aag ctt gct gct ttg cgc ccc atc atg	835
Arg Pro Gly Thr Thr Val Glu Lys Leu Ala Ala Leu Arg Pro Ile Met	
230 235 240 245	
ggc cgc cag gat gcg gaa gca acc gtc acc gct ggc aac gcg tcc ggc	883
Gly Arg Gln Asp Ala Glu Ala Thr Val Thr Ala Gly Asn Ala Ser Gly	
250 255 260	
caa aat gat ggc gct gct gcc gtc atc gtg acc act cgc gcc aag gcc	931
Gln Asn Asp Gly Ala Ala Ala Val Ile Val Thr Thr Arg Ala Lys Ala	
265 270 275	
gag gag aag ggc ctg cgc cca gtc atg cgt ttg gct ggc tgg tct gtg	979
Glu Glu Lys Gly Leu Arg Pro Val Met Arg Leu Ala Gly Trp Ser Val	
280 285 290	
gct gct gtt ccc cca gag acc atg ggt att gga cct gtt cct gcc acc	1027
Ala Ala Val Pro Pro Glu Thr Met Gly Ile Gly Pro Val Pro Ala Thr	
295 300 305	
aag aag gtc ctg gat cgt ttg ggc ctt acc ctg gag gac atc ggc gcg	1075
Lys Lys Val Leu Asp Arg Leu Gly Leu Thr Leu Glu Asp Ile Gly Ala	
310 315 320 325	

```

atc gaa ctc aac gaa gct ttc gca gct cag gca ctg tct gtg ctg aag 1123
Ile Glu Leu Asn Glu Ala Phe Ala Ala Gln Ala Leu Ser Val Leu Lys
      330                      335                      340

gaa tgg aac att tct tgg gaa gat gag cgc gtc aac cca ctg ggt tcc 1171
Glu Trp Asn Ile Ser Trp Glu Asp Glu Arg Val Asn Pro Leu Gly Ser
      345                      350                      355

ggt att tcc atg gga cac cca gtc ggt gcc acc ggt gct cgc atg gca 1219
Gly Ile Ser Met Gly His Pro Val Gly Ala Thr Gly Ala Arg Met Ala
      360                      365                      370

gta acc ttg gct cac cgc atg cag cgt gaa aac act cag tac gga ctg 1267
Val Thr Leu Ala His Arg Met Gln Arg Glu Asn Thr Gln Tyr Gly Leu
      375                      380                      385

gcc acc atg tgc atc ggt ggc ggc cag ggt ctt gca gct gtc ttt gaa 1315
Ala Thr Met Cys Ile Gly Gly Gly Gln Gly Leu Ala Ala Val Phe Glu
      390                      395                      400                      405

aag gag aac taaaaatggc tattttgcac agc 1347
Lys Glu Asn

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<210> 252

<211> 408

<212> PRT

<213> Corynebacterium glutamicum...

<400> 252

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Met Asn Pro Gln Asp Ile Val Ile Cys Ser Pro Leu Arg Thr Pro Val
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Gly Ala Tyr Gly Gly Ser Phe Thr Gly Val Pro Val Glu Glu Leu Ala
      20                      25                      30

Thr Thr Val Ile Asn Ala Ile Val Glu Ala Thr Gly Ile Thr Gly Asp
      35                      40                      45

Asp Val Asp Asp Leu Ile Leu Gly Gln Ala Ser Pro Asn Gly Ala Ala
      50                      55                      60

Pro Ala Leu Gly Arg Val Val Ala Leu Asp Ser Lys Leu Gly Gln Asn
      65                      70                      75                      80

Val Pro Gly Met Gln Leu Asp Arg Arg Cys Gly Ser Gly Leu Gln Ala
      85                      90                      95

Ile Val Thr Ala Ala Ala His Val Ala Ser Gly Ala Ala Asp Leu Ile
      100                      105                      110

Ile Ala Gly Gly Ala Glu Ser Met Ser Arg Val Glu Tyr Thr Val Ser
      115                      120                      125

Gly Asp Ile Arg Trp Gly Val Lys Gly Gly Asp Met Gln Leu Arg Asp
      130                      135                      140

Arg Leu Ala Glu Ala Arg Glu Thr Ala Gly Gly Arg Asn His Pro Ile
      145                      150                      155                      160

```

Pro Gly Gly Met Ile Glu Thr Ala Glu Asn Leu Arg Arg Glu Tyr Gly
 165 170 175
 Ile Ser Arg Glu Glu Gln Asp Lys Ile Ser Ala Ala Ser Gln Gln Arg
 180 185 190
 Trp Gly Lys Ala Ala Asp Ala Gly Leu Phe Asp Asp Glu Ile Val Pro
 195 200 205
 Val Thr Val Pro Ala Lys Lys Arg Gly Gln Glu Pro Thr Ile Val Ser
 210 215 220
 Arg Asp Glu His Gly Arg Pro Gly Thr Thr Val Glu Lys Leu Ala Ala
 225 230 235 240
 Leu Arg Pro Ile Met Gly Arg Gln Asp Ala Glu Ala Thr Val Thr Ala
 245 250 255
 Gly Asn Ala Ser Gly Gln Asn Asp Gly Ala Ala Ala Val Ile Val Thr
 260 265 270
 Thr Arg Ala Lys Ala Glu Glu Lys Gly Leu Arg Pro Val Met Arg Leu
 275 280 285
 Ala Gly Trp Ser Val Ala Ala Val Pro Pro Glu Thr Met Gly Ile Gly
 290 295 300
 Pro Val Pro Ala Thr Lys Lys Val Leu Asp Arg Leu Gly Leu Thr Leu
 305 310 315 320
 Glu Asp Ile Gly Ala Ile Glu Leu Asn Glu Ala Phe Ala Ala Gln Ala
 325 330 335
 Leu Ser Val Leu Lys Glu Trp Asn Ile Ser Trp Glu Asp Glu Arg Val
 340 345 350
 Asn Pro Leu Gly Ser Gly Ile Ser Met Gly His Pro Val Gly Ala Thr
 355 360 365
 Gly Ala Arg Met Ala Val Thr Leu Ala His Arg Met Gln Arg Glu Asn
 370 375 380
 Thr Gln Tyr Gly Leu Ala Thr Met Cys Ile Gly Gly Gly Gln Gly Leu
 385 390 395 400
 Ala Ala Val Phe Glu Lys Glu Asn
 405

<210> 253

<211> 554

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(531)

<223> RXS01205

<400> 253

gta tcg gcc tat ccg ccg gcc atc atc gca gcg gct ctc gta gga att 48

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Val Ser Ala Tyr Pro Pro Ala Ile Ile Ala Ala Ala Leu Val Gly Ile
  1          5          10          15
tgc gcg gga gtt ttg ccc cat aat ttt gaa ccc tcg cga ata ttt atg   96
Cys Ala Gly Val Leu Pro His Asn Phe Glu Pro Ser Arg Ile Phe Met
          20          25          30
ggc gat tcc ggc tcc atg ctc atc ggc ctg ctg ttg gct gca gca tcg   144
Gly Asp Ser Gly Ser Met Leu Ile Gly Leu Leu Leu Ala Ala Ala Ser
          35          40          45
acc tca gcg tca gga aaa atc aac atg agc ctg tat ggc gca gct gat   192
Thr Ser Ala Ser Gly Lys Ile Asn Met Ser Leu Tyr Gly Ala Ala Asp
          50          55          60
ttt atc gca ttg atc tca ccc atc atc gtt gtt ctc gcc gcc gtg gcc   240
Phe Ile Ala Leu Ile Ser Pro Ile Ile Val Val Leu Ala Ala Val Ala
          65          70          75          80
atc cca ctg ctc gac ctc gtg atg gca gtg gtt agg cgc gtg ggc agg   288
Ile Pro Leu Leu Asp Leu Val Met Ala Val Val Arg Arg Val Gly Arg
          85          90          95
gga gca tca ccc ttt tcc ccg gac aaa atg cat ctg cac cac cga ctg   336
Gly Ala Ser Pro Phe Ser Pro Asp Lys Met His Leu His His Arg Leu
          100          105          110
ctg tcc atc gga cac acc cat agg cgc gtg gtc cta gtg ctc tac acc   384
Leu Ser Ile Gly His Thr His Arg Arg Val Val Leu Val Leu Tyr Thr
          115          120          125
tgg gcg agc gcc gtg gca ttc ggc gca gtg agc ttc tcc gtc gtt ccg   432
Trp Ala Ser Ala Val Ala Phe Gly Ala Val Ser Phe Ser Val Val Pro
          130          135          140
cca ctg ttt gcc acc gga tcg agc atc tgt ggc atc ctc atc gcc gtc   480
Pro Leu Phe Ala Thr Gly Ser Ser Ile Cys Gly Ile Leu Ile Ala Val
          145          150          155          160
gct gtc aca gcc gtg cca gtg atg aaa agc cgg cga gcc gcc aaa ctt   528
Ala Val Thr Ala Val Pro Val Met Lys Ser Arg Arg Ala Ala Lys Leu
          165          170          175
gat taagtgattg tcactttgga ttg   554
Asp

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<210> 254

<211> 177

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 254

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Val Ser Ala Tyr Pro Pro Ala Ile Ile Ala Ala Ala Leu Val Gly Ile
  1          5          10          15
Cys Ala Gly Val Leu Pro His Asn Phe Glu Pro Ser Arg Ile Phe Met
          20          25          30
Gly Asp Ser Gly Ser Met Leu Ile Gly Leu Leu Leu Ala Ala Ala Ser

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35					40					45					
Thr	Ser	Ala	Ser	Gly	Lys	Ile	Asn	Met	Ser	Leu	Tyr	Gly	Ala	Ala	Asp
50						55					60				
Phe	Ile	Ala	Leu	Ile	Ser	Pro	Ile	Ile	Val	Val	Leu	Ala	Ala	Val	Ala
65					70					75					80
Ile	Pro	Leu	Leu	Asp	Leu	Val	Met	Ala	Val	Val	Arg	Arg	Val	Gly	Arg
				85					90					95	
Gly	Ala	Ser	Pro	Phe	Ser	Pro	Asp	Lys	Met	His	Leu	His	His	Arg	Leu
			100					105					110		
Leu	Ser	Ile	Gly	His	Thr	His	Arg	Arg	Val	Val	Leu	Val	Leu	Tyr	Thr
		115					120					125			
Trp	Ala	Ser	Ala	Val	Ala	Phe	Gly	Ala	Val	Ser	Phe	Ser	Val	Val	Pro
	130					135					140				
Pro	Leu	Phe	Ala	Thr	Gly	Ser	Ser	Ile	Cys	Gly	Ile	Leu	Ile	Ala	Val
145					150					155					160
Ala	Val	Thr	Ala	Val	Pro	Val	Met	Lys	Ser	Arg	Arg	Ala	Ala	Lys	Leu
				165				170						175	

Asp

<210> 255
 <211> 564
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(541)
 <223> RXS01269

<400> 255
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tccgattcta tttcgtcaac caccgacctg gaaagacggt gtg gta ttt gag atg 115
 Val Val Phe Glu Met
 1 5

att aag ttt cga acc atg ctt gaa cca gat gaa aaa cat gta act gat 163
 Ile Lys Phe Arg Thr Met Leu Glu Pro Asp Glu Lys His Val Thr Asp
 10 15 20

gaa cag cgt cta act aaa gtt gga aag ctt ctg cgg gaa acg agt tta 211
 Glu Gln Arg Leu Thr Lys Val Gly Lys Leu Leu Arg Glu Thr Ser Leu
 25 30 35

gat gag tta cct aca ctc tgg aat gta ttt aaa ggt gat atg agc ctt 259
 Asp Glu Leu Pro Thr Leu Trp Asn Val Phe Lys Gly Asp Met Ser Leu
 40 45 50

gta ggg cct cga cct ttg ctt gtt agc tat ctg gaa cat tac tct tct 307
 Val Gly Pro Arg Pro Leu Leu Val Ser Tyr Leu Glu His Tyr Ser Ser

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      55              60              65
gaa caa gct cga cgc cat gaa gtt cgt cct ggg att act ggt ttg gct 355
Glu Gln Ala Arg Arg His Glu Val Arg Pro Gly Ile Thr Gly Leu Ala
 70              75              80              85

cag gtg aat ggc cgt aat caa act act tgg gat gaa cga ctt aag ttg 403
Gln Val Asn Gly Arg Asn Gln Thr Thr Trp Asp Glu Arg Leu Lys Leu
      90              95              100

gat gtc gaa tat gtg gat cgc tgt agt ttg aaa cta gat ttc aaa ata 451
Asp Val Glu Tyr Val Asp Arg Cys Ser Leu Lys Leu Asp Phe Lys Ile
      105              110              115

tta atc gcc act gta aaa aca gtt ctt tct aaa aag ggc att agt aat 499
Leu Ile Ala Thr Val Lys Thr Val Leu Ser Lys Lys Gly Ile Ser Asn
      120              125              130

gaa ggt cat gtc acg atg cca tcc ttc att gaa gaa aga aaa 541
Glu Gly His Val Thr Met Pro Ser Phe Ile Glu Glu Arg Lys
      135              140              145

tagcaggtaa aaattttact ttc 564

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<210> 256

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 256

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Val Val Phe Glu Met Ile Lys Phe Arg Thr Met Leu Glu Pro Asp Glu
  1              5              10              15

Lys His Val Thr Asp Glu Gln Arg Leu Thr Lys Val Gly Lys Leu Leu
      20              25              30

Arg Glu Thr Ser Leu Asp Glu Leu Pro Thr Leu Trp Asn Val Phe Lys
      35              40              45

Gly Asp Met Ser Leu Val Gly Pro Arg Pro Leu Leu Val Ser Tyr Leu
      50              55              60

Glu His Tyr Ser Ser Glu Gln Ala Arg Arg His Glu Val Arg Pro Gly
      65              70              75              80

Ile Thr Gly Leu Ala Gln Val Asn Gly Arg Asn Gln Thr Thr Trp Asp
      85              90              95

Glu Arg Leu Lys Leu Asp Val Glu Tyr Val Asp Arg Cys Ser Leu Lys
      100              105              110

Leu Asp Phe Lys Ile Leu Ile Ala Thr Val Lys Thr Val Leu Ser Lys
      115              120              125

Lys Gly Ile Ser Asn Glu Gly His Val Thr Met Pro Ser Phe Ile Glu
      130              135              140

Glu Arg Lys
145

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<400> 257																	
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ttactgcagg gatcctgcga gatcgagtaa acgcctaaag atg acg tcg aaa agc																	115
Met Thr Ser Lys Ser																	
1 5																	
att agc ggc aag cgc ccg aat ctg ccg tcg ctc act gga gcg cgg tgg																	163
Ile	Ser	Gly	Lys	Arg	Pro	Asn	Leu	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Trp		
10 15 20																	
ctc gcg gcg ctc gct gtt tat ttt ttg cat gcg ttg gtg ttt ttg tcg																	211
Leu	Ala	Ala	Leu	Ala	Val	Tyr	Phe	Leu	His	Ala	Leu	Val	Phe	Leu	Ser		
25 30 35																	
gtg tat ccg ttc cag cag tcg gaa ctg ttt gcc aca atc cat aaa ttt																	259
Val	Tyr	Pro	Phe	Gln	Gln	Ser	Glu	Leu	Phe	Ala	Thr	Ile	His	Lys	Phe		
40 45 50																	
gtc ccc atg cag ctg ggt tca gct ggt gta acc ttc ttc ttt atc ttg																	307
Val	Pro	Met	Gln	Leu	Gly	Ser	Ala	Gly	Val	Thr	Phe	Phe	Phe	Ile	Leu		
55 60 65																	
tcc gga ttt ttg atc tat tgg tca aat agc cag ctc aag ggc atg aag																	355
Ser	Gly	Phe	Leu	Ile	Tyr	Trp	Ser	Asn	Ser	Gln	Leu	Lys	Gly	Met	Lys		
70 75 80 85																	
aat gtg ctg tat tac tgc aag cgc cgc atc acc aag att tat ccc atg																	403
Asn	Val	Leu	Tyr	Tyr	Cys	Lys	Arg	Arg	Ile	Thr	Lys	Ile	Tyr	Pro	Met		
90 95 100																	
cac ttg att gcg ttg ccg atg ttt att gag gcg tcg gcg aag ttc acg																	451
His	Leu	Ile	Ala	Leu	Pro	Met	Phe	Ile	Glu	Ala	Ser	Ala	Lys	Phe	Thr		
105 110 115																	
act aca ggc att acc tgg gtg ctg att ttg cgc gag taaagctgtg																	497
Thr	Thr	Gly	Ile	Thr	Trp	Val	Leu	Ile	Leu	Arg	Glu						
120 125																	
gctgcggaat gcg																	510

<400> 258
Met Thr Ser Lys Ser Ile Ser Gly Lys Arg Pro Asn Leu Pro Ser Leu
1 5 10 15

Thr Gly Ala Arg Trp Leu Ala Ala Leu Ala Val Tyr Phe Leu His Ala
 20 25 30
 Leu Val Phe Leu Ser Val Tyr Pro Phe Gln Gln Ser Glu Leu Phe Ala
 35 40 45
 Thr Ile His Lys Phe Val Pro Met Gln Leu Gly Ser Ala Gly Val Thr
 50 55 60
 Phe Phe Phe Ile Leu Ser Gly Phe Leu Ile Tyr Trp Ser Asn Ser Gln
 65 70 75 80
 Leu Lys Gly Met Lys Asn Val Leu Tyr Tyr Cys Lys Arg Arg Ile Thr
 85 90 95
 Lys Ile Tyr Pro Met His Leu Ile Ala Leu Pro Met Phe Ile Glu Ala
 100 105 110
 Ser Ala Lys Phe Thr Thr Thr Gly Ile Thr Trp Val Leu Ile Leu Arg
 115 120 125
 Glu

<210> 259
 <211> 774
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(751)
 <223> RXS01491

<400> 259
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 gggcagcatg tgtggccata tccagtgatg gaggtggaca atg ctg gat gag tct 115
 Met Leu Asp Glu Ser
 1 5
 ttg ttt cca aat tcg gca aag ttt tct ttc att aaa act ggc gat gct 163
 Leu Phe Pro Asn Ser Ala Lys Phe Ser Phe Ile Lys Thr Gly Asp Ala
 10 15 20
 gtt aat tta gac cat ttc cat cag ttg cat ccg ttg gaa aag gca ctg 211
 Val Asn Leu Asp His Phe His Gln Leu His Pro Leu Glu Lys Ala Leu
 25 30 35
 gta gcg cac tcg gtt gat att aga aaa gca gag ttt gga gat gcc agg 259
 Val Ala His Ser Val Asp Ile Arg Lys Ala Glu Phe Gly Asp Ala Arg
 40 45 50
 tgg tgt gca cat cag gca ctc caa gct ttg gga cga gat agc ggt gat 307
 Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly Arg Asp Ser Gly Asp
 55 60 65
 ccc att ttg cgt ggg gaa cga gga atg cca ttg tgg cct tct tcg gtg 355
 Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu Trp Pro Ser Ser Val

70	75	80	85	
tct ggt tca ttg acc cac act gac gga ttc cga gct gct gtt gtg gcg				403
Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg Ala Ala Val Val Ala				
	90	95	100	
cca cga ttg ttg gtg cgt tct atg gga ttg gat gcc gaa cct gcg gag				451
Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp Ala Glu Pro Ala Glu				
	105	110	115	
ccg ttg ccc aag gat gtt ttg ggt tca atc gct cgg gtg ggg gag att				499
Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala Arg Val Gly Glu Ile				
	120	125	130	
cct caa ctt aag cgc ttg gag gaa caa ggt gtg cac tgc gcg gat cgc				547
Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val His Cys Ala Asp Arg				
	135	140	145	
ctg ctg ttt tgt gcc aag gaa gca aca tac aaa gcg tgg ttc ccg ctg				595
Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys Ala Trp Phe Pro Leu				
	150	155	160	165
acg cat agg tgg ctt ggt ttt gaa caa gct gag atc gac ttg cgt gat				643
Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu Ile Asp Leu Arg Asp				
	170	175	180	
gat ggc act ttt gtg tcc tat ttg ctg gtt cga cca act cca gtg ccg				691
Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg Pro Thr Pro Val Pro				
	185	190	195	
ttt att tca ggt aaa tgg gta ctg cgt gat ggt tat gtc ata gct gcg				739
Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly Tyr Val Ile Ala Ala				
	200	205	210	
act gca gtg act tgaactggat ggagaggata cct				774
Thr Ala Val Thr				
	215			

<210> 260

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 260

Met	Leu	Asp	Glu	Ser	Leu	Phe	Pro	Asn	Ser	Ala	Lys	Phe	Ser	Phe	Ile
1				5					10					15	

Lys	Thr	Gly	Asp	Ala	Val	Asn	Leu	Asp	His	Phe	His	Gln	Leu	His	Pro
		20						25					30		

Leu	Glu	Lys	Ala	Leu	Val	Ala	His	Ser	Val	Asp	Ile	Arg	Lys	Ala	Glu
		35					40					45			

Phe	Gly	Asp	Ala	Arg	Trp	Cys	Ala	His	Gln	Ala	Leu	Gln	Ala	Leu	Gly
	50					55					60				

Arg	Asp	Ser	Gly	Asp	Pro	Ile	Leu	Arg	Gly	Glu	Arg	Gly	Met	Pro	Leu
65					70					75				80	

Trp	Pro	Ser	Ser	Val	Ser	Gly	Ser	Leu	Thr	His	Thr	Asp	Gly	Phe	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85					90					95					
Ala	Ala	Val	Val	Ala	Pro	Arg	Leu	Leu	Val	Arg	Ser	Met	Gly	Leu	Asp
			100					105					110		
Ala	Glu	Pro	Ala	Glu	Pro	Leu	Pro	Lys	Asp	Val	Leu	Gly	Ser	Ile	Ala
		115					120					125			
Arg	Val	Gly	Glu	Ile	Pro	Gln	Leu	Lys	Arg	Leu	Glu	Glu	Gln	Gly	Val
	130					135					140				
His	Cys	Ala	Asp	Arg	Leu	Leu	Phe	Cys	Ala	Lys	Glu	Ala	Thr	Tyr	Lys
145						150					155				160
Ala	Trp	Phe	Pro	Leu	Thr	His	Arg	Trp	Leu	Gly	Phe	Glu	Gln	Ala	Glu
			165						170					175	
Ile	Asp	Leu	Arg	Asp	Asp	Gly	Thr	Phe	Val	Ser	Tyr	Leu	Leu	Val	Arg
			180					185					190		
Pro	Thr	Pro	Val	Pro	Phe	Ile	Ser	Gly	Lys	Trp	Val	Leu	Arg	Asp	Gly
		195					200					205			
Tyr	Val	Ile	Ala	Ala	Thr	Ala	Val	Thr							
	210					215									

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<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(592)

<223> RXS01572

<400> 261

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					Met	Gly	Val	Gln	Ile	
					1				5	

gct	gca	gcc	aag	ggt	gct	gag	gtt	acc	gtt	ctg	tcc	cgt	tcc	ctg	cgc	163
Ala	Ala	Ala	Lys	Gly	Ala	Glu	Val	Thr	Val	Leu	Ser	Arg	Ser	Leu	Arg	
			10					15						20		

aag	gca	gaa	ctt	gcc	aag	gaa	ctc	ggc	gca	gct	cgc	acg	ctt	gcg	act	211
Lys	Ala	Glu	Leu	Ala	Lys	Glu	Leu	Gly	Ala	Ala	Arg	Thr	Leu	Ala	Thr	
		25						30					35			

tct	gat	gag	gat	ttc	ttc	acc	gaa	cac	gcc	ggt	gaa	ttc	gac	ttc	atc	259
Ser	Asp	Glu	Asp	Phe	Phe	Thr	Glu	His	Ala	Gly	Glu	Phe	Asp	Phe	Ile	
		40					45				50					

ctc	aac	acc	att	agc	gca	tcc	atc	cca	gtc	gac	aag	tac	ctg	agc	ctt	307
Leu	Asn	Thr	Ile	Ser	Ala	Ser	Ile	Pro	Val	Asp	Lys	Tyr	Leu	Ser	Leu	
	55						60				65					

ctc	aag	cca	cac	ggt	gtc	atg	gct	gtt	gtc	ggt	ctg	cca	cca	gag	aag	355
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Leu Lys Pro His Gly Val Met Ala Val Val Gly Leu Pro Pro Glu Lys
 70 75 80 85
 cag cca ctg agc ttc ggt gcg ctc atc ggc ggc gga aaa gtc ctc acc 403
 Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly Gly Lys Val Leu Thr
 90 95 100
 gga tcc aac att ggc ggc atc cct gaa acc cag gaa atg ctc gac ttc 451
 Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln Glu Met Leu Asp Phe
 105 110 115
 tgt gca aaa cac ggc ctc ggt gcg atg atc gaa act gtc ggc gtc aac 499
 Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu Thr Val Gly Val Asn
 120 125 130
 gat gtt gat gca gcc tac gac cgt gtt gtt gcc ggc gac gtt cag ttc 547
 Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala Gly Asp Val Gln Phe
 135 140 145
 cgc gtt gtc att gat act gct tcg ttt gct gag gtt gag gcg gtt 592
 Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu Val Glu Ala Val
 150 155 160
 taggtttact gaagttcaga ctt 615

<210> 262
 <211> 164
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 262
 Met Gly Val Gln Ile Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu
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 Ser Arg Ser Leu Arg Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala
 20 25 30
 Arg Thr Leu Ala Thr Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly
 35 40 45
 Glu Phe Asp Phe Ile Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp
 50 55 60
 Lys Tyr Leu Ser Leu Leu Lys Pro His Gly Val Met Ala Val Val Gly
 65 70 75 80
 Leu Pro Pro Glu Lys Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly
 85 90 95
 Gly Lys Val Leu Thr Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln
 100 105 110
 Glu Met Leu Asp Phe Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu
 115 120 125
 Thr Val Gly Val Asn Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala
 130 135 140
 Gly Asp Val Gln Phe Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu
 145 150 155 160

<400> 263																
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tcgtgccagc tcagggcata tctcacctaa agtaaacacc atg aaa tca atc ttc 115																
Met Lys Ser Ile Phe 1 5																
att tcc ggt gcg gcg aac gga att ggc aaa gct gtg gcg ttg aaa ttt 163																
Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala Val Ala Leu Lys Phe 10 15 20																
ctt cac gaa ggt tgg ctc gtt gga gcc tac gac ctc gcg gaa atc acc 211																
Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp Leu Ala Glu Ile Thr 25 30 35																
tac tca cac ccc aat ctt cgc tgg ggc tac ctc aat gtt cga cag tcc 259																
Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu Asn Val Arg Gln Ser 40 45 50																
gag tcg tgg gac aaa gcc cta gaa gac ttt gcg acg cac acc gga ggc 307																
Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala Thr His Thr Gly Gly 55 60 65																
acc atc gat gtg gtg gac aat aat gcc ggc gta att att gag gga ccg 355																
Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val Ile Ile Glu Gly Pro 70 75 80 85																
ctg cag gac gca gag gag ggg agc gtc gac aag ctt ctt gca atc aac 403																
Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys Leu Leu Ala Ile Asn 90 95 100																
gtc aat ggc gtg act ctt ggt gcc cgc gcc gct cat cct tat ttg gcg 451																
Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala His Pro Tyr Leu Ala 105 110 115																
cgc acg ccg ggc gcc cag ttg tta aac atg tcc tcg gcg tcg gcg gtg 499																
Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser Ser Ala Ser Ala Val 120 125 130																
tac ggg cag ccc cag atc gcg gtg tat tcg gct tcg aag ttt tac gtc 547																
Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala Ser Lys Phe Tyr Val 135 140 145																
gca ggt ctt act gag gcg ctg aat ttg gag tgg cgg aaa gac gat att 595																
Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp Arg Lys Asp Asp Ile 150 155 160 165																

cgc gtg gtc gat gtt tgg cct ttg tgg gcg aaa acc gat ttg gtg aac 643
 Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys Thr Asp Leu Val Asn
 170 175 180

ggc gtg aag gct aag tca ctg aag cgt ttg ggt gtc cgg atc act ccg 691
 Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly Val Arg Ile Thr Pro
 185 190 195

gaa cag gtg gca cag gcg gta tgg gat gcg gtg cat ccg aaa tct cgg 739
 Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val His Pro Lys Ser Arg
 200 205 210

tgg gcg aag gga aag gtg cat cac ggg gtg tca aag ttg gat aag gcg 787
 Trp Ala Lys Gly Lys Val His His Gly Val Ser Lys Leu Asp Lys Ala
 215 220 225

ctg tat ctc atg aaa tct ctg tcg cct gat cgg gta gcg atg tgt ttt 835
 Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg Val Ala Met Cys Phe
 230 235 240 245

gcg cga cta atc gcc gga taaatgaatt gattatttta ggc 876
 Ala Arg Leu Ile Ala Gly
 250

<210> 264

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 264

Met Lys Ser Ile Phe Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala
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Val Ala Leu Lys Phe Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp
 20 25 30

Leu Ala Glu Ile Thr Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu
 35 40 45

Asn Val Arg Gln Ser Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala
 50 55 60

Thr His Thr Gly Gly Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val
 65 70 75 80

Ile Ile Glu Gly Pro Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys
 85 90 95

Leu Leu Ala Ile Asn Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala
 100 105 110

His Pro Tyr Leu Ala Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser
 115 120 125

Ser Ala Ser Ala Val Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala
 130 135 140

Ser Lys Phe Tyr Val Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp
 145 150 155 160

Arg Lys Asp Asp Ile Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys
 165 170 175

Thr Asp Leu Val Asn Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly
 180 185 190

Val Arg Ile Thr Pro Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val
 195 200 205

His Pro Lys Ser Arg Trp Ala Lys Gly Lys Val His His Gly Val Ser
 210 215 220

Lys Leu Asp Lys Ala Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg
 225 230 235 240

Val Ala Met Cys Phe Ala Arg Leu Ile Ala Gly
 245 250

<210> 265
 <211> 897
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(874)
 <223> RXS02474

<400> 265
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aatcttgaga atttatatttg aggaagcaag aggaagtgtc atg agc aaa gtt gca 115
 Met Ser Lys Val Ala
 1 5

atg gtt acc ggt ggt gca caa ggc atc ggt cgt gga att tca gag aag 163
 Met Val Thr Gly Gly Ala Gln Gly Ile Gly Arg Gly Ile Ser Glu Lys
 10 15 20

ctg gca gca gat ggt ttc gat att gcc gta gcc gac ctg cca caa cag 211
 Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala Asp Leu Pro Gln Gln
 25 30 35

gaa gaa caa gct gca gag acc atc aag ttg att gaa gct gca ggt caa 259
 Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile Glu Ala Ala Gly Gln
 40 45 50

aag gct gta ttc gtt gga tta gat gtc acc gat aag gct aat ttc gac 307
 Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp Lys Ala Asn Phe Asp
 55 60 65

agt gca att gat gag gca gca gag aaa ctt ggc ggc ttc gat gtg cta 355
 Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly Gly Phe Asp Val Leu
 70 75 80 85

gta aac aac gcc ggc atc gca caa att aag cca ctt ctg gaa gtc acc 403
 Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro Leu Leu Glu Val Thr
 90 95 100

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gaa gaa gac cta aag cag atc tac tcc gtg aac gtt ttt agc gta ttt 451
Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn Val Phe Ser Val Phe
      105                      110                      115

ttt ggt att caa gca gca tcc cga aag ttc gat gag ctt ggc gta aaa 499
Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp Glu Leu Gly Val Lys
      120                      125                      130

ggc aag atc atc aac gct gca tca atc gct gct atc caa ggt ttc cca 547
Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala Ile Gln Gly Phe Pro
      135                      140                      145

atc ttg agc gcc tac tcc acc acc aaa ttc gcg gtt cgt ggc ctc acc 595
Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala Val Arg Gly Leu Thr
      150                      155                      160                      165

cag gct gct gcg caa gaa ctc gca ccc aag ggt cac acc gtg aat gcc 643
Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly His Thr Val Asn Ala
      170                      175                      180

tac gca cct ggc atc gtg ggc acc gga atg tgg gag caa atc gat gcc 691
Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp Glu Gln Ile Asp Ala
      185                      190                      195

gag ctt tcc aag atc aac ggc aag cca atc ggt gag aac ttc aag gag 739
Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly Glu Asn Phe Lys Glu
      200                      205                      210

tac tcc tcc tca atc gca ttg ggc cga cca tca gta cct gag gat gta 787
Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser Val Pro Glu Asp Val
      215                      220                      225

gcc ggt ctg gtt tcg ttc ctg gct tct gaa aac tcc aac tac atc acc 835
Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn Ser Asn Tyr Ile Thr
      230                      235                      240                      245

gga cag gtc atg ctt gtc gac ggc ggc atg ctc tac aac tagggggttgc 884
Gly Gln Val Met Leu Val Asp Gly Gly Met Leu Tyr Asn
      250                      255

tttcccgcac tca 897

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<210> 266

<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 266

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Met Ser Lys Val Ala Met Val Thr Gly Gly Ala Gln Gly Ile Gly Arg
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Gly Ile Ser Glu Lys Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala
  20           25           30

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Asp Leu Pro Gln Gln Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile
  35           40           45

```

```

Glu Ala Ala Gly Gln Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp
  50           55           60

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Lys Ala Asn Phe Asp Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly
 65 70 75 80
 Gly Phe Asp Val Leu Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro
 85 90 95
 Leu Leu Glu Val Thr Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn
 100 105 110
 Val Phe Ser Val Phe Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp
 115 120 125
 Glu Leu Gly Val Lys Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala
 130 135 140
 Ile Gln Gly Phe Pro Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala
 145 150 155 160
 Val Arg Gly Leu Thr Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly
 165 170 175
 His Thr Val Asn Ala Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp
 180 185 190
 Glu Gln Ile Asp Ala Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly
 195 200 205
 Glu Asn Phe Lys Glu Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser
 210 215 220
 Val Pro Glu Asp Val Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn
 225 230 235 240
 Ser Asn Tyr Ile Thr Gly Gln Val Met Leu Val Asp Gly Gly Met Leu
 245 250 255

Tyr Asn

<210> 267
 <211> 1224
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1201)
 <223> RXS02485

<400> 267
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tacgcgttgc catgaggata agactaccgt tagtgggggtg ttg gat tca tcg cta 115
 Leu Asp Ser Ser Leu
 1 5

gcc cag gaa atc gcc gcg atc gac ggc gtc gaa ctc gat tcg gaa gtc 163
 Ala Gln Glu Ile Ala Ala Ile Asp Gly Val Glu Leu Asp Ser Glu Val
 10 15 20

act	ttc	gcc	gat	ctg	acg	acc	ctc	cgc	atc	ggc	gga	aaa	ccc	cgc	agc	211
Thr	Phe	Ala	Asp	Leu	Thr	Thr	Leu	Arg	Ile	Gly	Gly	Lys	Pro	Arg	Ser	
			25					30					35			
gcc	gta	cgt	tgc	cag	acc	acg	gag	gcg	ctg	gtc	agc	gcc	ata	aaa	ttg	259
Ala	Val	Arg	Cys	Gln	Thr	Thr	Glu	Ala	Leu	Val	Ser	Ala	Ile	Lys	Leu	
		40					45					50				
ctt	gac	gac	gcc	tcc	ctc	ccc	ctc	ctc	att	gtc	ggc	ggc	ggg	tcc	aat	307
Leu	Asp	Asp	Ala	Ser	Leu	Pro	Leu	Leu	Ile	Val	Gly	Gly	Gly	Ser	Asn	
	55					60					65					
ctc	gtc	gtg	gcc	gac	ggc	gat	ctg	gat	gtt	att	gcc	gtc	atc	atc	gaa	355
Leu	Val	Val	Ala	Asp	Gly	Asp	Leu	Asp	Val	Ile	Ala	Val	Ile	Ile	Glu	
	70				75					80					85	
acc	gac	gac	gtc	tcc	atc	aac	ctc	acc	gac	ggc	ctc	ctc	acc	gcc	gat	403
Thr	Asp	Asp	Val	Ser	Ile	Asn	Leu	Thr	Asp	Gly	Leu	Leu	Thr	Ala	Asp	
				90					95					100		
gca	ggc	gct	gtt	tgg	gac	gat	gtt	gtc	cac	ctt	tcg	gtg	gat	gcc	ggc	451
Ala	Gly	Ala	Val	Trp	Asp	Asp	Val	Val	His	Leu	Ser	Val	Asp	Ala	Gly	
			105					110					115			
ctc	ggc	gga	att	gaa	tgc	ctc	tcc	gga	atc	ccc	ggc	tcc	gcc	ggc	gcc	499
Leu	Gly	Gly	Ile	Glu	Cys	Leu	Ser	Gly	Ile	Pro	Gly	Ser	Ala	Gly	Ala	
		120					125					130				
acc	cca	gtc	caa	aac	gtg	ggc	gcc	tac	ggc	acg	gaa	gtt	tcc	gat	gta	547
Thr	Pro	Val	Gln	Asn	Val	Gly	Ala	Tyr	Gly	Thr	Glu	Val	Ser	Asp	Val	
	135					140					145					
ctc	acc	cgc	gtc	cag	ctt	ctc	gac	cgc	acc	acc	cac	caa	gtc	tcc	tgg	595
Leu	Thr	Arg	Val	Gln	Leu	Leu	Asp	Arg	Thr	Thr	His	Gln	Val	Ser	Trp	
	150				155					160					165	
gtc	gac	gcc	tcc	gaa	ctc	gac	ctc	tct	tac	cga	tac	tcc	aat	ctc	aaa	643
Val	Asp	Ala	Ser	Glu	Leu	Asp	Leu	Ser	Tyr	Arg	Tyr	Ser	Asn	Leu	Lys	
				170					175					180		
ttc	acc	aac	cgc	gca	gtc	gtc	ttg	gcg	atc	gaa	ctc	cag	ctc	ctc	acc	691
Phe	Thr	Asn	Arg	Ala	Val	Val	Leu	Ala	Ile	Glu	Leu	Gln	Leu	Leu	Thr	
			185					190					195			
gac	gga	ttg	tcc	gcg	ccg	cta	cgt	ttt	ggc	gaa	ttg	gga	cgt	cga	tta	739
Asp	Gly	Leu	Ser	Ala	Pro	Leu	Arg	Phe	Gly	Glu	Leu	Gly	Arg	Arg	Leu	
		200					205					210				
gcg	atc	tcc	gag	gcc	gaa	ccc	cac	cca	cgt	cgc	ccc	gtc	cgc	atg	gtc	787
Ala	Ile	Ser	Glu	Ala	Glu	Pro	His	Pro	Arg	Arg	Pro	Val	Arg	Met	Val	
	215					220					225					
cgc	gac	gcc	gtc	cta	gaa	ctc	cgc	cgc	gcc	aaa	ggc	atg	gtc	gtg	gaa	835
Arg	Asp	Ala	Val	Leu	Glu	Leu	Arg	Arg	Ala	Lys	Gly	Met	Val	Val	Glu	
	230				235					240					245	
cac	acc	gac	cac	gac	acc	tgg	tcc	gcc	gga	tcc	ttc	ttc	acc	aac	cca	883
His	Thr	Asp	His	Asp	Thr	Trp	Ser	Ala	Gly	Ser	Phe	Phe	Thr	Asn	Pro	
				250					255					260		
atc	gtc	gac	cca	gcc	ctt	gcc	gac	gca	gtc	ttt	gaa	aaa	gtc	ggc	gaa	931

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Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe Glu Lys Val Gly Glu
      265                                270                                275

ccc acc atg ccc cgc ttc cca gcc ggc gat ggc aaa gaa aaa ctc tcc 979
Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly Lys Glu Lys Leu Ser
      280                                285                                290

gca gcc tgg ctc atc gaa cgc gcc ggc ttc aaa aag gga cac ccc ggc 1027
Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys Lys Gly His Pro Gly
      295                                300                                305

gca ggc gca aaa gcc tcc ctg agc acc aaa cac acc ctc gca ctc acc 1075
Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His Thr Leu Ala Leu Thr
310                                315                                320                                325

aac cgt ggc gac gcc cgc gcc tcc gac ctc gtc gca tta gcc aaa gaa 1123
Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val Ala Leu Ala Lys Glu
      330                                335                                340

atc cgc gac gga gtc ctc gaa acc ttc ggc gtc acc ctc gtc cca gaa 1171
Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val Thr Leu Val Pro Glu
      345                                350                                355

ccc gtc tgg att gga atc agc atc gat gac tgaattttcc gacgtccctg 1221
Pro Val Trp Ile Gly Ile Ser Ile Asp Asp
      360                                365

gca 1224

<210> 268
<211> 367
<212> PRT
<213> Corynebacterium glutamicum

<400> 268
Leu Asp Ser Ser Leu Ala Gln Glu Ile Ala Ala Ile Asp Gly Val Glu
 1          5          10          15

Leu Asp Ser Glu Val Thr Phe Ala Asp Leu Thr Thr Leu Arg Ile Gly
      20          25          30

Gly Lys Pro Arg Ser Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val
      35          40          45

Ser Ala Ile Lys Leu Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val
      50          55          60

Gly Gly Gly Ser Asn Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile
      65          70          75          80

Ala Val Ile Ile Glu Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly
      85          90          95

Leu Leu Thr Ala Asp Ala Gly Ala Val Trp Asp Asp Val Val His Leu
      100         105         110

Ser Val Asp Ala Gly Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro
      115         120         125

Gly Ser Ala Gly Ala Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr

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130	135	140
Glu Val Ser Asp Val Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr 145 150 155 160		
His Gln Val Ser Trp Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg 165 170 175		
Tyr Ser Asn Leu Lys Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu 180 185 190		
Leu Gln Leu Leu Thr Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu 195 200 205		
Leu Gly Arg Arg Leu Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg 210 215 220		
Pro Val Arg Met Val Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys 225 230 235 240		
Gly Met Val Val Glu His Thr Asp His Asp Thr Trp Ser Ala Gly Ser 245 250 255		
Phe Phe Thr Asn Pro Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe 260 265 270		
Glu Lys Val Gly Glu Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly 275 280 285		
Lys Glu Lys Leu Ser Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys 290 295 300		
Lys Gly His Pro Gly Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His 305 310 315 320		
Thr Leu Ala Leu Thr Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val 325 330 335		
Ala Leu Ala Lys Glu Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val 340 345 350		
Thr Leu Val Pro Glu Pro Val Trp Ile Gly Ile Ser Ile Asp Asp 355 360 365		

<210> 269

<211> 1641

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1618)

<223> RXS02539

<400> 269

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				Met Thr Val Tyr Ala	
				1 5	

aat Asn	cca Pro	gga Gly	acc Thr	gaa Glu 10	ggc Gly	tcg Ser	atc Ile	gtt Val	aac Asn 15	tat Tyr	gaa Glu	aag Lys	cgc Arg	tac Tyr 20	gag Glu	163
aac Asn	tac Tyr	att Ile	ggt Gly 25	ggc Gly	aag Lys	tgg Trp	gtt Val	cca Pro 30	ccg Pro	gta Val	gag Glu	ggc Gly	cag Gln 35	tac Tyr	ctt Leu	211
gag Glu	aac Asn	att Ile 40	tca Ser	cct Pro	gtc Val	act Thr	ggt Gly 45	gaa Glu	gtt Val	ttc Phe	tgt Cys	gag Glu 50	gtc Val	gca Ala	cgt Arg	259
ggc Gly	acc Thr 55	gca Ala	gcg Ala	gac Asp	gtg Val	gag Glu 60	ctt Leu	gca Ala	ctg Leu	gat Asp	gct Ala 65	gca Ala	cat His	gca Ala	gcc Ala	307
gct Ala 70	gat Asp	gcg Ala	tgg Trp	ggc Gly	aag Lys 75	act Thr	tct Ser	gtc Val	gct Ala	gaa Glu 80	cgt Arg	gct Ala	ctg Leu	atc Ile	ctg Leu 85	355
cac His	cgc Arg	att Ile	gcg Ala	gac Asp 90	cgc Arg	atg Met	gaa Glu	gag Glu	cac His 95	ctg Leu	gaa Glu	gaa Glu	atc Ile	gca Ala 100	gtt Val	403
gca Ala	gaa Glu	acc Thr 105	tgg Trp	gag Glu	aac Asn	ggc Gly	aag Lys	gca Ala 110	gtc Val	cgt Arg	gag Glu	act Thr 115	ctt Leu	gct Ala	gca Ala	451
gat Asp	atc Ile 120	cca Pro	ctg Leu	gca Ala	atc Ile	gac Asp	cac His 125	ttc Phe	cgc Arg	tac Tyr	ttt Phe 130	gct Ala	ggc Gly	gcg Ala	atc Ile	499
cgt Arg 135	gct Ala	cag Gln	gaa Glu	gat Asp	cgt Arg	tcc Ser 140	tca Ser	cag Gln	atc Ile	gac Asp 145	cac His	aac Asn	act Thr	gtt Val	gct Ala	547
tac Tyr 150	cac His	ttc Phe	aac Asn	gag Glu 155	cca Pro	atc Ile	ggt Gly	gtt Val	gtt Val	ggt Gly 160	cag Gln	atc Ile	att Ile	cct Pro	tgg Trp 165	595
aac Asn	ttc Phe	cca Pro	atc Ile 170	ctc Leu	atg Met	gct Ala	acc Thr	tgg Trp 175	aag Lys	ctc Leu	gca Ala	ccg Pro	gca Ala	ctt Leu 180	gct Ala	643
gca Ala	ggt Gly	aac Asn	gcg Ala 185	atc Ile	gtc Val	atg Met	aag Lys	cca Pro 190	gct Ala	gag Glu	cag Gln	acc Thr 195	cca Pro	gca Ala	tcc Ser	691
att Ile	ttg Leu 200	tat Tyr	ctg Leu	att Ile	aac Asn	atc Ile	atc Ile 205	ggc Gly	gat Asp	ctc Leu	atc Ile 210	cca Pro	gag Glu	ggc Gly	gtc Val	739
ctc Leu 215	aac Asn	atc Ile	gtc Val	aac Asn	gga Gly	ctc Leu 220	ggc Gly	ggt Gly	gaa Glu	gca Ala	ggc Gly 225	gct Ala	gca Ala	ctg Leu	tcc Ser	787
ggc Gly 230	tct Ser	aat Asn	cgg Arg	att Ile 235	ggc Gly	aag Lys	att Ile	gct Ala	ttc Phe 240	acc Thr	ggg Gly	tcc Ser	acc Thr	gag Glu	gtc Val 245	835

ggc aag ctg atc aac cgc gct gca tcc gac aag atc att cct gtc acc	883
Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys Ile Ile Pro Val Thr	
250 255 260	
ctg gag ctc ggc ggt aag tcc cca tcc atc ttc ttc tcc gat gtt ctg	931
Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe Phe Ser Asp Val Leu	
265 270 275	
tca cag gat gac gcc ttc gca gag aag gca gtt gaa ggc ttc gcg atg	979
Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val Glu Gly Phe Ala Met	
280 285 290	
ttc gcc ctc aat cag ggt gaa gtt tgt acc tgt cct tcc cgt gca ctt	1027
Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys Pro Ser Arg Ala Leu	
295 300 305	
gtt cat gag tcc atc gct gat gaa ttc ctc gag ctt ggc gtg aag cga	1075
Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu Leu Gly Val Lys Arg	
310 315 320 325	
gtt cag aac atc aag ctg ggt aac cca ctt gat act gaa acc atg atg	1123
Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp Thr Glu Thr Met Met	
330 335 340	
ggt gct cag gcg tcc cag gag cag atg gac aag atc tcc tcc tac ctg	1171
Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys Ile Ser Ser Tyr Leu	
345 350 355	
aag atc ggc cca gaa gaa ggc gct caa acc ctc act ggt ggc aag gtc	1219
Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu Thr Gly Gly Lys Val	
360 365 370	
aac aag gtt gat ggc atg gag aac ggt tac tac att gag cca acc gtt	1267
Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr Ile Glu Pro Thr Val	
375 380 385	
ttc cgc ggc acc aac gac atg agg atc ttc cgc gag gaa atc ttc gga	1315
Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg Glu Glu Ile Phe Gly	
390 395 400 405	
cca gtc ctt tct gtt gct acc ttc agc gac ttc gat gag gcc atc cgt	1363
Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe Asp Glu Ala Ile Arg	
410 415 420	
att gca aac gac acc aac tac ggc ctc ggc gct ggt gtc tgg agc cgt	1411
Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala Gly Val Trp Ser Arg	
425 430 435	
gac caa aac acc att tat cgt gca ggt cgc gca atc cag gct ggt cga	1459
Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala Ile Gln Ala Gly Arg	
440 445 450	
gtt tgg gtc aac cag tac cac aac tac cca gcg cac tcc gct ttc ggt	1507
Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala His Ser Ala Phe Gly	
455 460 465	
gga tac aag gag tcc ggc atc ggc cgt gag aac cac ctc atg atg ctg	1555
Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn His Leu Met Met Leu	
470 475 480 485	
aac cac tac cag cag acc aag aac ctg ttg gtc tcc tac gat cca aac	1603

Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val Ser Tyr Asp Pro Asn
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 Pro Thr Gly Leu Phe
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1641

<210> 270

<211> 506

<212> PRT

<213> Corynebacterium glutamicum

<400> 270

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Glu Gly Gln Tyr Leu Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe
 35 40 45

Cys Glu Val Ala Arg Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp
 50 55 60

Ala Ala His Ala Ala Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu
 65 70 75 80

Arg Ala Leu Ile Leu His Arg Ile Ala Asp Arg Met Glu Glu His Leu
 85 90 95

Glu Glu Ile Ala Val Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg
 100 105 110

Glu Thr Leu Ala Ala Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr
 115 120 125

Phe Ala Gly Ala Ile Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp
 130 135 140

His Asn Thr Val Ala Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly
 145 150 155 160

Gln Ile Ile Pro Trp Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu
 165 170 175

Ala Pro Ala Leu Ala Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu
 180 185 190

Gln Thr Pro Ala Ser Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu
 195 200 205

Ile Pro Glu Gly Val Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala
 210 215 220

Gly Ala Ala Leu Ser Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr
 225 230 235 240

Gly Ser Thr Glu Val Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys
 245 250 255

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Ile Ile Pro Val Thr Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe
      260                      265                      270

Phe Ser Asp Val Leu Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val
      275                      280                      285

Glu Gly Phe Ala Met Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys
      290                      295                      300

Pro Ser Arg Ala Leu Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu
305                      310                      315                      320

Leu Gly Val Lys Arg Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp
      325                      330                      335

Thr Glu Thr Met Met Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys
      340                      345                      350

Ile Ser Ser Tyr Leu Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu
      355                      360                      365

Thr Gly Gly Lys Val Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr
      370                      375                      380

Ile Glu Pro Thr Val Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg
385                      390                      395                      400

Glu Glu Ile Phe Gly Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe
      405                      410                      415

Asp Glu Ala Ile Arg Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala
      420                      425                      430

Gly Val Trp Ser Arg Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala
      435                      440                      445

Ile Gln Ala Gly Arg Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala
      450                      455                      460

His Ser Ala Phe Gly Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn
465                      470                      475                      480

His Leu Met Met Leu Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val
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Ser Tyr Asp Pro Asn Pro Thr Gly Leu Phe
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<210> 271

<211> 1227

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1204)

<223> RXS02578

<400> 271


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aacagcccac acctttccgc taaactcgca tgttgaaata atg tct acc caa tca 115
                                         Met Ser Thr Gln Ser
                                         1 5
tat gca ccc atc cgc cat cgc gga ttc atc agc tca ctc gag gga cta 163
Tyr Ala Pro Ile Arg His Arg Gly Phe Ile Ser Ser Leu Glu Gly Leu
                                         10 15 20
cgc gca atc gcc tcc ctg gga gtc ttg gcg acc cac gtt gca ttc caa 211
Arg Ala Ile Ala Ser Leu Gly Val Leu Ala Thr His Val Ala Phe Gln
                                         25 30 35
acc tcc gtc gac ccc gcc agc aac atc ggt gca gta ctc gcg cgt ttc 259
Thr Ser Val Asp Pro Ala Ser Asn Ile Gly Ala Val Leu Ala Arg Phe
                                         40 45 50
gac ttt ttc gtc gcc gtc ttc ttc gcc ctc tcc gcc ttc gtt ctt tgg 307
Asp Phe Phe Val Ala Val Phe Phe Ala Leu Ser Ala Phe Val Leu Trp
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cga cgc cgc gcc ggg caa cca gtg gga ctg tac tac ctc aaa cgc cta 355
Arg Arg Arg Ala Gly Gln Pro Val Gly Leu Tyr Tyr Leu Lys Arg Leu
                                         70 75 80 85
gcc cgc atc atg ccc gca tac tgg gca acg gtc att gca gtc ctg ctg 403
Ala Arg Ile Met Pro Ala Tyr Trp Ala Thr Val Ile Ala Val Leu Leu
                                         90 95 100
ttt att ccc acc ggc ccc tgg tta gcc aac ctg acg atg acc caa atc 451
Phe Ile Pro Thr Gly Pro Trp Leu Ala Asn Leu Thr Met Thr Gln Ile
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Tyr Trp Pro Asp Gly Leu Met Thr Gly Leu Thr His Leu Trp Ser Leu
                                         120 125 130
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Cys Val Glu Val Ala Phe Tyr Leu Val Met Pro Leu Leu Ala Trp Val
                                         135 140 145
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Leu Asp Arg Phe Gly Arg Pro Val Arg Ile Leu Leu Ile Val Gly Gly
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gca gtg ttg agt ctg gcg tgg ccg tgg att ccc ctt gtg gag cat gcg 643
Ala Val Leu Ser Leu Ala Trp Pro Trp Ile Pro Leu Val Glu His Ala
                                         170 175 180
ttg gac gag ggg tgg gcg aac atg cag atc tgg cca ccc gct tac gct 691
Leu Asp Glu Gly Trp Ala Asn Met Gln Ile Trp Pro Pro Ala Tyr Ala
                                         185 190 195
tgc tgg ttt gca gtc ggc atg atc gcc gca gaa att gaa gga gtt cga 739
Cys Trp Phe Ala Val Gly Met Ile Ala Ala Glu Ile Glu Gly Val Arg
                                         200 205 210
ttc cca cgg gtt ccg agc ttt gtg tgg gtg ggt tta gct tta gtg gtc 787
Phe Pro Arg Val Pro Ser Phe Val Trp Val Gly Leu Ala Leu Val Val
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gct tgg atc gcg ggc caa gaa tgg ttc gga cca cta ggt tta gtg cac 835
 Ala Trp Ile Ala Gly Gln Glu Trp Phe Gly Pro Leu Gly Leu Val His
 230 235 240 245
 ccc agc ccc tgg gaa ttc aac tta aga gtc ctc gcg ggc aca ctt ttc 883
 Pro Ser Pro Trp Glu Phe Asn Leu Arg Val Leu Ala Gly Thr Leu Phe
 250 255 260
 gct gta ttt ctg gtg gtt ccc tac gcg ctg ggt acg ccc tct cgg ctt 931
 Ala Val Phe Leu Val Val Pro Tyr Ala Leu Gly Thr Pro Ser Arg Leu
 265 270 275
 ctt gat tcc agt tgg atg aaa acg ctc ggc acc tgg tcg tat tcc atc 979
 Leu Asp Ser Ser Trp Met Lys Thr Leu Gly Thr Trp Ser Tyr Ser Ile
 280 285 290
 ttc ctc tgg cac ctt ccc gtg ctg acg att gtg ttc cca ctg ctc ggg 1027
 Phe Leu Trp His Leu Pro Val Leu Thr Ile Val Phe Pro Leu Leu Gly
 295 300 305
 ttg cct tta ttt agt gga aat ttc ctg ttg gtg ttc atc gtg acg gtc 1075
 Leu Pro Leu Phe Ser Gly Asn Phe Leu Leu Val Phe Ile Val Thr Val
 310 315 320 325
 ttg ttg acg atc cca gtt gcc gcc atc agc tac acc ttc atc gaa gag 1123
 Leu Leu Thr Ile Pro Val Ala Ala Ile Ser Tyr Thr Phe Ile Glu Glu
 330 335 340
 ccc atc agc ggt gga ccc ggc gcg cca ttc agg ctg ggg gtc gtt agg 1171
 Pro Ile Ser Gly Gly Pro Gly Ala Pro Phe Arg Leu Gly Val Val Arg
 345 350 355
 att cac cat ttt tct ggg ggt agg tct gga aaa tgatgaattg gcaccacgtc 1224
 Ile His His Phe Ser Gly Gly Arg Ser Gly Lys
 360 365
 aag 1227

<210> 272

<211> 368

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

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 Ser Leu Glu Gly Leu Arg Ala Ile Ala Ser Leu Gly Val Leu Ala Thr
 20 25 30
 His Val Ala Phe Gln Thr Ser Val Asp Pro Ala Ser Asn Ile Gly Ala
 35 40 45
 Val Leu Ala Arg Phe Asp Phe Phe Val Ala Val Phe Phe Ala Leu Ser
 50 55 60
 Ala Phe Val Leu Trp Arg Arg Arg Ala Gly Gln Pro Val Gly Leu Tyr
 65 70 75 80

Tyr Leu Lys Arg Leu Ala Arg Ile Met Pro Ala Tyr Trp Ala Thr Val
 85 90 95
 Ile Ala Val Leu Leu Phe Ile Pro Thr Gly Pro Trp Leu Ala Asn Leu
 100 105 110
 Thr Met Thr Gln Ile Tyr Trp Pro Asp Gly Leu Met Thr Gly Leu Thr
 115 120 125
 His Leu Trp Ser Leu Cys Val Glu Val Ala Phe Tyr Leu Val Met Pro
 130 135 140
 Leu Leu Ala Trp Val Leu Asp Arg Phe Gly Arg Pro Val Arg Ile Leu
 145 150 155 160
 Leu Ile Val Gly Gly Ala Val Leu Ser Leu Ala Trp Pro Trp Ile Pro
 165 170 175
 Leu Val Glu His Ala Leu Asp Glu Gly Trp Ala Asn Met Gln Ile Trp
 180 185 190
 Pro Pro Ala Tyr Ala Cys Trp Phe Ala Val Gly Met Ile Ala Ala Glu
 195 200 205
 Ile Glu Gly Val Arg Phe Pro Arg Val Pro Ser Phe Val Trp Val Gly
 210 215 220
 Leu Ala Leu Val Val Ala Trp Ile Ala Gly Gln Glu Trp Phe Gly Pro
 225 230 235 240
 Leu Gly Leu Val His Pro Ser Pro Trp Glu Phe Asn Leu Arg Val Leu
 245 250 255
 Ala Gly Thr Leu Phe Ala Val Phe Leu Val Val Pro Tyr Ala Leu Gly
 260 265 270
 Thr Pro Ser Arg Leu Leu Asp Ser Ser Trp Met Lys Thr Leu Gly Thr
 275 280 285
 Trp Ser Tyr Ser Ile Phe Leu Trp His Leu Pro Val Leu Thr Ile Val
 290 295 300
 Phe Pro Leu Leu Gly Leu Pro Leu Phe Ser Gly Asn Phe Leu Leu Val
 305 310 315 320
 Phe Ile Val Thr Val Leu Leu Thr Ile Pro Val Ala Ala Ile Ser Tyr
 325 330 335
 Thr Phe Ile Glu Glu Pro Ile Ser Gly Gly Pro Gly Ala Pro Phe Arg
 340 345 350
 Leu Gly Val Val Arg Ile His His Phe Ser Gly Gly Arg Ser Gly Lys
 355 360 365

<210> 273

<211> 1089

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1066)

<223> RXS02741

<400> 273

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ttcccaacct tgtcttttcag tcatgggttag tgtgggaacc atg aag gca atc tta 115
Met Lys Ala Ile Leu
1 5

gtt tcc cgc acc ggc gga cca gag gtg ttg gag ttc acc gac act gac 163
Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu Phe Thr Asp Thr Asp
10 15 20

gcc cca aag ccc act gat gat cag gtt tta gtt gaa gtt gat atg gct 211
Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val Glu Val Asp Met Ala
25 30 35

ggc gtc aac ttt att gat act tac tat cgc cag ggt gaa tat cac gct 259
Gly Val Asn Phe Ile Asp Thr Tyr Arg Gln Gly Glu Tyr His Ala
40 45 50

cgc ctg ccg ttt atc cca ggt ttt gaa ggc act ggt cgg gtg ttg gag 307
Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr Gly Arg Val Leu Glu
55 60 65

gat ccg cag ggg ttg att gcg gcg ggt acc aag gtg gcg tgg tgt gat 355
Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys Val Ala Trp Cys Asp
70 75 80 85

gcc atg ggt tcg tat gct cag cag gtg tgt gtg ccg cgg gat cgc ttg 403
Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val Pro Arg Asp Arg Leu
90 95 100

gtg gcg gtt ccc gag ggc gtg agt tcg gaa gtg gct gcg tcg atg ttg 451
Val Ala Val Pro Glu Gly Val Ser Ser Glu Val Ala Ala Ser Met Leu
105 110 115

atg cag gga atc act gcg cat tat cta acc aat ggt gtg tat gag ctt 499
Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn Gly Val Tyr Glu Leu
120 125 130

gaa gag ggc gat tct tgc ctc atc act gct ggc gcg ggt ggt gtt gga 547
Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly Ala Gly Gly Val Gly
135 140 145

ttg ttg gct acg cag atg gcg gcg gcc aag gga gtg cgc gtg tac agc 595
Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly Val Arg Val Tyr Ser
150 155 160 165

gtg gtg tcc acg gat gaa aaa gct gag ctt gct ttg gat gcc ggt gct 643
Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala Leu Asp Ala Gly Ala
170 175 180

tat gag gtg ttt cgt tat tcc gat aat ttg gcg gag cag gtt cgt cgg 691
Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala Glu Gln Val Arg Arg
185 190 195

cac aac ggg ggt cgc gga gtt gat gtg gtg tat gac ggt gtc ggc cag 739
His Asn Gly Gly Arg Gly Val Asp Val Val Tyr Asp Gly Val Gly Gln

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Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg Pro Arg Gly Thr Val			
215	220	225	
tgt ttg ttt ggt gcg gcg tcg ggt cct gtg gag cct ttt gat ccg cag			835
Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu Pro Phe Asp Pro Gln			
230	235	240	245
ctg ttg aac act cac ggt tcg atc ttc ttg acc cgc cca agc att ggc			883
Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr Arg Pro Ser Ile Gly			
	250	255	260
gcg tgg acg tct gag gag ggc gaa ttt gcc aag cgt gca cag gcg gtc			931
Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys Arg Ala Gln Ala Val			
	265	270	275
acg cag gcc atc gtc gaa ggc acc ttg cgg gtt cgc gtt act ggc aca			979
Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val Arg Val Thr Gly Thr			
	280	285	290
tat tcg ctt gcc gac gcc tac atc gcc cac cgc gac ctt cag gcg cgt			1027
Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg Asp Leu Gln Ala Arg			
	295	300	305
agc acg agc ggt tct ttg gtc ttg gaa atc ccg aag gac taaacacgca			1076
Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro Lys Asp			
310	315	320	
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<210> 274

<211> 322

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

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			20					25					30		

Glu	Val	Asp	Met	Ala	Gly	Val	Asn	Phe	Ile	Asp	Thr	Tyr	Tyr	Arg	Gln
		35					40					45			

Gly	Glu	Tyr	His	Ala	Arg	Leu	Pro	Phe	Ile	Pro	Gly	Phe	Glu	Gly	Thr
	50					55					60				

Gly	Arg	Val	Leu	Glu	Asp	Pro	Gln	Gly	Leu	Ile	Ala	Ala	Gly	Thr	Lys
	65				70					75					80

Val	Ala	Trp	Cys	Asp	Ala	Met	Gly	Ser	Tyr	Ala	Gln	Gln	Val	Cys	Val
				85					90					95	

Pro	Arg	Asp	Arg	Leu	Val	Ala	Val	Pro	Glu	Gly	Val	Ser	Ser	Glu	Val
			100					105					110		

Ala	Ala	Ser	Met	Leu	Met	Gln	Gly	Ile	Thr	Ala	His	Tyr	Leu	Thr	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115	120	125
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Val Arg Val Tyr Ser Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala 165 170 175		
Leu Asp Ala Gly Ala Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala 180 185 190		
Glu Gln Val Arg Arg His Asn Gly Gly Arg Gly Val Asp Val Val Tyr 195 200 205		
Asp Gly Val Gly Gln Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg 210 215 220		
Pro Arg Gly Thr Val Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu 225 230 235 240		
Pro Phe Asp Pro Gln Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr 245 250 255		
Arg Pro Ser Ile Gly Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys 260 265 270		
Arg Ala Gln Ala Val Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val 275 280 285		
Arg Val Thr Gly Thr Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg 290 295 300		
Asp Leu Gln Ala Arg Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro 305 310 315 320		
Lys Asp		

<210> 275
 <211> 430
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(430)
 <223> RXS03061

<400> 275
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 Val Ser Leu Thr Phe
 1 5

cca gta atc aac ccc agc gat ggc tcc acc atc acc gag cta gaa aac 163
 Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile Thr Glu Leu Glu Asn

10										15					20					
cac	gat	tcc	acc	cag	tgg	atg	tcc	gcg	ctc	tct	gat	gca	gtt	gca	gct	211				
His	Asp	Ser	Thr	Gln	Trp	Met	Ser	Ala	Leu	Ser	Asp	Ala	Val	Ala	Ala					
25					30					35										
ggt	cct	tca	tgg	gct	gcg	aaa	act	ccc	cgc	gaa	aga	tcc	gtg	gta	ctc	259				
Gly	Pro	Ser	Trp	Ala	Ala	Lys	Thr	Pro	Arg	Glu	Arg	Ser	Val	Val	Leu					
40					45					50										
acc	gca	atc	ttc	gaa	gca	ctg	acc	gaa	cgc	gcc	caa	gaa	ctt	gca	gag	307				
Thr	Ala	Ile	Phe	Glu	Ala	Leu	Thr	Glu	Arg	Ala	Gln	Glu	Leu	Ala	Glu					
55					60					65										
atc	atc	cac	ctg	gaa	gct	gga	aaa	tcc	gat	gca	gaa	gct	ctt	ggt	gaa	355				
Ile	Ile	His	Leu	Glu	Ala	Gly	Lys	Ser	Asp	Ala	Glu	Ala	Leu	Gly	Glu					
70					75					80					85					
gtc	gct	tat	ggt	gca	gaa	tac	ttc	cgt	tgg	ttt	gcg	gaa	gaa	gca	gtg	403				
Val	Ala	Tyr	Gly	Ala	Glu	Tyr	Phe	Arg	Trp	Phe	Ala	Glu	Glu	Ala	Val					
90					95					100										
cgc	ctg	ccc	ggc	cgc	tac	gga	cag	tca								430				
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105					110															

<210> 276

<211> 110

<212> PRT

<213> Corynebacterium glutamicum

<400> 276

Val	Ser	Leu	Thr	Phe	Pro	Val	Ile	Asn	Pro	Ser	Asp	Gly	Ser	Thr	Ile	
1				5					10					15		
Thr	Glu	Leu	Glu	Asn	His	Asp	Ser	Thr	Gln	Trp	Met	Ser	Ala	Leu	Ser	
20					25					30						
Asp	Ala	Val	Ala	Ala	Gly	Pro	Ser	Trp	Ala	Ala	Lys	Thr	Pro	Arg	Glu	
35					40					45						
Arg	Ser	Val	Val	Leu	Thr	Ala	Ile	Phe	Glu	Ala	Leu	Thr	Glu	Arg	Ala	
50					55					60						
Gln	Glu	Leu	Ala	Glu	Ile	Ile	His	Leu	Glu	Ala	Gly	Lys	Ser	Asp	Ala	
65					70					75					80	
Glu	Ala	Leu	Gly	Glu	Val	Ala	Tyr	Gly	Ala	Glu	Tyr	Phe	Arg	Trp	Phe	
85					90					95						
Ala	Glu	Glu	Ala	Val	Arg	Leu	Pro	Gly	Arg	Tyr	Gly	Gln	Ser			
100					105					110						

<210> 277

<211> 747

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(724)

<223> RXS03150

<400> 277

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acccaaggct gaattcctga gctcaccttg tacaagatca gtg gaa gcc cag ttc 115
Val Glu Ala Gln Phe
1 5

acc tct ccc ctg ctc aac aat ggg caa acc tgt ttc ctt ggt acc cga 163
Thr Ser Pro Leu Leu Asn Asn Gly Gln Thr Cys Phe Leu Gly Thr Arg
10 15 20

atc ctt gct cca aaa tca cgt tac gcg gaa gta gtc gat gca ttc acc 211
Ile Leu Ala Pro Lys Ser Arg Tyr Ala Glu Val Val Asp Ala Phe Thr
25 30 35

gct ttc gct ggc agc ctg cag gtt gga gtc acg tcc tcc cct gac act 259
Ala Phe Ala Gly Ser Leu Gln Val Gly Val Thr Ser Ser Pro Asp Thr
40 45 50

cag atc gga ccg atg gcg act gcc cgg cag cgt gag cgc gtg gaa tcc 307
Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg Glu Arg Val Glu Ser
55 60 65

tac att tcc caa ggc aaa aat gct gga gcc cgc atc act gtc ggt ggc 355
Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg Ile Thr Val Gly Gly
70 75 80 85

agc cgt cca cga gat ctt gac gcc gga ttc ttc gtt gag cca aca gtg 403
Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe Val Glu Pro Thr Val
90 95 100

ttc gcc gat gta gac aat cgc gca gcc att gcc caa gat gaa atc ttc 451
Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala Gln Asp Glu Ile Phe
105 110 115

gga ccg gtg ccc tct gtt gtt tcc tac caa gac gat gaa cac gcc atc 499
Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp Asp Glu His Ala Ile
120 125 130

caa cta gcc aac gat tcc gaa ttc ggt ctc ggc gga act gtc tgg acg 547
Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly Gly Thr Val Trp Thr
135 140 145

agc gat ccc gag cgc ggc gct gca ttg gcc cgc cga gtt cac aca gga 595
Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg Arg Val His Thr Gly
150 155 160 165

acc att ggc atc aac cgc tat atc cct gat ccc gcc gca cca ttt gga 643
Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro Ala Ala Pro Phe Gly
170 175 180

ggt gtg aaa aac agt ggc ctt ggc aga gaa ctc ggc ccc gaa ggt ctt 691
Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu Gly Pro Glu Gly Leu
185 190 195

gct tcc tac caa gaa acc caa acc att tat ctc taatccaaac tgcacctata 744
Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu

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200

205

tat

747

<210> 278

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 278

Val Glu Ala Gln Phe Thr Ser Pro Leu Leu Asn Asn Gly Gln Thr Cys
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Phe Leu Gly Thr Arg Ile Leu Ala Pro Lys Ser Arg Tyr Ala Glu Val
 20 25 30

Val Asp Ala Phe Thr Ala Phe Ala Gly Ser Leu Gln Val Gly Val Thr
 35 40 45

Ser Ser Pro Asp Thr Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg
 50 55 60

Glu Arg Val Glu Ser Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg
 65 70 75 80

Ile Thr Val Gly Gly Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe
 85 90 95

Val Glu Pro Thr Val Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala
 100 105 110

Gln Asp Glu Ile Phe Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp
 115 120 125

Asp Glu His Ala Ile Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly
 130 135 140

Gly Thr Val Trp Thr Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg
 145 150 155 160

Arg Val His Thr Gly Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro
 165 170 175

Ala Ala Pro Phe Gly Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu
 180 185 190

Gly Pro Glu Gly Leu Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu
 195 200 205

<210> 279

<211> 747

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(724)

<223> RXS02554

<400> 279

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ggataggctc cataaaaaata accaaaggcg gaaaatttca atg tca cac act aag 115
Met Ser His Thr Lys
1 5

cca tcc att gcc atc ctc ggt gct ggc cga gtg ggt tct tca ctt gcc 163
Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val Gly Ser Ser Leu Ala
10 15 20

agg tca gcg gtc gcc gca ggc tat gag gta aag gtt gct ggt tca ggt 211
Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys Val Ala Gly Ser Gly
25 30 35

gct gtg gac aaa atc gct ctt acc gct gag atc ctt atg ccc ggc gcg 259
Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile Leu Met Pro Gly Ala
40 45 50

gtt cca agc act gct gac cag gct gta aag gat gca gat att gtg ttc 307
Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp Ala Asp Ile Val Phe
55 60 65

ttg gct gtt ccc ctg cat aaa ttc cgc agt gtc aat cca gcc act tta 355
Leu Ala Val Pro Leu His Lys Phe Arg Ser Val Asn Pro Ala Thr Leu
70 75 80 85

gag ggc aag atc gtt att gac acg atg aac cac tgg gtt ccg gtc aat 403
Glu Gly Lys Ile Val Ile Asp Thr Met Asn His Trp Val Pro Val Asn
90 95 100

ggt gag ttg gag gaa att gat cag gat ccg cgc agc act tcg gag att 451
Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg Ser Thr Ser Glu Ile
105 110 115

att gcg gag ttt ttc gcg gga tca acc atg gtg aag tct ttt aac cac 499
Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val Lys Ser Phe Asn His
120 125 130

att ggt tat cac gag att gag cag gat gcg ggt acc ggg cgt gcg att 547
Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly Thr Gly Arg Ala Ile
135 140 145

gcg tat gcc acg gat gat gtg gat gca ggt gcc cag gtt gca cag cta 595
Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala Gln Val Ala Gln Leu
150 155 160 165

att aag agt ttt ggg ttt gtt cct tta aat att ggc gca ttg gaa aac 643
Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile Gly Ala Leu Glu Asn
170 175 180

ggc cgt att ctg gaa cct ggc caa gaa gct ttc ggc gcg cac ctt aat 691
Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe Gly Ala His Leu Asn
185 190 195

aaa gat tcg cgc cta gaa ctt gtt aat cag cgg tagtacctcg atcttcagcc 744
Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
200 205

aac

747

<210> 280
 <211> 208
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 280
 Met Ser His Thr Lys Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val
 1 5 10 15
 Gly Ser Ser Leu Ala Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys
 20 25 30
 Val Ala Gly Ser Gly Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile
 35 40 45
 Leu Met Pro Gly Ala Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp
 50 55 60
 Ala Asp Ile Val Phe Leu Ala Val Pro Leu His Lys Phe Arg Ser Val
 65 70 75 80
 Asn Pro Ala Thr Leu Glu Gly Lys Ile Val Ile Asp Thr Met Asn His
 85 90 95
 Trp Val Pro Val Asn Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg
 100 105 110
 Ser Thr Ser Glu Ile Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val
 115 120 125
 Lys Ser Phe Asn His Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly
 130 135 140
 Thr Gly Arg Ala Ile Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala
 145 150 155 160
 Gln Val Ala Gln Leu Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile
 165 170 175
 Gly Ala Leu Glu Asn Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe
 180 185 190
 Gly Ala His Leu Asn Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
 195 200 205

<210> 281
 <211> 606
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(583)
 <223> RXS03058

<400> 281
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 gcccatattgg aatcacaaca ccgcatatcg gccatggctg gtg tca aag ctc aaa 115

	Val	Ser	Lys	Leu	Lys	
	1				5	
ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc						163
Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala						
				10	15	20
gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt						211
Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu						
				25	30	35
att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc						259
Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala						
				40	45	50
atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt						307
Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu						
				55	60	65
aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta						355
Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val						
				70	75	80
ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta						403
Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu						
				90	95	100
caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa						451
Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln						
				105	110	115
atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata						499
Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile						
				120	125	130
cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga						547
Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly						
				135	140	145
atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc						593
Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro						
				150	155	160
tataaacc aa aaa						606

<210> 282

<211> 161

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

Val Ser Lys Leu Lys Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly															
1				5				10					15		
Asp His Ser Phe Ala Asp Leu Ala Gly Arg Gln Val Ala His Val Asp															
				20			25						30		
Val Val Asp Pro Leu Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr															
				35			40						45		

Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn
 50 55 60
 Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly
 65 70 75 80
 Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp
 85 90 95
 Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile
 100 105 110
 Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu
 115 120 125
 Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg
 130 135 140
 Arg Ile Arg Arg Gly Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys
 145 150 155 160
 Pro

<210> 283

<211> 544

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(514)

<223> RXS03218

<400> 283

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 atcaacaatt gccctttaac caggagtatt cttagcttct atg act cct gat ctt 115
 Met Thr Pro Asp Leu
 1 5
 gca gct ttt ctg gac aaa ctt tat gcc gag ggg cag gaa ttt gat gca 163
 Ala Ala Phe Leu Asp Lys Leu Tyr Ala Glu Gly Gln Glu Phe Asp Ala
 10 15 20
 gag caa ccg gat cgg ctt gat cgc agg aga aac ctt gaa tct gaa agc 211
 Glu Gln Pro Asp Arg Leu Asp Arg Arg Arg Asn Leu Glu Ser Glu Ser
 25 30 35
 gct gcg cta ctt cgc tcg ctc atc tac gga att agt cca aag tca gtt 259
 Ala Ala Leu Leu Arg Ser Leu Ile Tyr Gly Ile Ser Pro Lys Ser Val
 40 45 50
 ctc gag cta ggc aca tcc aat ggt tac tcg act att tgg atg gca gat 307
 Leu Glu Leu Gly Thr Ser Asn Gly Tyr Ser Thr Ile Trp Met Ala Asp
 55 60 65
 gtc gtg aat tta aca aca gta gac aat gat cct gag cgg tct ttg gat 355
 Val Val Asn Leu Thr Thr Val Asp Asn Asp Pro Glu Arg Ser Leu Asp
 70 75 80 85

gct gca gca aac ctt cgc gcc gct gga gtt gaa gaa aaa gtt caa cga 403
 Ala Ala Ala Asn Leu Arg Ala Ala Gly Val Glu Glu Lys Val Gln Arg
 90 95 100

atc gtc gcc gat gga gca acc gta ctt gcc gat tcc gcc gat gaa caa 451
 Ile Val Ala Asp Gly Ala Thr Val Leu Ala Asp Ser Ala Asp Glu Gln
 105 110 115

tgg gat ttc att ttc ctt gat gcc gaa caa tca ctc tat gta aat tgg 499
 Trp Asp Phe Ile Phe Leu Asp Ala Glu Gln Ser Leu Tyr Val Asn Trp
 120 125 130

tgg cct gac ctg caa tgagttctag caaatggcgg cttgttagtg 544
 Trp Pro Asp Leu Gln
 135

<210> 284

<211> 138

<212> PRT

<213> Corynebacterium glutamicum

<400> 284

Met Thr Pro Asp Leu Ala Ala Phe Leu Asp Lys Leu Tyr Ala Glu Gly
 1 5 10 15

Gln Glu Phe Asp Ala Glu Gln Pro Asp Arg Leu Asp Arg Arg Arg Asn
 20 25 30

Leu Glu Ser Glu Ser Ala Ala Leu Leu Arg Ser Leu Ile Tyr Gly Ile
 35 40 45

Ser Pro Lys Ser Val Leu Glu Leu Gly Thr Ser Asn Gly Tyr Ser Thr
 50 55 60

Ile Trp Met Ala Asp Val Val Asn Leu Thr Thr Val Asp Asn Asp Pro
 65 70 75 80

Glu Arg Ser Leu Asp Ala Ala Ala Asn Leu Arg Ala Ala Gly Val Glu
 85 90 95

Glu Lys Val Gln Arg Ile Val Ala Asp Gly Ala Thr Val Leu Ala Asp
 100 105 110

Ser Ala Asp Glu Gln Trp Asp Phe Ile Phe Leu Asp Ala Glu Gln Ser
 115 120 125

Leu Tyr Val Asn Trp Trp Pro Asp Leu Gln
 130 135

<210> 285

<211> 537

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(514)

<223> FRXA01918

<400> 285

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atcaacaatt gccctttaac caggagtatt cttagcttct atg act cct gat ctt 115
                               Met Thr Pro Asp Leu
                               1           5

gca gct ttt ctg gac aaa ctt tat gcc gag ggg cag gaa ttt gat gca 163
Ala Ala Phe Leu Asp Lys Leu Tyr Ala Glu Gly Gln Glu Phe Asp Ala
                               10           15           20

gag caa ccg gat cgg ctt gat cgc agg aga aac ctt gaa tct gaa agc 211
Glu Gln Pro Asp Arg Leu Asp Arg Arg Arg Asn Leu Glu Ser Glu Ser
                               25           30           35

gct gcg cta ctt cgc tcg ctc atc tac gga att agt cca aag tca gtt 259
Ala Ala Leu Leu Arg Ser Leu Ile Tyr Gly Ile Ser Pro Lys Ser Val
                               40           45           50

ctc gag cta ggc aca tcc aat ggt tac tcg act att tgg atg gca gat 307
Leu Glu Leu Gly Thr Ser Asn Gly Tyr Ser Thr Ile Trp Met Ala Asp
                               55           60           65

gtc gtg aat tta aca aca gta gac aat gat cct gag cgg tct ttg gat 355
Val Val Asn Leu Thr Thr Val Asp Asn Asp Pro Glu Arg Ser Leu Asp
                               70           75           80           85

gct gca gca aac ctt cgc gcc gct gga gtt gaa gaa aaa gtt caa cga 403
Ala Ala Ala Asn Leu Arg Ala Ala Gly Val Glu Glu Lys Val Gln Arg
                               90           95           100

atc gtc gcc gat gga gca acc gta ctt gcc gat tcc gcc gat gaa caa 451
Ile Val Ala Asp Gly Ala Thr Val Leu Ala Asp Ser Ala Asp Glu Gln
                               105           110           115

tgg gat ttc att ttc ctt gat gcc gaa caa tca ctc tat gta aat tgg 499
Trp Asp Phe Ile Phe Leu Asp Ala Glu Gln Ser Leu Tyr Val Asn Trp
                               120           125           130

tgg cct gac ctg caa tgagttctag caaatggcgg ctt 537
Trp Pro Asp Leu Gln
                               135

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<210> 286

<211> 138

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 286

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Met Thr Pro Asp Leu Ala Ala Phe Leu Asp Lys Leu Tyr Ala Glu Gly
 1           5           10           15

Gln Glu Phe Asp Ala Glu Gln Pro Asp Arg Leu Asp Arg Arg Arg Asn
 20           25           30

Leu Glu Ser Glu Ser Ala Ala Leu Leu Arg Ser Leu Ile Tyr Gly Ile
 35           40           45

Ser Pro Lys Ser Val Leu Glu Leu Gly Thr Ser Asn Gly Tyr Ser Thr

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50	55	60
Ile Trp Met Ala Asp Val Val Asn Leu Thr Thr Val Asp Asn Asp Pro		
65	70	75 80
Glu Arg Ser Leu Asp Ala Ala Ala Asn Leu Arg Ala Ala Gly Val Glu		
	85	90 95
Glu Lys Val Gln Arg Ile Val Ala Asp Gly Ala Thr Val Leu Ala Asp		
	100	105 110
Ser Ala Asp Glu Gln Trp Asp Phe Ile Phe Leu Asp Ala Glu Gln Ser		
	115	120 125
Leu Tyr Val Asn Trp Trp Pro Asp Leu Gln		
130	135	

<210> 287

<211> 672

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(649)

<223> RXC00110

<400> 287

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aataacgaac gctaatttta aacactggag gagcttccac gtg agc aac aaa gac 115
                                         Val Ser Asn Lys Asp
                                         1 5
ggc ctt ttt act gac ggt aac agc acg ttt gca cct aag gtg gat tca 163
Gly Leu Phe Thr Asp Gly Asn Ser Thr Phe Ala Pro Lys Val Asp Ser
                                         10 15 20
att ccc ctc agc gat gtg gat acc agc gtt agc ggt gaa gcc tcc atc 211
Ile Pro Leu Ser Asp Val Asp Thr Ser Val Ser Gly Glu Ala Ser Ile
                                         25 30 35
ggc acg ctg atc tcc aac gca acc tcc caa atg tcc agc ctt ttc cgc 259
Gly Thr Leu Ile Ser Asn Ala Thr Ser Gln Met Ser Ser Leu Phe Arg
                                         40 45 50
gca gaa gtt gag ctg gcg aag act gaa ctc gca ggc gaa gcc aag aaa 307
Ala Glu Val Glu Leu Ala Lys Thr Glu Leu Ala Gly Glu Ala Lys Lys
                                         55 60 65
gct gcc atc ggc ggc ggc gca ttc agc gtt gct ggc gta atc gca ctg 355
Ala Ala Ile Gly Gly Gly Ala Phe Ser Val Ala Gly Val Ile Ala Leu
                                         70 75 80 85
tac agc tcc ttc ttc ttt ttc ttc ttc gtc gca gca ctg ctg agc gag 403
Tyr Ser Ser Phe Phe Phe Phe Phe Phe Val Ala Ala Leu Leu Ser Glu
                                         90 95 100
tgg att aag cct tgg gca gca ttc ctc atc gtg ttc ctc ttc atg ctg 451
Trp Ile Lys Pro Trp Ala Ala Phe Leu Ile Val Phe Leu Phe Met Leu

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105 110 115
 gtc atc gcc gca gct ctc gca ctg ttc ggc tgg cgc aag gtg aag aag 499
 Val Ile Ala Ala Ala Leu Ala Leu Phe Gly Trp Arg Lys Val Lys Lys
 120 125 130
 atg ggc gct ccg aag aac acc atc caa tcg gtc aac caa ctg aag aac 547
 Met Gly Ala Pro Lys Asn Thr Ile Gln Ser Val Asn Gln Leu Lys Asn
 135 140 145
 ctg gtc cca ggt cag gca tcc gag aag ctg gag aag gcc aac aag cgt 595
 Leu Val Pro Gly Gln Ala Ser Glu Lys Leu Glu Lys Ala Asn Lys Arg
 150 155 160 165
 ggc ctc tac acc tcc gcg tcc ttc cac agc ccc ggc gcc atc act ggc 643
 Gly Leu Tyr Thr Ser Ala Ser Phe His Ser Pro Gly Ala Ile Thr Gly
 170 175 180
 gac cac taaaaaagga gacttcgatg gcc 672
 Asp His

<210> 288

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 288

Val Ser Asn Lys Asp Gly Leu Phe Thr Asp Gly Asn Ser Thr Phe Ala
 1 5 10 15
 Pro Lys Val Asp Ser Ile Pro Leu Ser Asp Val Asp Thr Ser Val Ser
 20 25 30
 Gly Glu Ala Ser Ile Gly Thr Leu Ile Ser Asn Ala Thr Ser Gln Met
 35 40 45
 Ser Ser Leu Phe Arg Ala Glu Val Glu Leu Ala Lys Thr Glu Leu Ala
 50 55 60
 Gly Glu Ala Lys Lys Ala Ala Ile Gly Gly Gly Ala Phe Ser Val Ala
 65 70 75 80
 Gly Val Ile Ala Leu Tyr Ser Ser Phe Phe Phe Phe Phe Phe Val Ala
 85 90 95
 Ala Leu Leu Ser Glu Trp Ile Lys Pro Trp Ala Ala Phe Leu Ile Val
 100 105 110
 Phe Leu Phe Met Leu Val Ile Ala Ala Ala Leu Ala Leu Phe Gly Trp
 115 120 125
 Arg Lys Val Lys Lys Met Gly Ala Pro Lys Asn Thr Ile Gln Ser Val
 130 135 140
 Asn Gln Leu Lys Asn Leu Val Pro Gly Gln Ala Ser Glu Lys Leu Glu
 145 150 155 160
 Lys Ala Asn Lys Arg Gly Leu Tyr Thr Ser Ala Ser Phe His Ser Pro
 165 170 175

Gly Ala Ile Thr Gly Asp His
180

<210> 289

<211> 954

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(931)

<223> RXC01971

<400> 289

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cagttcagta tctttgagcc acggctagaa tgtgaatcct atg tct aag aag aag 115
Met Ser Lys Lys Lys
1 5

cct cgc ccc att ccg gtt cct gcc caa ttt atc cct ggt ctc att gat 163
Pro Arg Pro Ile Pro Val Pro Ala Gln Phe Ile Pro Gly Leu Ile Asp
10 15 20

gcg cat aca cat ttg gca tcg tgt gga gga gat ctt gca ggg ttg gtg 211
Ala His Thr His Leu Ala Ser Cys Gly Gly Asp Leu Ala Gly Leu Val
25 30 35

gaa agg gcc aag gag gcg ggc gtc gaa aag ctt tgt acc gtc ggt gat 259
Glu Arg Ala Lys Glu Ala Gly Val Glu Lys Leu Cys Thr Val Gly Asp
40 45 50

ggt ttg gct gag gcc gag ctt gcg ctg gag gcc gcg caa cag ttt ggc 307
Gly Leu Ala Glu Ala Glu Leu Ala Leu Glu Ala Ala Gln Gln Phe Gly
55 60 65

aat gtg ttt gct gcg tgt gcg att cat ccg acg aag gct gat cag ttg 355
Asn Val Phe Ala Ala Cys Ala Ile His Pro Thr Lys Ala Asp Gln Leu
70 75 80 85

gat ggg gct gcg cgt gcg cgg ctg acg cag atg gcg gcg gat ccg aat 403
Asp Gly Ala Ala Arg Ala Arg Leu Thr Gln Met Ala Ala Asp Pro Asn
90 95 100

tgt gtg gcc att ggt gag act ggt ttg gat tcg tat tgg atc aag cac 451
Cys Val Ala Ile Gly Glu Thr Gly Leu Asp Ser Tyr Trp Ile Lys His
105 110 115

gat cca gag gac acg gcg gcg ttg gat gtg caa gag gag gcg ctg cgc 499
Asp Pro Glu Asp Thr Ala Ala Leu Asp Val Gln Glu Glu Ala Leu Arg
120 125 130

tgg cat att gat ttg gca att agt gcg gat aag ccg ttg atg att cac 547
Trp His Ile Asp Leu Ala Ile Ser Ala Asp Lys Pro Leu Met Ile His
135 140 145

aat cgt gag gcg gat gct gat ttg atg cga gtg ttg gcg gat gct cca 595
Asn Arg Glu Ala Asp Ala Asp Leu Met Arg Val Leu Ala Asp Ala Pro
150 155 160 165

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cct cca aaa gat acg att ctg cat tgt ttt tct tcg ccg ttg gac gtg 643
Pro Pro Lys Asp Thr Ile Leu His Cys Phe Ser Ser Pro Leu Asp Val
      170                      175                      180

gcg aag gaa gcg ttg gat cgt gga tat gtg ttg agt ttt gcg ggc aat 691
Ala Lys Glu Ala Leu Asp Arg Gly Tyr Val Leu Ser Phe Ala Gly Asn
      185                      190                      195

gtg acg ttt aag cgt aat gag gag ttg cgg gag gct gct cgt att gcg 739
Val Thr Phe Lys Arg Asn Glu Glu Leu Arg Glu Ala Ala Arg Ile Ala
      200                      205                      210

ccg att tcc cag att ttg att gaa acc gat gcg ccg tat atg acg ccg 787
Pro Ile Ser Gln Ile Leu Ile Glu Thr Asp Ala Pro Tyr Met Thr Pro
      215                      220                      225

gag ccg ttt cgg ggg agt agg aat gag ccg tcg ttg att ggt cat acg 835
Glu Pro Phe Arg Gly Ser Arg Asn Glu Pro Ser Leu Ile Gly His Thr
      230                      235                      240                      245

gcg cta tgc att gcg gag gtt cgg ggg atg gct gtg gag gat gtt gcg 883
Ala Leu Cys Ile Ala Glu Val Arg Gly Met Ala Val Glu Asp Val Ala
      250                      255                      260

gcg gct ttg aat gag aat ttt gat cgc gtt tat ggg gtc aca aat cta 931
Ala Ala Leu Asn Glu Asn Phe Asp Arg Val Tyr Gly Val Thr Asn Leu
      265                      270                      275

taacgtgagg tagctcacag tca 954

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<210> 290

<211> 277

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 290

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Met Ser Lys Lys Lys Pro Arg Pro Ile Pro Val Pro Ala Gln Phe Ile
 1                      5                      10                      15

Pro Gly Leu Ile Asp Ala His Thr His Leu Ala Ser Cys Gly Gly Asp
      20                      25                      30

Leu Ala Gly Leu Val Glu Arg Ala Lys Glu Ala Gly Val Glu Lys Leu
      35                      40                      45

Cys Thr Val Gly Asp Gly Leu Ala Glu Ala Glu Leu Ala Leu Glu Ala
      50                      55                      60

Ala Gln Gln Phe Gly Asn Val Phe Ala Ala Cys Ala Ile His Pro Thr
      65                      70                      75                      80

Lys Ala Asp Gln Leu Asp Gly Ala Ala Arg Ala Arg Leu Thr Gln Met
      85                      90                      95

Ala Ala Asp Pro Asn Cys Val Ala Ile Gly Glu Thr Gly Leu Asp Ser
      100                      105                      110

Tyr Trp Ile Lys His Asp Pro Glu Asp Thr Ala Ala Leu Asp Val Gln
      115                      120                      125

```

Glu Glu Ala Leu Arg Trp His Ile Asp Leu Ala Ile Ser Ala Asp Lys
 130 135 140
 Pro Leu Met Ile His Asn Arg Glu Ala Asp Ala Asp Leu Met Arg Val
 145 150 155 160
 Leu Ala Asp Ala Pro Pro Pro Lys Asp Thr Ile Leu His Cys Phe Ser
 165 170 175
 Ser Pro Leu Asp Val Ala Lys Glu Ala Leu Asp Arg Gly Tyr Val Leu
 180 185 190
 Ser Phe Ala Gly Asn Val Thr Phe Lys Arg Asn Glu Glu Leu Arg Glu
 195 200 205
 Ala Ala Arg Ile Ala Pro Ile Ser Gln Ile Leu Ile Glu Thr Asp Ala
 210 215 220
 Pro Tyr Met Thr Pro Glu Pro Phe Arg Gly Ser Arg Asn Glu Pro Ser
 225 230 235 240
 Leu Ile Gly His Thr Ala Leu Cys Ile Ala Glu Val Arg Gly Met Ala
 245 250 255
 Val Glu Asp Val Ala Ala Ala Leu Asn Glu Asn Phe Asp Arg Val Tyr
 260 265 270
 Gly Val Thr Asn Leu
 275

<210> 291
 <211> 465
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(442)
 <223> RXA02118

<400> 291
 gggctggtgc gggttgcttt aatggaggtc atgctcgcag gctaacagaa ttggtggttt 60
 tagtgctggt accagggaca tcggctagaa tctgctgaat atg tct gat caa tta 115
 Met Ser Asp Gln Leu
 1 5
 gct ccc tgc cct gag tgc agc agt gaa tat acc tac gaa aac ggc ggc 163
 Ala Pro Cys Pro Glu Cys Ser Ser Glu Tyr Thr Tyr Glu Asn Gly Gly
 10 15 20
 gtt ctg gtc tgc cca atg tgt gcc cac gaa tgg gtc gaa ggt gaa gta 211
 Val Leu Val Cys Pro Met Cys Ala His Glu Trp Val Glu Gly Glu Val
 25 30 35
 gcg gaa gaa acc gcg act gtc atc aaa gac tct gtg gga aat atc ctc 259
 Ala Glu Glu Thr Ala Thr Val Ile Lys Asp Ser Val Gly Asn Ile Leu
 40 45 50

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aat gat ggc gat tcc gta tcg att gtg aag agc ctc aaa gtc aag ggt 307
Asn Asp Gly Asp Ser Val Ser Ile Val Lys Ser Leu Lys Val Lys Gly
  55                      60                      65

ggc ggt gcc atc aag att ggc acc aaa gtc agc gga att cgt ctt ctt 355
Gly Gly Ala Ile Lys Ile Gly Thr Lys Val Ser Gly Ile Arg Leu Leu
  70                      75                      80                      85

gaa gag cca gtt gac ggc cac gac atc gac gct aag gtc cct gga ttt 403
Glu Glu Pro Val Asp Gly His Asp Ile Asp Ala Lys Val Pro Gly Phe
          90                      95                      100

ggc caa atg cga ctc aag tcc agt gtt gta aag aag gcc taaacccttt 452
Gly Gln Met Arg Leu Lys Ser Ser Val Val Lys Lys Ala
          105                      110

taaggagctt tag 465

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<210> 292
 <211> 114
 <212> PRT
 <213> *Corynebacterium glutamicum*

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<400> 292
Met Ser Asp Gln Leu Ala Pro Cys Pro Glu Cys Ser Ser Glu Tyr Thr
  1                      5                      10                      15

Tyr Glu Asn Gly Gly Val Leu Val Cys Pro Met Cys Ala His Glu Trp
          20                      25                      30

Val Glu Gly Glu Val Ala Glu Glu Thr Ala Thr Val Ile Lys Asp Ser
          35                      40                      45

Val Gly Asn Ile Leu Asn Asp Gly Asp Ser Val Ser Ile Val Lys Ser
          50                      55                      60

Leu Lys Val Lys Gly Gly Gly Ala Ile Lys Ile Gly Thr Lys Val Ser
          65                      70                      75                      80

Gly Ile Arg Leu Leu Glu Glu Pro Val Asp Gly His Asp Ile Asp Ala
          85                      90                      95

Lys Val Pro Gly Phe Gly Gln Met Arg Leu Lys Ser Ser Val Val Lys
          100                      105                      110

Lys Ala

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<210> 293
 <211> 537
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(514)
 <223> RXA00078

<400> 293

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<210> 294
<211> 138
<212> PRT
<213> Corynebacterium glutamicum
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<400> 294
Met Lys Ala Asp Leu Thr Pro Tyr Arg Gln Phe Asn Gly Asn Ala Lys
  1          5          10          15

Glu Ala Met Glu Phe Tyr Gln Thr Val Phe Gly Gly Glu Leu Gln Met
  20          25          30

Met Pro Phe Ser Ala Met His Ser Glu Glu Glu Val Gly Gly Asp Gly
  35          40          45

Glu Lys Ile Met His Ala Glu Leu Val Val Asp Gly Gln Lys Leu Leu
  50          55          60

```

Phe Ala Ser Asp Ile Pro Arg Val Met Gln Arg Met Lys Gly Glu Asp
 65 70 75 80
 Thr Pro Leu Ser Leu Thr Gly Gly Ala Glu Leu Glu Glu Glu Ile Arg
 85 90 95
 Gly Tyr Trp Glu Lys Leu Ser Glu Gly Gly Thr Val Thr Met Pro Leu
 100 105 110
 Glu Ala Val Pro Trp Gly Ala Val Tyr Gly Ala Leu Glu Asp Arg Phe
 115 120 125
 Gly Thr His Trp Met Phe Asn Ile Gly Gly
 130 135

<210> 295

<211> 391

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(391)

<223> RXA02105

<400> 295

gcggggcggtcg aaaagcggcg acctgcggat ctgtgacccg cgccataaat ggggtacgatg 60

gcgggttgaa aattccgtaa cttctttgag ggagaaaccc atg gtc ggc acg att 115
 Met Val Gly Thr Ile
 1 5

tcc acc tac atc gca ttc aat gga aac acc acg gaa gct ctg aaa cat 163
 Ser Thr Tyr Ile Ala Phe Asn Gly Asn Thr Thr Glu Ala Leu Lys His
 10 15 20

tgg caa gag gtt ttt ggt ggt gaa ctt aat ctt tta acc tac ggt cag 211
 Trp Gln Glu Val Phe Gly Gly Glu Leu Asn Leu Leu Thr Tyr Gly Gln
 25 30 35

ctc acc ttg gaa ggt atg ccg ttt gat cct cca gcg gat gcg ttg gcg 259
 Leu Thr Leu Glu Gly Met Pro Phe Asp Pro Pro Ala Asp Ala Leu Ala
 40 45 50

cac ggc gtc ctc acg ttg gac aat ggt ggt ttg att tct ggc agt gat 307
 His Gly Val Leu Thr Leu Asp Asn Gly Gly Leu Ile Ser Gly Ser Asp
 55 60 65

tct ttt gag gga gaa atg ctc gtc aaa gac acc gcg tac tcc atg ttg 355
 Ser Phe Glu Gly Glu Met Leu Val Lys Asp Thr Ala Tyr Ser Met Leu
 70 75 80 85

tat aac gcg gag tca gtg gaa gat ggt cgc gcg cgg 391
 Tyr Asn Ala Glu Ser Val Glu Asp Gly Arg Ala Arg
 90 95

<210> 296

<211> 97

<212> PRT

<213> Corynebacterium glutamicum

<400> 296

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Met Val Gly Thr Ile Ser Thr Tyr Ile Ala Phe Asn Gly Asn Thr Thr
  1           5           10           15

Glu Ala Leu Lys His Trp Gln Glu Val Phe Gly Gly Glu Leu Asn Leu
      20           25           30

Leu Thr Tyr Gly Gln Leu Thr Leu Glu Gly Met Pro Phe Asp Pro Pro
      35           40           45

Ala Asp Ala Leu Ala His Gly Val Leu Thr Leu Asp Asn Gly Gly Leu
      50           55           60

Ile Ser Gly Ser Asp Ser Phe Glu Gly Glu Met Leu Val Lys Asp Thr
      65           70           75           80

Ala Tyr Ser Met Leu Tyr Asn Ala Glu Ser Val Glu Asp Gly Arg Ala
      85           90           95
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Arg

<210> 297

<211> 1497

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1474)

<223> RXN00663

<400> 297

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ctgaacgatt ggtgaccggc tcatgaaaac ttgacgagtc cccggtattc gccagcgggtg 60

actactaccg tgggcgacaa gccacttag aggaggactt gtg aca acc acc tat 115
                               Val Thr Thr Thr Tyr
                               1           5

cca gat ttc ctt gga aat tct tcg ctc caa aca gat acg gag cac tgg 163
Pro Asp Phe Leu Gly Asn Ser Ser Leu Gln Thr Asp Thr Glu His Trp
      10           15           20

gaa atg gaa gga ggt gcg cag gaa gtc tct gtt act tat gtt ttg gac 211
Glu Met Glu Gly Gly Ala Gln Glu Val Ser Val Thr Tyr Val Leu Asp
      25           30           35

acg tca gtg ttg ctg tct gat ccg ttg tcg ttg aca cgg ttc gcg gag 259
Thr Ser Val Leu Leu Ser Asp Pro Leu Ser Leu Thr Arg Phe Ala Glu
      40           45           50

cac gat gta gtt ctg cca att gtt gta att acg gaa tta gaa gcc aag 307
His Asp Val Val Leu Pro Ile Val Val Ile Thr Glu Leu Glu Ala Lys
      55           60           65

cgt cat cac ccg gac ctt ggc ttt ttt gct cgc caa gcg ctt cgg atg 355
Arg His His Pro Asp Leu Gly Phe Phe Ala Arg Gln Ala Leu Arg Met
      70           75           80           85
```


ctg gat gag ctg cgt gag atc cat ggg gat ttg tcc aag cca ctg cca	403
Leu Asp Glu Leu Arg Glu Ile His Gly Asp Leu Ser Lys Pro Leu Pro	
90 95 100	
att ggc gat gaa ggc gga cac atc cat gtt gag ctg aat cac caa aac	451
Ile Gly Asp Glu Gly Gly His Ile His Val Glu Leu Asn His Gln Asn	
105 110 115	
acg ggg tcc ttg ccc gtg gga ttc cgc ctt ggt gac aat gac acc cgc	499
Thr Gly Ser Leu Pro Val Gly Phe Arg Leu Gly Asp Asn Asp Thr Arg	
120 125 130	
atc ctt gca gtg gcc aag aat ctg cag gaa gag ggc cac aat gtg gtt	547
Ile Leu Ala Val Ala Lys Asn Leu Gln Glu Glu Gly His Asn Val Val	
135 140 145	
ctg gtg tcg aag gac ctg ccg atg cgg att aag gcg tcg gca agc gga	595
Leu Val Ser Lys Asp Leu Pro Met Arg Ile Lys Ala Ser Ala Ser Gly	
150 155 160 165	
atc gcc gca cag gaa tac cgc gct gcc ctg gcg cgc gac cgt ggt tac	643
Ile Ala Ala Gln Glu Tyr Arg Ala Ala Leu Ala Arg Asp Arg Gly Tyr	
170 175 180	
acc ggc atg acc cac gcc aat atc acc gat gac cag ctc agc gag ctc	691
Thr Gly Met Thr His Ala Asn Ile Thr Asp Asp Gln Leu Ser Glu Leu	
185 190 195	
tac gac acc ggc gag gtg cgc att gag gag ctc gaa aag ctg ccc gtc	739
Tyr Asp Thr Gly Glu Val Arg Ile Glu Glu Leu Glu Lys Leu Pro Val	
200 205 210	
aac cac ggc ttc acc ctc aaa tcc aac agc ggt tcg gcg ctt ggt cgt	787
Asn His Gly Phe Thr Leu Lys Ser Asn Ser Gly Ser Ala Leu Gly Arg	
215 220 225	
atg aat tcc gac aag atc atc gag ctt gtc ccc ggc gac cag cag gta	835
Met Asn Ser Asp Lys Ile Ile Glu Leu Val Pro Gly Asp Gln Gln Val	
230 235 240 245	
ttc ggt atc agc ggg cgt agc gct gag cag cgg gtt gcc att gat ttg	883
Phe Gly Ile Ser Gly Arg Ser Ala Glu Gln Arg Val Ala Ile Asp Leu	
250 255 260	
ctt aac gac gac gcc gtc ggc atc gta tcc atc ggc ggc ccc gcg ggt	931
Leu Asn Asp Asp Ala Val Gly Ile Val Ser Ile Gly Gly Pro Ala Gly	
265 270 275	
aca ggt aaa agc gca ctc gca ctg tgt gcc ggc ctg gaa gct gtg atg	979
Thr Gly Lys Ser Ala Leu Ala Leu Cys Ala Gly Leu Glu Ala Val Met	
280 285 290	
gag cgt cgc att cag cgc aag att atc gtg ttc cgc cca ctc ttt gcc	1027
Glu Arg Arg Ile Gln Arg Lys Ile Ile Val Phe Arg Pro Leu Phe Ala	
295 300 305	
gtt ggc gga cag gaa ctt ggc tac ctg cct ggc gac caa gaa gaa aaa	1075
Val Gly Gly Gln Glu Leu Gly Tyr Leu Pro Gly Asp Gln Glu Glu Lys	
310 315 320 325	

atg ggg cct tgg gcg caa gcg gtt ttt gac acc cta agc tcc atg gtc 1123
 Met Gly Pro Trp Ala Gln Ala Val Phe Asp Thr Leu Ser Ser Met Val
 330 335 340

agc caa aac atc atc gat gaa gcc ctc tcc cgc ggc ctc atc gaa gtt 1171
 Ser Gln Asn Ile Ile Asp Glu Ala Leu Ser Arg Gly Leu Ile Glu Val
 345 350 355

ctc cca ctt act cac atc cgc gga cgc tca ctc cac gat gct ttc gtc 1219
 Leu Pro Leu Thr His Ile Arg Gly Arg Ser Leu His Asp Ala Phe Val
 360 365 370

atc gtc gac gag gcc caa tcc cta gaa cgc aac gtg ttg ctc acc atg 1267
 Ile Val Asp Glu Ala Gln Ser Leu Glu Arg Asn Val Leu Leu Thr Met
 375 380 385

ctg tct cgc atc ggc cag aat tcc cga gta gtt ctc acc cat gac gta 1315
 Leu Ser Arg Ile Gly Gln Asn Ser Arg Val Val Leu Thr His Asp Val
 390 395 400 405

gcg cag cgc gac aac ctg cgc gtt ggt cgc tac gac ggc atc gtc tct 1363
 Ala Gln Arg Asp Asn Leu Arg Val Gly Arg Tyr Asp Gly Ile Val Ser
 410 415 420

gtg gtg gaa gca ctc aag gat cac gaa ctg ttt ggc cac atc acg ttg 1411
 Val Val Glu Ala Leu Lys Asp His Glu Leu Phe Gly His Ile Thr Leu
 425 430 435

cag cgt tcc gaa cgc tcc cga atc gct gag ttg gtc acc caa gtt ttg 1459
 Gln Arg Ser Glu Arg Ser Arg Ile Ala Glu Leu Val Thr Gln Val Leu
 440 445 450

gat gcg ccg tct ctg tagtcgcgca gtctgtggcg att 1497
 Asp Ala Pro Ser Leu
 455

<210> 298

<211> 458

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 298

Val Thr Thr Thr Tyr Pro Asp Phe Leu Gly Asn Ser Ser Leu Gln Thr
 1 5 10 15

Asp Thr Glu His Trp Glu Met Glu Gly Gly Ala Gln Glu Val Ser Val
 20 25 30

Thr Tyr Val Leu Asp Thr Ser Val Leu Leu Ser Asp Pro Leu Ser Leu
 35 40 45

Thr Arg Phe Ala Glu His Asp Val Val Leu Pro Ile Val Val Ile Thr
 50 55 60

Glu Leu Glu Ala Lys Arg His His Pro Asp Leu Gly Phe Phe Ala Arg
 65 70 75 80

Gln Ala Leu Arg Met Leu Asp Glu Leu Arg Glu Ile His Gly Asp Leu
 85 90 95

Ser Lys Pro Leu Pro Ile Gly Asp Glu Gly Gly His Ile His Val Glu
 100 105 110
 Leu Asn His Gln Asn Thr Gly Ser Leu Pro Val Gly Phe Arg Leu Gly
 115 120 125
 Asp Asn Asp Thr Arg Ile Leu Ala Val Ala Lys Asn Leu Gln Glu Glu
 130 135 140
 Gly His Asn Val Val Leu Val Ser Lys Asp Leu Pro Met Arg Ile Lys
 145 150 155 160
 Ala Ser Ala Ser Gly Ile Ala Ala Gln Glu Tyr Arg Ala Ala Leu Ala
 165 170 175
 Arg Asp Arg Gly Tyr Thr Gly Met Thr His Ala Asn Ile Thr Asp Asp
 180 185 190
 Gln Leu Ser Glu Leu Tyr Asp Thr Gly Glu Val Arg Ile Glu Glu Leu
 195 200 205
 Glu Lys Leu Pro Val Asn His Gly Phe Thr Leu Lys Ser Asn Ser Gly
 210 215 220
 Ser Ala Leu Gly Arg Met Asn Ser Asp Lys Ile Ile Glu Leu Val Pro
 225 230 235 240
 Gly Asp Gln Gln Val Phe Gly Ile Ser Gly Arg Ser Ala Glu Gln Arg
 245 250 255
 Val Ala Ile Asp Leu Leu Asn Asp Asp Ala Val Gly Ile Val Ser Ile
 260 265 270
 Gly Gly Pro Ala Gly Thr Gly Lys Ser Ala Leu Ala Leu Cys Ala Gly
 275 280 285
 Leu Glu Ala Val Met Glu Arg Arg Ile Gln Arg Lys Ile Ile Val Phe
 290 295 300
 Arg Pro Leu Phe Ala Val Gly Gly Gln Glu Leu Gly Tyr Leu Pro Gly
 305 310 315 320
 Asp Gln Glu Glu Lys Met Gly Pro Trp Ala Gln Ala Val Phe Asp Thr
 325 330 335
 Leu Ser Ser Met Val Ser Gln Asn Ile Ile Asp Glu Ala Leu Ser Arg
 340 345 350
 Gly Leu Ile Glu Val Leu Pro Leu Thr His Ile Arg Gly Arg Ser Leu
 355 360 365
 His Asp Ala Phe Val Ile Val Asp Glu Ala Gln Ser Leu Glu Arg Asn
 370 375 380
 Val Leu Leu Thr Met Leu Ser Arg Ile Gly Gln Asn Ser Arg Val Val
 385 390 395 400
 Leu Thr His Asp Val Ala Gln Arg Asp Asn Leu Arg Val Gly Arg Tyr
 405 410 415
 Asp Gly Ile Val Ser Val Val Glu Ala Leu Lys Asp His Glu Leu Phe

420	425	430
Gly His Ile Thr Leu Gln Arg	Ser Glu Arg Ser Arg	Ile Ala Glu Leu
435	440	445
Val Thr Gln Val Leu Asp	Ala Pro Ser Leu	
450	455	

<210> 299
 <211> 1019
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(996)
 <223> FRXA00663

<400> 299	
ctt ggt gac aat gac acc cgc atc ctt gca gtg gcc aag aat ctg cag	48
Leu Gly Asp Asn Asp Thr Arg Ile Leu Ala Val Ala Lys Asn Leu Gln	
1 5 10 15	
gaa gag ggc cac aat gtg gtt ctg gtg tcg aag gac ctg ccg atg cgg	96
Glu Glu Gly His Asn Val Val Leu Val Ser Lys Asp Leu Pro Met Arg	
20 25 30	
att aag gcg tcg gca agc gga atc gcc gca cag gaa tac cgc gct gcc	144
Ile Lys Ala Ser Ala Ser Gly Ile Ala Ala Gln Glu Tyr Arg Ala Ala	
35 40 45	
ctg gcg cgc gac cgt ggt tac acc ggc atg acc cac gcc aat atc acc	192
Leu Ala Arg Asp Arg Gly Tyr Thr Gly Met Thr His Ala Asn Ile Thr	
50 55 60	
gat gac cag ctc agc gag ctc tac gac acc ggc gag gtg cgc att gag	240
Asp Asp Gln Leu Ser Glu Leu Tyr Asp Thr Gly Glu Val Arg Ile Glu	
65 70 75 80	
gag ctc gaa aag ctg ccc gtc aac cac ggc ttc acc ctc aaa tcc aac	288
Glu Leu Glu Lys Leu Pro Val Asn His Gly Phe Thr Leu Lys Ser Asn	
85 90 95	
agc ggt tcg gcg ctt ggt cgt atg aat tcc gac aag atc atc gag ctt	336
Ser Gly Ser Ala Leu Gly Arg Met Asn Ser Asp Lys Ile Ile Glu Leu	
100 105 110	
gtc ccc ggc gac cag cag gta ttc ggt atc agc ggg cgt agc gct gag	384
Val Pro Gly Asp Gln Gln Val Phe Gly Ile Ser Gly Arg Ser Ala Glu	
115 120 125	
cag cgg gtt gcc att gat ttg ctt aac gac gac gcc gtc ggc atc gta	432
Gln Arg Val Ala Ile Asp Leu Leu Asn Asp Asp Ala Val Gly Ile Val	
130 135 140	
tcc atc ggc ggc ccc gcg ggt aca ggt aaa agc gca ctc gca ctg tgt	480
Ser Ile Gly Gly Pro Ala Gly Thr Gly Lys Ser Ala Leu Ala Leu Cys	
145 150 155 160	
gcc ggc ctg gaa gct gtg atg gag cgt cgc att cag cgc aag att atc	528

Ala Gly Leu Glu Ala Val Met Glu Arg Arg Ile Gln Arg Lys Ile Ile
165 170 175

gtg ttc cgc cca ctc ttt gcc gtt ggc gga cag gaa ctt ggc tac ctg 576
Val Phe Arg Pro Leu Phe Ala Val Gly Gly Gln Glu Leu Gly Tyr Leu
180 185 190

cct ggc gac caa gaa gaa aaa atg ggg cct tgg gcg caa gcg gtt ttt 624
Pro Gly Asp Gln Glu Glu Lys Met Gly Pro Trp Ala Gln Ala Val Phe
195 200 205

gac acc cta agc tcc atg gtc agc caa aac atc atc gat gaa gcc ctc 672
Asp Thr Leu Ser Ser Met Val Ser Gln Asn Ile Ile Asp Glu Ala Leu
210 215 220

tcc cgc ggc ctc atc gaa gtt ctc cca ctt act cac atc cgc gga cgc 720
Ser Arg Gly Leu Ile Glu Val Leu Pro Leu Thr His Ile Arg Gly Arg
225 230 235 240

tca ctc cac gat gct ttc gtc atc gtc gac gag gcc caa tcc cta gaa 768
Ser Leu His Asp Ala Phe Val Ile Val Asp Glu Ala Gln Ser Leu Glu
245 250 255

cgc aac gtg ttg ctc acc atg ctg tct cgc atc ggc cag aat tcc cga 816
Arg Asn Val Leu Leu Thr Met Leu Ser Arg Ile Gly Gln Asn Ser Arg
260 265 270

gta gtt ctc acc cat gac gta gcg cag cgc gac aac ctg cgc gtt ggt 864
Val Val Leu Thr His Asp Val Ala Gln Arg Asp Asn Leu Arg Val Gly
275 280 285

cgc tac gac ggc atc gtc tct gtg gtg gaa gca ctc aag gat cac gaa 912
Arg Tyr Asp Gly Ile Val Ser Val Val Glu Ala Leu Lys Asp His Glu
290 295 300

ctg ttt ggc cac atc acg ttg cag cgt tcc gaa cgc tcc cga atc gct 960
Leu Phe Gly His Ile Thr Leu Gln Arg Ser Glu Arg Ser Arg Ile Ala
305 310 315 320

gag ttg gtc acc caa gtt ttg gat gcg ccg tct ctg tagtcgcgca 1006
Glu Leu Val Thr Gln Val Leu Asp Ala Pro Ser Leu
325 330

gtctgtggcg att 1019

<210> 300

<211> 332

<212> PRT

<213> Corynebacterium glutamicum

<400> 300

Leu Gly Asp Asn Asp Thr Arg Ile Leu Ala Val Ala Lys Asn Leu Gln
1 5 10 15

Glu Glu Gly His Asn Val Val Leu Val Ser Lys Asp Leu Pro Met Arg
20 25 30

Ile Lys Ala Ser Ala Ser Gly Ile Ala Ala Gln Glu Tyr Arg Ala Ala
35 40 45

Leu Ala Arg Asp Arg Gly Tyr Thr Gly Met Thr His Ala Asn Ile Thr
 50 55 60
 Asp Asp Gln Leu Ser Glu Leu Tyr Asp Thr Gly Glu Val Arg Ile Glu
 65 70 75 80
 Glu Leu Glu Lys Leu Pro Val Asn His Gly Phe Thr Leu Lys Ser Asn
 85 90 95
 Ser Gly Ser Ala Leu Gly Arg Met Asn Ser Asp Lys Ile Ile Glu Leu
 100 105 110
 Val Pro Gly Asp Gln Gln Val Phe Gly Ile Ser Gly Arg Ser Ala Glu
 115 120 125
 Gln Arg Val Ala Ile Asp Leu Leu Asn Asp Asp Ala Val Gly Ile Val
 130 135 140
 Ser Ile Gly Gly Pro Ala Gly Thr Gly Lys Ser Ala Leu Ala Leu Cys
 145 150 155 160
 Ala Gly Leu Glu Ala Val Met Glu Arg Arg Ile Gln Arg Lys Ile Ile
 165 170 175
 Val Phe Arg Pro Leu Phe Ala Val Gly Gly Gln Glu Leu Gly Tyr Leu
 180 185 190
 Pro Gly Asp Gln Glu Glu Lys Met Gly Pro Trp Ala Gln Ala Val Phe
 195 200 205
 Asp Thr Leu Ser Ser Met Val Ser Gln Asn Ile Ile Asp Glu Ala Leu
 210 215 220
 Ser Arg Gly Leu Ile Glu Val Leu Pro Leu Thr His Ile Arg Gly Arg
 225 230 235 240
 Ser Leu His Asp Ala Phe Val Ile Val Asp Glu Ala Gln Ser Leu Glu
 245 250 255
 Arg Asn Val Leu Leu Thr Met Leu Ser Arg Ile Gly Gln Asn Ser Arg
 260 265 270
 Val Val Leu Thr His Asp Val Ala Gln Arg Asp Asn Leu Arg Val Gly
 275 280 285
 Arg Tyr Asp Gly Ile Val Ser Val Val Glu Ala Leu Lys Asp His Glu
 290 295 300
 Leu Phe Gly His Ile Thr Leu Gln Arg Ser Glu Arg Ser Arg Ile Ala
 305 310 315 320
 Glu Leu Val Thr Gln Val Leu Asp Ala Pro Ser Leu
 325 330

<210> 301

<211> 1140

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1117)

<223> RXA00888

<400> 301

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acctttcttg aacattccga aagcaggccg aactagcact gtg act gcc ccg cga 115
                                   Val Thr Ala Pro Arg
                                   1 5

aaa acc cgc aca gaa gta atc acc act gtc ctc aat cta gaa cgc acg 163
Lys Thr Arg Thr Glu Val Ile Thr Thr Val Leu Asn Leu Glu Arg Thr
                                   10 15 20

ctc gcg caa acc gtt tta gga atc aac gac gaa aac ctg cgt gtg ttg 211
Leu Ala Gln Thr Val Leu Gly Ile Asn Asp Glu Asn Leu Arg Val Leu
                                   25 30 35

gac aat caa att gat tgc gat att cac gtg cgt ggc acc cac gtg gaa 259
Asp Asn Gln Ile Asp Cys Asp Ile His Val Arg Gly Thr His Val Glu
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ctc acc ggg cca gcc cac gaa gtc tcc cgc gcc tcg aaa ata ttt gag 307
Leu Thr Gly Pro Ala His Glu Val Ser Arg Ala Ser Lys Ile Phe Glu
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gaa ctg cag gcg att gcc cgt cga gga cat gtg att agc cct gag aca 355
Glu Leu Gln Ala Ile Ala Arg Arg Gly His Val Ile Ser Pro Glu Thr
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gta aaa aat gtc atc agc atg att aac gtg gag acg ccg caa acc gtc 403
Val Lys Asn Val Ile Ser Met Ile Asn Val Glu Thr Pro Gln Thr Val
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tct gaa atc ttg acc ggc gat atc ctt gct cgc cgt ggc aaa gtg atc 451
Ser Glu Ile Leu Thr Gly Asp Ile Leu Ala Arg Arg Gly Lys Val Ile
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cgc cct aag acg ctt ggc caa aag cac tac gtg gac gcg att gat acc 499
Arg Pro Lys Thr Leu Gly Gln Lys His Tyr Val Asp Ala Ile Asp Thr
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aac acg att gtg ttc ggt ctg ggc cca gcc ggt tcc ggt aaa acc tat 547
Asn Thr Ile Val Phe Gly Leu Gly Pro Ala Gly Ser Gly Lys Thr Tyr
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ctg gcc atg gca aaa gcc gtc caa gcg ctg caa tca aag cag gtc agc 595
Leu Ala Met Ala Lys Ala Val Gln Ala Leu Gln Ser Lys Gln Val Ser
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cgc atc atc ttg acc cgc ccc gca gtg gaa gcc ggc gag aaa ctc ggc 643
Arg Ile Ile Leu Thr Arg Pro Ala Val Glu Ala Gly Glu Lys Leu Gly
                                   170 175 180

ttc ttg ccc ggc acc ctg aac gaa aag atc gac ccc tac ctg cgc ccg 691
Phe Leu Pro Gly Thr Leu Asn Glu Lys Ile Asp Pro Tyr Leu Arg Pro
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ctt cac gac gcg ctg cgc gac atg gtc gaa cca gaa gtc att cca aaa 739
Leu His Asp Ala Leu Arg Asp Met Val Glu Pro Glu Val Ile Pro Lys

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gga cgc acc ctc aac gat gca ttc gtg atc ctg gat gaa gcc cag aac Gly Arg Thr Leu Asn Asp Ala Phe Val Ile Leu Asp Glu Ala Gln Asn 230 235 240 245			835
acc acc cca gca cag atg aag atg ttc ctc acc cgc ctg gga ttc ggt Thr Thr Pro Ala Gln Met Lys Met Phe Leu Thr Arg Leu Gly Phe Gly 250 255 260			883
tcc aaa atg gta gtc aca ggt gac atc acc cag gtg gac ctc cca gga Ser Lys Met Val Val Thr Gly Asp Ile Thr Gln Val Asp Leu Pro Gly 265 270 275			931
ggc caa aag tcc ggc ctg cgc ctg gtt cgc cac atc ctg cgc gga gta Gly Gln Lys Ser Gly Leu Arg Leu Val Arg His Ile Leu Arg Gly Val 280 285 290			979
gac gat gtg cac ttc tcc gag ctc acc tca tcc gac gtg gtc cgc cac Asp Asp Val His Phe Ser Glu Leu Thr Ser Ser Asp Val Val Arg His 295 300 305			1027
caa ctg gtt gga cac att gtg gat gca tac gaa gac tat gaa gaa cgc Gln Leu Val Gly His Ile Val Asp Ala Tyr Glu Asp Tyr Glu Glu Arg 310 315 320 325			1075
gag gcc cgc gaa ttg aaa cgc aaa cgc cag gag aca cgg cca Glu Ala Arg Glu Leu Lys Arg Lys Arg Gln Glu Thr Arg Pro 330 335			1117
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Gly Thr His Val Glu Leu Thr Gly Pro Ala His Glu Val Ser Arg Ala 50 55 60			
Ser Lys Ile Phe Glu Glu Leu Gln Ala Ile Ala Arg Arg Gly His Val 65 70 75 80			
Ile Ser Pro Glu Thr Val Lys Asn Val Ile Ser Met Ile Asn Val Glu 85 90 95			

Thr Pro Gln Thr Val Ser Glu Ile Leu Thr Gly Asp Ile Leu Ala Arg
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 Arg Gly Lys Val Ile Arg Pro Lys Thr Leu Gly Gln Lys His Tyr Val
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 Asp Ala Ile Asp Thr Asn Thr Ile Val Phe Gly Leu Gly Pro Ala Gly
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 Ser Gly Lys Thr Tyr Leu Ala Met Ala Lys Ala Val Gln Ala Leu Gln
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 Ser Lys Gln Val Ser Arg Ile Ile Leu Thr Arg Pro Ala Val Glu Ala
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 Gly Glu Lys Leu Gly Phe Leu Pro Gly Thr Leu Asn Glu Lys Ile Asp
 180 185 190
 Pro Tyr Leu Arg Pro Leu His Asp Ala Leu Arg Asp Met Val Glu Pro
 195 200 205
 Glu Val Ile Pro Lys Leu Met Glu Ala Gly Ile Val Glu Val Ala Pro
 210 215 220
 Leu Ala Tyr Met Arg Gly Arg Thr Leu Asn Asp Ala Phe Val Ile Leu
 225 230 235 240
 Asp Glu Ala Gln Asn Thr Thr Pro Ala Gln Met Lys Met Phe Leu Thr
 245 250 255
 Arg Leu Gly Phe Gly Ser Lys Met Val Val Thr Gly Asp Ile Thr Gln
 260 265 270
 Val Asp Leu Pro Gly Gly Gln Lys Ser Gly Leu Arg Leu Val Arg His
 275 280 285
 Ile Leu Arg Gly Val Asp Asp Val His Phe Ser Glu Leu Thr Ser Ser
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 Asp Val Val Arg His Gln Leu Val Gly His Ile Val Asp Ala Tyr Glu
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Thr Arg Pro

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<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<222> (101)..(1483)

<223> RXA01437

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	Met Ser Asp Thr Pro	
	1 5	
acc tca gct ctg atc acc acg gtc aac cgc agc ttc gat gga ttc gat	163	
Thr Ser Ala Leu Ile Thr Thr Val Asn Arg Ser Phe Asp Gly Phe Asp		
10 15 20		
ttg gaa gaa gta gca gca gac ctt gga gtt cgg ctc acc tac ctg ccc	211	
Leu Glu Glu Val Ala Ala Asp Leu Gly Val Arg Leu Thr Tyr Leu Pro		
25 30 35		
gac gaa gaa cta gaa gta tcc aaa gtt ctc gcg gcg gac ctc ctc gct	259	
Asp Glu Glu Leu Glu Val Ser Lys Val Leu Ala Ala Asp Leu Leu Ala		
40 45 50		
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Glu Gly Pro Ala Leu Ile Ile Gly Val Gly Asn Thr Phe Phe Asp Ala		
55 60 65		
cag gtc gcc gct gcc ctc ggc gtc cca gtg cta ctg ctg gta gac aag	355	
Gln Val Ala Ala Leu Gly Val Pro Val Leu Leu Leu Val Asp Lys		
70 75 80 85		
caa ggc aag cac gtt gct ctt gct cgc acc cag gta aac aat gcc ggc	403	
Gln Gly Lys His Val Ala Leu Ala Arg Thr Gln Val Asn Asn Ala Gly		
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gca gtt gtt gca gca gca ttt acc gct gaa caa gag cca atg ccg gat	451	
Ala Val Val Ala Ala Ala Phe Thr Ala Glu Gln Glu Pro Met Pro Asp		
105 110 115		
aag ctg cgc aag gct gtg cgc aac cac agc aac ctc gaa cca gtc atg	499	
Lys Leu Arg Lys Ala Val Arg Asn His Ser Asn Leu Glu Pro Val Met		
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agc gcc gaa ctc ttt gaa aac tgg ctg ctc aag cgc gca cgc gca gag	547	
Ser Ala Glu Leu Phe Glu Asn Trp Leu Leu Lys Arg Ala Arg Ala Glu		
135 140 145		
cac tcc cac att gtg ctg cca gaa ggt gac gac gac cgc atc ttg atg	595	
His Ser His Ile Val Leu Pro Glu Gly Asp Asp Asp Arg Ile Leu Met		
150 155 160 165		
gct gcc cac cag ctg ctt gat caa gac atc tgt gac atc acg atc ctg	643	
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ggc gat cca gta aag atc aag gag cgc gct acc gaa ctt ggc ctg cac	691	
Gly Asp Pro Val Lys Ile Lys Glu Arg Ala Thr Glu Leu Gly Leu His		
185 190 195		
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Leu Asn Thr Ala Tyr Leu Val Asn Pro Leu Thr Asp Pro Arg Leu Glu		
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gaa ttc gcc gaa caa ttc gcg gag ctg cgc aag tca aag agc gtc act	787	
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215 220 225		

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aac acc acc gca cac acc att aag cca agc ttc cag atc atc aaa act Asn Thr Thr Ala His Thr Ile Lys Pro Ser Phe Gln Ile Ile Lys Thr 265 270 275	931
gtt cca gaa gca tcc gtc gtt tct tcc atc ttc ctc atg gtg ctg cgc Val Pro Glu Ala Ser Val Val Ser Ser Ile Phe Leu Met Val Leu Arg 280 285 290	979
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gct gaa cag ctt ggt gaa atc gcc gtt gtg tca gca aaa act gca gca Ala Glu Gln Leu Gly Glu Ile Ala Val Val Ser Ala Lys Thr Ala Ala 310 315 320 325	1075
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aac tcc ggc gga ggc tca gat gtg gat cgc gcc atc gac gct ctt gca Asn Ser Gly Gly Gly Ser Asp Val Asp Arg Ala Ile Asp Ala Leu Ala 345 350 355	1171
gaa gca cgc cga ctt aac cca gaa cta tgc gtc gat gga cca ctt cag Glu Ala Arg Arg Leu Asn Pro Glu Leu Cys Val Asp Gly Pro Leu Gln 360 365 370	1219
ttc gac gcc gcc gtc gac ccg ggt gtg gcg cgc aag aag atg cca gac Phe Asp Ala Ala Val Asp Pro Gly Val Ala Arg Lys Lys Met Pro Asp 375 380 385	1267
tct gac gtc gct ggc cag gca aat gtg ttt atc ttc cct gac ctg gaa Ser Asp Val Ala Gly Gln Ala Asn Val Phe Ile Phe Pro Asp Leu Glu 390 395 400 405	1315
gcc gga aac atc ggc tac aaa act gca caa cgc acc ggt cac gcc ctg Ala Gly Asn Ile Gly Tyr Lys Thr Ala Gln Arg Thr Gly His Ala Leu 410 415 420	1363
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tcc cgt ggc gca aca gtc cct gac atc gtc aac aca gta gcc atc aca Ser Arg Gly Ala Thr Val Pro Asp Ile Val Asn Thr Val Ala Ile Thr 440 445 450	1459
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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 304

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Leu Thr Tyr Leu Pro Asp Glu Glu Leu Glu Val Ser Lys Val Leu Ala
      35              40              45

Ala Asp Leu Leu Ala Glu Gly Pro Ala Leu Ile Ile Gly Val Gly Asn
      50              55              60

Thr Phe Phe Asp Ala Gln Val Ala Ala Ala Leu Gly Val Pro Val Leu
      65              70              75              80

Leu Leu Val Asp Lys Gln Gly Lys His Val Ala Leu Ala Arg Thr Gln
      85              90              95

Val Asn Asn Ala Gly Ala Val Val Ala Ala Ala Phe Thr Ala Glu Gln
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Glu Pro Met Pro Asp Lys Leu Arg Lys Ala Val Arg Asn His Ser Asn
      115              120              125

Leu Glu Pro Val Met Ser Ala Glu Leu Phe Glu Asn Trp Leu Leu Lys
      130              135              140

Arg Ala Arg Ala Glu His Ser His Ile Val Leu Pro Glu Gly Asp Asp
      145              150              155              160

Asp Arg Ile Leu Met Ala Ala His Gln Leu Leu Asp Gln Asp Ile Cys
      165              170              175

Asp Ile Thr Ile Leu Gly Asp Pro Val Lys Ile Lys Glu Arg Ala Thr
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Glu Leu Gly Leu His Leu Asn Thr Ala Tyr Leu Val Asn Pro Leu Thr
      195              200              205

Asp Pro Arg Leu Glu Glu Phe Ala Glu Gln Phe Ala Glu Leu Arg Lys
      210              215              220

Ser Lys Ser Val Thr Ile Asp Glu Ala Arg Glu Ile Met Lys Asp Ile
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Ser Tyr Phe Gly Thr Met Met Val His Asn Gly Asp Ala Asp Gly Met
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Val Ser Gly Ala Ala Asn Thr Thr Ala His Thr Ile Lys Pro Ser Phe
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Gln Ile Ile Lys Thr Val Pro Glu Ala Ser Val Val Ser Ser Ile Phe
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Leu Met Val Leu Arg Gly Arg Leu Trp Ala Phe Gly Asp Cys Ala Val

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Ala	Lys	Thr	Ala	Ala	Gln	Phe	Gly	Ile	Asp	Pro	Arg	Val	Ala	Ile	Leu
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Ser	Tyr	Ser	Thr	Gly	Asn	Ser	Gly	Gly	Gly	Ser	Asp	Val	Asp	Arg	Ala
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Ile	Asp	Ala	Leu	Ala	Glu	Ala	Arg	Arg	Leu	Asn	Pro	Glu	Leu	Cys	Val
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Pro	Val	Asn	Asp	Leu	Ser	Arg	Gly	Ala	Thr	Val	Pro	Asp	Ile	Val	Asn
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1225)

<223> RXN00778

<400> 305

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aag	cgc	tcc	atc	gcc	ctt	gtg	ggc	gca	ggt	act	gca	ggc	tcc	ttc	gct	163
Lys	Arg	Ser	Ile	Ala	Leu	Val	Gly	Ala	Val	Thr	Ala	Gly	Ser	Phe	Ala	
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ctt	gta	gct	tgc	tcc	gac	tcc	aat	gag	tct	gat	tcc	acc	tcc	tca	tct	211
Leu	Val	Ala	Cys	Ser	Asp	Ser	Asn	Glu	Ser	Asp	Ser	Thr	Ser	Ser	Ser	
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gca	gct	tcc	acc	ggt	tct	tcc	gat	gct	gca	tcc	att	gag	ggc	ctt	tcc	259
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Ser Leu Ala Tyr Thr Pro Ser Gly Ser Gly Ser Gly Arg Thr Asn Phe	
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Ala Ala Gly Gln Val Ala Phe Gly Gly Ser Asp Ser Ala Met Lys Asp	
105 110 115	
gac cag gct gca gaa gca gaa gca cgt tgc aac ggc aac gaa gca tgg	499
Asp Gln Ala Ala Glu Ala Glu Ala Arg Cys Asn Gly Asn Glu Ala Trp	
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His Leu Pro Phe Val Ile Gly Pro Val Ala Val Ala Tyr Asn Leu Pro	
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Gly Val Asp Thr Leu Asn Leu Asp Thr Asn Ile Ile Ala Gln Ile Phe	
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Lys Gly Glu Ile Thr Lys Trp Asn Asp Glu Ala Ile Ala Ser Gln Asn	
170 175 180	
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Glu Gly Thr Asp Leu Pro Asp Gln Asp Ile Ser Val Leu Tyr Arg Ser	
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gaa gag tcc ggt acc tcc gac aac ttc cag aag ttc ctc gga gct tcc	739
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Thr Asp Ile Trp Glu Thr Glu Gly Gln Gln Phe Pro Thr Glu Val Gly	
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Ser Gly Ala Gln Gly Ser Asn Gly Val Ala Ser Glu Ala Ser Asn Ile	
230 235 240 245	
gag ggt gca atc acc tac gtt gaa gct ggt ttc gct aac cag tcc ggc	883
Glu Gly Ala Ile Thr Tyr Val Glu Ala Gly Phe Ala Asn Gln Ser Gly	
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ctg ggc gtt gca aac atc gac ttc ggt tcc ggc cca gtt gaa ctc aac	931
Leu Gly Val Ala Asn Ile Asp Phe Gly Ser Gly Pro Val Glu Leu Asn	
265 270 275	
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Ala Glu Ser Val Gly Val Ala Leu Gly Ala Leu Asp Phe Leu Thr Glu	
280 285 290	

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 Gly His Asn Met Val Val Asp Thr Asp Ala Met Phe Ala Met Asn Glu
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 Ala Gly Ala Tyr Pro Leu Ile Leu Thr Thr Tyr Glu Ile Val Cys Ser
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 Ala Gly Tyr Asp Glu Thr Thr Arg Asp Gln Val Lys Asp Phe Leu Thr
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gtt gca ctg gac tcc cag gat gac cag ctc gag gct ctc ggc tac atc 1171
 Val Ala Leu Asp Ser Gln Asp Asp Gln Leu Glu Ala Leu Gly Tyr Ile
 345 350 355

cca gtt acc ggc gag cac tac gat cgc ctc gtt gca gca gtt gaa gca 1219
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 Ile Gln
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<210> 306

<211> 375

<212> PRT

<213> Corynebacterium glutamicum

<400> 306

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 35 40 45

Ile Glu Gly Leu Ser Gly Val Thr Gly Gln Leu Val Ala Glu Gly Ala
 50 55 60

Ser Ser Gln Gln Ser Ala Met Asp Tyr Phe Gly Ile Arg Tyr Ser Glu
 65 70 75 80

Ala Val Ser Gly Ala Ser Leu Ala Tyr Thr Pro Ser Gly Ser Gly Ser
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Gly Arg Thr Asn Phe Ala Ala Gly Gln Val Ala Phe Gly Gly Ser Asp
 100 105 110

Ser Ala Met Lys Asp Asp Gln Ala Ala Glu Ala Glu Ala Arg Cys Asn
 115 120 125

Gly Asn Glu Ala Trp His Leu Pro Phe Val Ile Gly Pro Val Ala Val
 130 135 140

Ala Tyr Asn Leu Pro Gly Val Asp Thr Leu Asn Leu Asp Thr Asn Ile
 145 150 155 160

Ile Ala Gln Ile Phe Lys Gly Glu Ile Thr Lys Trp Asn Asp Glu Ala
 165 170 175
 Ile Ala Ser Gln Asn Glu Gly Thr Asp Leu Pro Asp Gln Asp Ile Ser
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 Val Leu Tyr Arg Ser Glu Glu Ser Gly Thr Ser Asp Asn Phe Gln Lys
 195 200 205
 Phe Leu Gly Ala Ser Thr Asp Ile Trp Glu Thr Glu Gly Gln Gln Phe
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 Pro Thr Glu Val Gly Ser Gly Ala Gln Gly Ser Asn Gly Val Ala Ser
 225 230 235 240
 Glu Ala Ser Asn Ile Glu Gly Ala Ile Thr Tyr Val Glu Ala Gly Phe
 245 250 255
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 260 265 270
 Pro Val Glu Leu Asn Ala Glu Ser Val Gly Val Ala Leu Gly Ala Leu
 275 280 285
 Asp Phe Leu Thr Glu Gly His Asn Met Val Val Asp Thr Asp Ala Met
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 325 330 335
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<210> 307

<211> 857

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(834)

<223> FRXA00778

<400> 307

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gca atg aag gac gac cag gct gca gaa gca gaa gca cgt tgc aac ggc 96
 Ala Met Lys Asp Asp Gln Ala Ala Glu Ala Glu Ala Arg Cys Asn Gly
 20 25 30

aac gaa gca tgg cac ctg cca ttc gtt atc ggc cca gtt gca gtt gct	144
Asn Glu Ala Trp His Leu Pro Phe Val Ile Gly Pro Val Ala Val Ala	
35 40 45	
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Tyr Asn Leu Pro Gly Val Asp Thr Leu Asn Leu Asp Thr Asn Ile Ile	
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gct cag atc ttc aag ggc gag atc acc aag tgg aac gac gaa gca atc	240
Ala Gln Ile Phe Lys Gly Glu Ile Thr Lys Trp Asn Asp Glu Ala Ile	
65 70 75 80	
gct tcc cag aac gag ggc acc gac ctc cca gac cag gac atc tcc gtt	288
Ala Ser Gln Asn Glu Gly Thr Asp Leu Pro Asp Gln Asp Ile Ser Val	
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100 105 110	
ctc gga gct tcc acc gac atc tgg gag acc gaa ggc cag cag ttc cca	384
Leu Gly Ala Ser Thr Asp Ile Trp Glu Thr Glu Gly Gln Gln Phe Pro	
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acc gag gtt ggc tcc ggt gcg cag ggc tcc aac ggt gta gct tct gag	432
Thr Glu Val Gly Ser Gly Ala Gln Gly Ser Asn Gly Val Ala Ser Glu	
130 135 140	
gct tcc aac atc gag ggt gca atc acc tac gtt gaa gct ggt ttc gct	480
Ala Ser Asn Ile Glu Gly Ala Ile Thr Tyr Val Glu Ala Gly Phe Ala	
145 150 155 160	
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Asn Gln Ser Gly Leu Gly Val Ala Asn Ile Asp Phe Gly Ser Gly Pro	
165 170 175	
gtt gaa ctc aac gct gag tcc gtt ggc gtt gca ctt ggt gca ctc gac	576
Val Glu Leu Asn Ala Glu Ser Val Gly Val Ala Leu Gly Ala Leu Asp	
180 185 190	
ttc ctg act gag ggc cac aac atg gtt gtt gac acc gac gct atg ttc	624
Phe Leu Thr Glu Gly His Asn Met Val Val Asp Thr Asp Ala Met Phe	
195 200 205	
gca atg aac gaa gcc ggt gct tac cca ctg atc ctc acc acc tac gaa	672
Ala Met Asn Glu Ala Gly Ala Tyr Pro Leu Ile Leu Thr Thr Tyr Glu	
210 215 220	
atc gtc tgc tcc gca ggc tac gac gag acc acc cgc gac cag gtc aag	720
Ile Val Cys Ser Ala Gly Tyr Asp Glu Thr Thr Arg Asp Gln Val Lys	
225 230 235 240	
gac ttc ctg acc gtt gca ctg gac tcc cag gat gac cag ctc gag gct	768
Asp Phe Leu Thr Val Ala Leu Asp Ser Gln Asp Asp Gln Leu Glu Ala	
245 250 255	
ctc ggc tac atc cca gtt acc ggc gag cac tac gat cgc ctc gtt gca	816
Leu Gly Tyr Ile Pro Val Thr Gly Glu His Tyr Asp Arg Leu Val Ala	
260 265 270	

gca gtt gaa gca att cag taataaacgc ctgccgtagc ttc
 Ala Val Glu Ala Ile Gln
 275

857

<210> 308

<211> 278

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 308

Arg Asn Asn Phe Ala Ala Ala Gln Val Ala Phe Gly Gly Ser Asp Ser
 1 5 10 15

Ala Met Lys Asp Asp Gln Ala Ala Glu Ala Glu Ala Arg Cys Asn Gly
 20 25 30

Asn Glu Ala Trp His Leu Pro Phe Val Ile Gly Pro Val Ala Val Ala
 35 40 45

Tyr Asn Leu Pro Gly Val Asp Thr Leu Asn Leu Asp Thr Asn Ile Ile
 50 55 60

Ala Gln Ile Phe Lys Gly Glu Ile Thr Lys Trp Asn Asp Glu Ala Ile
 65 70 75 80

Ala Ser Gln Asn Glu Gly Thr Asp Leu Pro Asp Gln Asp Ile Ser Val
 85 90 95

Leu Tyr Arg Ser Glu Glu Ser Gly Thr Ser Asp Asn Phe Gln Lys Phe
 100 105 110

Leu Gly Ala Ser Thr Asp Ile Trp Glu Thr Glu Gly Gln Gln Phe Pro
 115 120 125

Thr Glu Val Gly Ser Gly Ala Gln Gly Ser Asn Gly Val Ala Ser Glu
 130 135 140

Ala Ser Asn Ile Glu Gly Ala Ile Thr Tyr Val Glu Ala Gly Phe Ala
 145 150 155 160

Asn Gln Ser Gly Leu Gly Val Ala Asn Ile Asp Phe Gly Ser Gly Pro
 165 170 175

Val Glu Leu Asn Ala Glu Ser Val Gly Val Ala Leu Gly Ala Leu Asp
 180 185 190

Phe Leu Thr Glu Gly His Asn Met Val Val Asp Thr Asp Ala Met Phe
 195 200 205

Ala Met Asn Glu Ala Gly Ala Tyr Pro Leu Ile Leu Thr Thr Tyr Glu
 210 215 220

Ile Val Cys Ser Ala Gly Tyr Asp Glu Thr Thr Arg Asp Gln Val Lys
 225 230 235 240

Asp Phe Leu Thr Val Ala Leu Asp Ser Gln Asp Asp Gln Leu Glu Ala
 245 250 255

Leu Gly Tyr Ile Pro Val Thr Gly Glu His Tyr Asp Arg Leu Val Ala
 260 265 270

Ala Val Glu Ala Ile Gln
275

<210> 309

<211> 1050

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1027)

<223> RXA02497

<400> 309

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gattcacact ttgccaccct agaccgtcta accttttaggt gtg aga tta ggt gta 115
Val Arg Leu Gly Val
1 5

tta gat gtg ggc agc aat act gtc cac cta gtt gca gta gac gcg cgt 163
Leu Asp Val Gly Ser Asn Thr Val His Leu Val Ala Val Asp Ala Arg
10 15 20

ccc ggt gga cac ccc acc ccg atg agc aat tgg cgt acc cca ctg cgc 211
Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp Arg Thr Pro Leu Arg
25 30 35

ctt gtt gag ctt ctt gat gac tcc ggg gcg atc tcc gaa aag ggc atc 259
Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile Ser Glu Lys Gly Ile
40 45 50

aac aaa ctc acc tca gca gtc ggg gaa gca gca gac cta gcg aaa acg 307
Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala Asp Leu Ala Lys Thr
55 60 65

ctc ggc tgc gct gaa ctg atg cca ttt gct aca tcg gca gtc cgc tcc 355
Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr Ser Ala Val Arg Ser
70 75 80 85

gcc acc aac agc gag gca gtg ctc gac cac gtg gag aag gaa acc ggc 403
Ala Thr Asn Ser Glu Ala Val Leu Asp His Val Glu Lys Glu Thr Gly
90 95 100

gtc cgc ctg tcc atc ctt tcc ggt gaa gac gaa gca cgc caa act ttc 451
Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu Ala Arg Gln Thr Phe
105 110 115

ctc gca gtt cga cgt tgg tat gga tgg tcc gca ggg cgc ata act aac 499
Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala Gly Arg Ile Thr Asn
120 125 130

ctc gac atc ggt ggc ggc tcc ctg gaa cta tcc tcc gga acc gac gaa 547
Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser Ser Gly Thr Asp Glu
135 140 145

tcc cca gac ctc gcg ttc tca ctg gat ctg ggt gcg ggc cgc ttg acc 595
Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly Ala Gly Arg Leu Thr
150 155 160 165

cac aac tgg ttc gac acc gat cca ccg gca cgt aag aaa atc aac ctc 643
 His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg Lys Lys Ile Asn Leu
 170 175 180

ctg cgc gat tat atc gat gcg gaa ctt gca gaa ccc gcc cgc cag atg 691
 Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu Pro Ala Arg Gln Met
 185 190 195

cgc acc cta ggg ccc gcg cgc ctg gca gtg gga aca tcc aaa act ttc 739
 Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly Thr Ser Lys Thr Phe
 200 205 210

cgc acc ctg gca cga ctg act ggt gct gcg ccc tca tcc gca gga cca 787
 Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro Ser Ser Ala Gly Pro
 215 220 225

cac gtc acc cga acc ctc acc gcg ccg ggt ctg cgc cag ctg atc gca 835
 His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu Arg Gln Leu Ile Ala
 230 235 240 245

ttt atc tca cga atg act gcg gcg gac cgc gct gag ctg gaa ggt atc 883
 Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala Glu Leu Glu Gly Ile
 250 255 260

agc tcg gat cgg tca cat cag atc gtg gca ggt gcg cta gtt gcg gaa 931
 Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly Ala Leu Val Ala Glu
 265 270 275

gct gcg atg cgt gcg ttg gat att gac aag gta gaa att tgt ccg tgg 979
 Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val Glu Ile Cys Pro Trp
 280 285 290

gca ctt cgt gaa ggt gtg atc ctc acc agg atc gac aaa gga ctc gag 1027
 Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile Asp Lys Gly Leu Glu
 295 300 305

taacatttac ccggaaagga gtt 1050

<210> 310

<211> 309

<212> PRT

<213> Corynebacterium glutamicum

<400> 310

Val Arg Leu Gly Val Leu Asp Val Gly Ser Asn Thr Val His Leu Val
 1 5 10 15

Ala Val Asp Ala Arg Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp
 20 25 30

Arg Thr Pro Leu Arg Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile
 35 40 45

Ser Glu Lys Gly Ile Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala
 50 55 60

Asp Leu Ala Lys Thr Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr
 65 70 75 80

Ser Ala Val Arg Ser Ala Thr Asn Ser Glu Ala Val Leu Asp His Val
85 90 95

Glu Lys Glu Thr Gly Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu
100 105 110

Ala Arg Gln Thr Phe Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala
115 120 125

Gly Arg Ile Thr Asn Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser
130 135 140

Ser Gly Thr Asp Glu Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly
145 150 155 160

Ala Gly Arg Leu Thr His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg
165 170 175

Lys Lys Ile Asn Leu Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu
180 185 190

Pro Ala Arg Gln Met Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly
195 200 205

Thr Ser Lys Thr Phe Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro
210 215 220

Ser Ser Ala Gly Pro His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu
225 230 235 240

Arg Gln Leu Ile Ala Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala
245 250 255

Glu Leu Glu Gly Ile Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly
260 265 270

Ala Leu Val Ala Glu Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val
275 280 285

Glu Ile Cys Pro Trp Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile
290 295 300

Asp Lys Gly Leu Glu
305

<210> 311

<211> 1671

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1648)

<223> RXA01477

<400> 311

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cattatttaa tgcatactcg gcgctatttt gaggagcctc atg cca cag tta agc 115
Met Pro Gln Leu Ser

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aga	cgc	cag	ttc	ttg	cag	aca	acc	gcc	gtt	act	gca	ggc	cta	gcc	act	163					
Arg	Arg	Gln	Phe	Leu	Gln	Thr	Thr	Ala	Val	Thr	Ala	Gly	Leu	Ala	Thr						
				10					15					20							
ttt	gcg	ggc	aca	cct	gca	cgc	gct	gaa	gaa	cgc	caa	ttc	cag	cat	ggc	211					
Phe	Ala	Gly	Thr	Pro	Ala	Arg	Ala	Glu	Glu	Arg	Gln	Phe	Gln	His	Gly						
				25					30					35							
gtg	gct	tcc	ggg	gac	ccc	acc	gca	acc	tct	gcc	att	ttg	tgg	act	cgg	259					
Val	Ala	Ser	Gly	Asp	Pro	Thr	Ala	Thr	Ser	Ala	Ile	Leu	Trp	Thr	Arg						
				40					45					50							
ctg	acc	cca	att	ccc	gac	gcc	aca	cct	gga	agt	ggc	ctt	ggc	ccc	gac	307					
Leu	Thr	Pro	Ile	Pro	Asp	Ala	Thr	Pro	Gly	Ser	Gly	Leu	Gly	Pro	Asp						
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tct	cct	gtc	acc	tgg	gaa	gtc	tcc	ccc	act	cct	gat	ttc	gcc	agc	atc	355					
Ser	Pro	Val	Thr	Trp	Glu	Val	Ser	Pro	Thr	Pro	Asp	Phe	Ala	Ser	Ile						
				70					75					80							
acg	cgc	tcg	gga	acc	gta	atc	acc	tcc	gca	gca	agc	gat	cac	acc	gtc	403					
Thr	Arg	Ser	Gly	Thr	Val	Ile	Thr	Ser	Ala	Ala	Ser	Asp	His	Thr	Val						
				90					95					100							
cac	gcg	cac	gcc	acg	ggc	ttg	agc	cca	tcc	acc	cgc	tat	ttc	tac	cgc	451					
His	Ala	His	Ala	Thr	Gly	Leu	Ser	Pro	Ser	Thr	Arg	Tyr	Phe	Tyr	Arg						
				105					110					115							
ttc	atc	tcc	tcc	acc	ggc	gag	gtc	tcc	cct	gtg	ggg	cgc	acg	caa	aca	499					
Phe	Ile	Ser	Ser	Thr	Gly	Glu	Val	Ser	Pro	Val	Gly	Arg	Thr	Gln	Thr						
				120					125					130							
aca	tcg	ctt	gtc	gac	gct	ccc	ctc	ccg	cac	ctt	cgc	ttt	gcc	ctt	gcg	547					
Thr	Ser	Leu	Val	Asp	Ala	Pro	Leu	Pro	His	Leu	Arg	Phe	Ala	Leu	Ala						
				135					140					145							
tcg	tgt	gcc	aat	tgg	gag	gca	gga	ttt	ttt	gcc	gcc	tac	ggc	gac	atc	595					
Ser	Cys	Ala	Asn	Trp	Glu	Ala	Gly	Phe	Phe	Ala	Ala	Tyr	Gly	Asp	Ile						
				150					155					160							
gcc	cgg	cgc	gct	gac	gcc	ggc	gaa	ttg	gag	atg	ttg	att	ttt	ttg	ggc	643					
Ala	Arg	Arg	Ala	Asp	Ala	Gly	Glu	Leu	Glu	Met	Leu	Ile	Phe	Leu	Gly						
				170					175					180							
gat	tac	atc	tac	gag	tac	gcc	acc	ggc	atg	ttc	gcc	gga	aag	gac	ggc	691					
Asp	Tyr	Ile	Tyr	Glu	Tyr	Ala	Thr	Gly	Met	Phe	Ala	Gly	Lys	Asp	Gly						
				185					190					195							
gtg	gtg	cgc	ccg	cat	cag	cct	ctt	cat	gaa	acc	atc	acg	ttg	gag	cac	739					
Val	Val	Arg	Pro	His	Gln	Pro	Leu	His	Glu	Thr	Ile	Thr	Leu	Glu	His						
				200					205					210							
tac	cgc	act	cgt	tat	ggc	cat	tac	cgc	agt	gac	aat	cac	ttg	cag	gca	787					
Tyr	Arg	Thr	Arg	Tyr	Gly	His	Tyr	Arg	Ser	Asp	Asn										

gcc aac aac tct aat cgt gag ggc gcg cag aat cat tcc gct gat gag	883
Ala Asn Asn Ser Asn Arg Glu Gly Ala Gln Asn His Ser Ala Asp Glu	
250 255 260	
ggt tcg tgg gtg gat cgt caa aat gct gct cgg cag gtc ttt ttg gag	931
Gly Ser Trp Val Asp Arg Gln Asn Ala Ala Arg Gln Val Phe Leu Glu	
265 270 275	
tgg atg ccg atc cgc cag gag gac acg ctc tat cgt tcc ttc act ttt	979
Trp Met Pro Ile Arg Gln Glu Asp Thr Leu Tyr Arg Ser Phe Thr Phe	
280 285 290	
ggt gac ctc gcc acg ctg tca ctt ctt gat ctt cga agt ttc aga gat	1027
Gly Asp Leu Ala Thr Leu Ser Leu Leu Asp Leu Arg Ser Phe Arg Asp	
295 300 305	
cca gca ccc tcc cag caa cag tgg ctg gag ggt caa cgt gcg gac acc	1075
Pro Ala Pro Ser Gln Gln Gln Trp Leu Glu Gly Gln Arg Ala Asp Thr	
310 315 320 325	
atg atg ggg tcg cag cag ttt gag tgg ctg aaa tcc aac gtg gaa cac	1123
Met Met Gly Ser Gln Gln Phe Glu Trp Leu Lys Ser Asn Val Glu His	
330 335 340	
acc acc acg acg tgg aat atc atc ggc agc tca gtg atg ttt gcc ccc	1171
Thr Thr Thr Thr Trp Asn Ile Ile Gly Ser Ser Val Met Phe Ala Pro	
345 350 355	
atg gca att acc ggg cag cct ctt ttc cag atc cct gaa cct att ccc	1219
Met Ala Ile Thr Gly Gln Pro Leu Phe Gln Ile Pro Glu Pro Ile Pro	
360 365 370	
gcc aat ttg gat cag tgg gac ggc tac tcc cgt gag cgc gac cga ctc	1267
Ala Asn Leu Asp Gln Trp Asp Gly Tyr Ser Arg Glu Arg Asp Arg Leu	
375 380 385	
cta gct gta ctt gcc gat ttc gcc act cca acg ctt ttt cta tct ggc	1315
Leu Ala Val Leu Ala Asp Phe Ala Thr Pro Thr Leu Phe Leu Ser Gly	
390 395 400 405	
gat atc cac tcc gaa tgg gca aac gcc atc cgg ttt aat ggt cga gaa	1363
Asp Ile His Ser Glu Trp Ala Asn Ala Ile Arg Phe Asn Gly Arg Glu	
410 415 420	
atc ggt gtc gag gca gta tgc agc tcc atc acc tca gct aat gtc aac	1411
Ile Gly Val Glu Ala Val Cys Ser Ser Ile Thr Ser Ala Asn Val Asn	
425 430 435	
gac ttc gcc aaa ctc cct gag gac aat ccg gtc tcc ctg caa gcg gaa	1459
Asp Phe Ala Lys Leu Pro Glu Asp Asn Pro Val Ser Leu Gln Ala Glu	
440 445 450	
caa gta atc cga gcc aac agt tcg cat gtg cgc cac gtt gat ctt gac	1507
Gln Val Ile Arg Ala Asn Ser Ser His Val Arg His Val Asp Leu Asp	
455 460 465	
gcc cac ggc tac gcc acg gtg aat ctc acc caa gat ggc gcg cac atg	1555
Ala His Gly Tyr Ala Thr Val Asn Leu Thr Gln Asp Gly Ala His Met	
470 475 480 485	

gtc tgg cac cgc gtc gcc gat ctc tcc ctt ccg gac tca gaa gtt gct 1603
 Val Trp His Arg Val Ala Asp Leu Ser Leu Pro Asp Ser Glu Val Ala
 490 495 500

ccg gca att gca ctt gag tgg aaa cca ggc gtc gga ttc act act 1648
 Pro Ala Ile Ala Leu Glu Trp Lys Pro Gly Val Gly Phe Thr Thr
 505 510 515

tgagctgctg attttaggt ttt 1671

<210> 312

<211> 516

<212> PRT

<213> Corynebacterium glutamicum

<400> 312

Met Pro Gln Leu Ser Arg Arg Gln Phe Leu Gln Thr Thr Ala Val Thr
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Ala Gly Leu Ala Thr Phe Ala Gly Thr Pro Ala Arg Ala Glu Glu Arg
 20 25 30

Gln Phe Gln His Gly Val Ala Ser Gly Asp Pro Thr Ala Thr Ser Ala
 35 40 45

Ile Leu Trp Thr Arg Leu Thr Pro Ile Pro Asp Ala Thr Pro Gly Ser
 50 55 60

Gly Leu Gly Pro Asp Ser Pro Val Thr Trp Glu Val Ser Pro Thr Pro
 65 70 75 80

Asp Phe Ala Ser Ile Thr Arg Ser Gly Thr Val Ile Thr Ser Ala Ala
 85 90 95

Ser Asp His Thr Val His Ala His Ala Thr Gly Leu Ser Pro Ser Thr
 100 105 110

Arg Tyr Phe Tyr Arg Phe Ile Ser Ser Thr Gly Glu Val Ser Pro Val
 115 120 125

Gly Arg Thr Gln Thr Thr Ser Leu Val Asp Ala Pro Leu Pro His Leu
 130 135 140

Arg Phe Ala Leu Ala Ser Cys Ala Asn Trp Glu Ala Gly Phe Phe Ala
 145 150 155 160

Ala Tyr Gly Asp Ile Ala Arg Arg Ala Asp Ala Gly Glu Leu Glu Met
 165 170 175

Leu Ile Phe Leu Gly Asp Tyr Ile Tyr Glu Tyr Ala Thr Gly Met Phe
 180 185 190

Ala Gly Lys Asp Gly Val Val Arg Pro His Gln Pro Leu His Glu Thr
 195 200 205

Ile Thr Leu Glu His Tyr Arg Thr Arg Tyr Gly His Tyr Arg Ser Asp
 210 215 220

Asn His Leu Gln Ala Ala His Ala Ala Leu Pro Trp Ile Val Met Trp
 225 230 235 240

Asp Asp His Glu Ser Ala Asn Asn Ser Asn Arg Glu Gly Ala Gln Asn
 245 250 255
 His Ser Ala Asp Glu Gly Ser Trp Val Asp Arg Gln Asn Ala Ala Arg
 260 265 270
 Gln Val Phe Leu Glu Trp Met Pro Ile Arg Gln Glu Asp Thr Leu Tyr
 275 280 285
 Arg Ser Phe Thr Phe Gly Asp Leu Ala Thr Leu Ser Leu Leu Asp Leu
 290 295 300
 Arg Ser Phe Arg Asp Pro Ala Pro Ser Gln Gln Gln Trp Leu Glu Gly
 305 310 315 320
 Gln Arg Ala Asp Thr Met Met Gly Ser Gln Gln Phe Glu Trp Leu Lys
 325 330 335
 Ser Asn Val Glu His Thr Thr Thr Thr Trp Asn Ile Ile Gly Ser Ser
 340 345 350
 Val Met Phe Ala Pro Met Ala Ile Thr Gly Gln Pro Leu Phe Gln Ile
 355 360 365
 Pro Glu Pro Ile Pro Ala Asn Leu Asp Gln Trp Asp Gly Tyr Ser Arg
 370 375 380
 Glu Arg Asp Arg Leu Leu Ala Val Leu Ala Asp Phe Ala Thr Pro Thr
 385 390 395 400
 Leu Phe Leu Ser Gly Asp Ile His Ser Glu Trp Ala Asn Ala Ile Arg
 405 410 415
 Phe Asn Gly Arg Glu Ile Gly Val Glu Ala Val Cys Ser Ser Ile Thr
 420 425 430
 Ser Ala Asn Val Asn Asp Phe Ala Lys Leu Pro Glu Asp Asn Pro Val
 435 440 445
 Ser Leu Gln Ala Glu Gln Val Ile Arg Ala Asn Ser Ser His Val Arg
 450 455 460
 His Val Asp Leu Asp Ala His Gly Tyr Ala Thr Val Asn Leu Thr Gln
 465 470 475 480
 Asp Gly Ala His Met Val Trp His Arg Val Ala Asp Leu Ser Leu Pro
 485 490 495
 Asp Ser Glu Val Ala Pro Ala Ile Ala Leu Glu Trp Lys Pro Gly Val
 500 505 510
 Gly Phe Thr Thr
 515

<210> 313

<211> 597

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(574)

<223> RXA01509

<400> 313

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	Met Ser Ile Glu Val	
	1 5	

acc gtc gaa atc cct aag gga tca cgc aac aag tac gaa atc gac cac	163
Thr Val Glu Ile Pro Lys Gly Ser Arg Asn Lys Tyr Glu Ile Asp His	
10 15 20	

gag acc gga aag gtc tac ctc gac cgc tac ctg ttc act cca atg gca	211
Glu Thr Gly Lys Val Tyr Leu Asp Arg Tyr Leu Phe Thr Pro Met Ala	
25 30 35	

tac cca ctg gac tac ggc tac atc gac cac acc ctc ggc gaa gac ggc	259
Tyr Pro Leu Asp Tyr Gly Tyr Ile Asp His Thr Leu Gly Glu Asp Gly	
40 45 50	

gac cca ttg gat gca ctg gtc atc ctc ccc gag tcc gtt ttt cca gca	307
Asp Pro Leu Asp Ala Leu Val Ile Leu Pro Glu Ser Val Phe Pro Ala	
55 60 65	

gtt gtg gtt aag tcc cga atc atc ggt gtt ttc aag atg acc gac gaa	355
Val Val Val Lys Ser Arg Ile Ile Gly Val Phe Lys Met Thr Asp Glu	
70 75 80 85	

gcc ggc ggc gac gac aag ctg ctc tcc gtt ctc gac gac cca cgc tac	403
Ala Gly Gly Asp Asp Lys Leu Leu Ser Val Leu Asp Asp Pro Arg Tyr	
90 95 100	

gac cac atc cag gac atc tcc gac gtg tcc gat ttc ctc aag gat gag	451
Asp His Ile Gln Asp Ile Ser Asp Val Ser Asp Phe Leu Lys Asp Glu	
105 110 115	

atc gag cac ttc ttc gtc cac tac aag gac ctg gaa aag ggc aag cac	499
Ile Glu His Phe Phe Val His Tyr Lys Asp Leu Glu Lys Gly Lys His	
120 125 130	

gtt gac ggt tcc ggc tgg ggc gac aag gct gag gct gaa aag atc cac	547
Val Asp Gly Ser Gly Trp Gly Asp Lys Ala Glu Ala Glu Lys Ile His	
135 140 145	

gct gag gca atc gac cgc tac aag gca taagtctttt gtaaattaag agc	597
Ala Glu Ala Ile Asp Arg Tyr Lys Ala	
150 155	

<210> 314

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 314

Met Ser Ile Glu Val Thr Val Glu Ile Pro Lys Gly Ser Arg Asn Lys
1 5 10 15

<400> 315																
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atccgcttgt ttcacatgcg gtgatcgcg ggagtaaacg atg att ttg gat tgg															115	
												Met	Ile	Leu	Asp	Trp
												1				5
gtt atc tcc atc atg gag gca ctc ggc gcc gtt ggc gtg ggt gtc gcg															163	
Val	Ile	Ser	Ile	Met	Glu	Ala	Leu	Gly	Ala	Val	Gly	Val	Gly	Val	Ala	
				10					15					20		
gtg ttt ttg gag aac gtt ttc ccg ccg att cca agt gag gtg gtg ctt															211	
Val	Phe	Leu	Glu	Asn	Val	Phe	Pro	Pro	Ile	Pro	Ser	Glu	Val	Val	Leu	
			25					30					35			
ccg ctc gcg ggt ttc acc acc acg caa ggc gat ctc aat gtg tgg gcg															259	
Pro	Leu	Ala	Gly	Phe	Thr	Thr	Thr	Gln	Gly	Asp	Leu	Asn	Val	Trp	Ala	

40	45	50	
gcg ctt atg tgg tgc gtg atc ggg tgc gtt tcc gga gcg ttt ttg ctt			307
Ala Leu Met Trp Ser Val Ile Gly Ser Val Ser Gly Ala Phe Leu Leu			
55	60	65	
tac ggg ttg ggg cgc tca atc ggg gcg gca cgg ttg cgg cag gtc gcc			355
Tyr Gly Leu Gly Arg Ser Ile Gly Ala Ala Arg Leu Arg Gln Val Ala			
70	75	80	85
gac tgg atg tgg ctt gtc gac gcg acc gac gtg gat aaa tcc cta tgc			403
Asp Trp Met Trp Leu Val Asp Ala Thr Asp Val Asp Lys Ser Leu Ser			
90	95	100	
tgg ttc gaa aag tac ggg aag tat tgc gtg ttt ttc ggt cgg ttg gtg			451
Trp Phe Glu Lys Tyr Gly Lys Tyr Ser Val Phe Phe Gly Arg Leu Val			
105	110	115	
ccg ggt gtc cga agt ttg att tgc att ccg gcg ggc gtc gac aag atg			499
Pro Gly Val Arg Ser Leu Ile Ser Ile Pro Ala Gly Val Asp Lys Met			
120	125	130	
aat ccg gtt ctc ttc ggt gtg ctc act gcg gtg ggc agc acc att tgg			547
Asn Pro Val Leu Phe Gly Val Leu Thr Ala Val Gly Ser Thr Ile Trp			
135	140	145	
aat gcg gtt ctg att tgg act ggt gtg tgg ttg ggg gcg gaa tgg gag			595
Asn Ala Val Leu Ile Trp Thr Gly Val Trp Leu Gly Ala Glu Trp Glu			
150	155	160	165
acg gtg tgc atg tgg ttt gag agc tat tca acg atc att tac gta ggt			643
Thr Val Ser Met Trp Phe Glu Ser Tyr Ser Thr Ile Ile Tyr Val Gly			
170	175	180	
atc gcg ctc att gtn gct tac gtg ttg ttt ggt tta gtc cgt cgc cga			691
Ile Ala Leu Ile Val Ala Tyr Val Leu Phe Gly Leu Val Arg Arg Arg			
185	190	195	
att aaa act taaccatcgg ttcgtagccg aag			723
Ile Lys Thr			
200			
<210> 316			
<211> 200			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 316			
Met Ile Leu Asp Trp Val Ile Ser Ile Met Glu Ala Leu Gly Ala Val			
1	5	10	15
Gly Val Gly Val Ala Val Phe Leu Glu Asn Val Phe Pro Pro Ile Pro			
20	25	30	
Ser Glu Val Val Leu Pro Leu Ala Gly Phe Thr Thr Thr Gln Gly Asp			
35	40	45	
Leu Asn Val Trp Ala Ala Leu Met Trp Ser Val Ile Gly Ser Val Ser			
50	55	60	

Gly Ala Phe Leu Leu Tyr Gly Leu Gly Arg Ser Ile Gly Ala Ala Arg
 65 70 75 80
 Leu Arg Gln Val Ala Asp Trp Met Trp Leu Val Asp Ala Thr Asp Val
 85 90 95
 Asp Lys Ser Leu Ser Trp Phe Glu Lys Tyr Gly Lys Tyr Ser Val Phe
 100 105 110
 Phe Gly Arg Leu Val Pro Gly Val Arg Ser Leu Ile Ser Ile Pro Ala
 115 120 125
 Gly Val Asp Lys Met Asn Pro Val Leu Phe Gly Val Leu Thr Ala Val
 130 135 140
 Gly Ser Thr Ile Trp Asn Ala Val Leu Ile Trp Thr Gly Val Trp Leu
 145 150 155 160
 Gly Ala Glu Trp Glu Thr Val Ser Met Trp Phe Glu Ser Tyr Ser Thr
 165 170 175
 Ile Ile Tyr Val Gly Ile Ala Leu Ile Val Ala Tyr Val Leu Phe Gly
 180 185 190
 Leu Val Arg Arg Arg Ile Lys Thr
 195 200

<210> 317
 <211> 705
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(682)
 <223> RXA00615

<400> 317
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 Met Thr Ala Ser Val 5
 1
 ttt tat ccg gtg ctg tca gtt gtg gtg ctc atc gac tgc att ttg ccg 163
 Phe Tyr Pro Val Leu Ser Val Val Val Leu Ile Asp Cys Ile Leu Pro 20
 10 15
 ctt atc ccc agt gag act gtt ctt gct ttg gca ggg gcg tgg tca gga 211
 Leu Ile Pro Ser Glu Thr Val Leu Ala Leu Ala Gly Ala Trp Ser Gly 35
 25 30
 gct cgg gga act cca aac ttg tgg ttg gtt att tca gta gca acg ttg 259
 Ala Arg Gly Thr Pro Asn Leu Trp Leu Val Ile Ser Val Ala Thr Leu 50
 40 45
 gcc gcg atc att ggt gac aac ctg tgt tat ttc ttt ggc acg cgg ttg 307
 Ala Ala Ile Ile Gly Asp Asn Leu Cys Tyr Phe Phe Gly Thr Arg Leu 65
 55 60

atc aat atg gtg aac agg att ccg gga gaa tcg agg cgc gga aaa gcg 355
 Ile Asn Met Val Asn Arg Ile Pro Gly Glu Ser Arg Arg Gly Lys Ala
 70 75 80 85

ctg gag tgg gcg cgg aag aac ctt aat gaa cgg gat gtt tcg aca atc 403
 Leu Glu Trp Ala Arg Lys Asn Leu Asn Glu Arg Asp Val Ser Thr Ile
 90 95 100

att atc gcc cgc ttt att ccg tgg gct agg tgg ttt gtc acc atc att 451
 Ile Ile Ala Arg Phe Ile Pro Trp Ala Arg Trp Phe Val Thr Ile Ile
 105 110 115

ttg gga tct gtg gga tat tcc tgg tcg agg ttt atc gtg tgg gat tcc 499
 Leu Gly Ser Val Gly Tyr Ser Trp Ser Arg Phe Ile Val Trp Asp Ser
 120 125 130

att gga gcg cta att tgg gca acc cag gca act ttg ttg ggt tat gtg 547
 Ile Gly Ala Leu Ile Trp Ala Thr Gln Ala Thr Leu Leu Gly Tyr Val
 135 140 145

ggc gga tgg ctt ttc caa gaa caa ccg ttg atc ggc ctg gtt gca ggc 595
 Gly Gly Trp Leu Phe Gln Glu Gln Pro Leu Ile Gly Leu Val Ala Gly
 150 155 160 165

gca gct ttg gga atc ttc ttc ggg ttc ttt ttg cag tgg ctc aac aaa 643
 Ala Ala Leu Gly Ile Phe Phe Gly Phe Phe Leu Gln Trp Leu Asn Lys
 170 175 180

atg tgg gag agg cgt cgt ctg gcg aaa gtg gct gca gaa tgaaaaatcag 692
 Met Trp Glu Arg Arg Arg Leu Ala Lys Val Ala Ala Glu
 185 190

gccagacagt ggg 705

<210> 318

<211> 194

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

Met Thr Ala Ser Val Phe Tyr Pro Val Leu Ser Val Val Val Leu Ile
 1 5 10 15

Asp Cys Ile Leu Pro Leu Ile Pro Ser Glu Thr Val Leu Ala Leu Ala
 20 25 30

Gly Ala Trp Ser Gly Ala Arg Gly Thr Pro Asn Leu Trp Leu Val Ile
 35 40 45

Ser Val Ala Thr Leu Ala Ala Ile Ile Gly Asp Asn Leu Cys Tyr Phe
 50 55 60

Phe Gly Thr Arg Leu Ile Asn Met Val Asn Arg Ile Pro Gly Glu Ser
 65 70 75 80

Arg Arg Gly Lys Ala Leu Glu Trp Ala Arg Lys Asn Leu Asn Glu Arg
 85 90 95

Asp Val Ser Thr Ile Ile Ile Ala Arg Phe Ile Pro Trp Ala Arg Trp
 100 105 110

Phe	Val	Thr	Ile	Ile	Leu	Gly	Ser	Val	Gly	Tyr	Ser	Trp	Ser	Arg	Phe
		115					120					125			
Ile	Val	Trp	Asp	Ser	Ile	Gly	Ala	Leu	Ile	Trp	Ala	Thr	Gln	Ala	Thr
		130				135					140				
Leu	Leu	Gly	Tyr	Val	Gly	Gly	Trp	Leu	Phe	Gln	Glu	Gln	Pro	Leu	Ile
145					150					155					160
Gly	Leu	Val	Ala	Gly	Ala	Ala	Leu	Gly	Ile	Phe	Phe	Gly	Phe	Phe	Leu
				165					170					175	
Gln	Trp	Leu	Asn	Lys	Met	Trp	Glu	Arg	Arg	Arg	Leu	Ala	Lys	Val	Ala
			180					185					190		

Ala Glu

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<210> 319
<211> 870
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (101) .. (847)  
<223> RXN00250.
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ccgtatagaa attcagtc aaagagttac tctgtccacc atg gtt ttt act ctt																115
Met Val Phe Thr Leu																5
gcg gac tcc gtc tcc cag gtt gcg cta ggt ccg tcc tgg ctg gac cct																163
Ala Asp Ser Val Ser Gln Val Ala Leu Gly Pro Ser Trp Leu Asp Pro																20
atg gaa ctt ctt tcc ggc tcc ggc ccg ttc ggt agc ttc att ctt ccg																211
Met Glu Leu Leu Ser Gly Ser Gly Pro Phe Gly Ser Phe Ile Leu Pro																35
gcg atg ctt gcc att gtc ttt atc gaa tca ggc cta ctt ttc cca ctt																259
Ala Met Leu Ala Ile Val Phe Ile Glu Ser Gly Leu Leu Phe Pro Leu																40
cta cca ggt gat tct ctc ctt ttc acc ggt ggt ctc cta gct aac cag																307
Leu Pro Gly Asp Ser Leu Leu Phe Thr Gly Gly Leu Leu Ala Asn Gln																65
gct gac cct ttt gca ccg ctg tgg ctg gtg ctg atc ctc tgc cct atc																355
Ala Asp Pro Phe Ala Pro Leu Trp Leu Val Leu Ile Leu Cys Pro Ile																70
gcc gca att ctt ggc gat cag gtg ggt tac tgg att ggc cac aag ttc																403
Ala Ala Ile Leu Gly Asp Gln Val Gly Tyr Trp Ile Gly His Lys Phe																90

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cac cct cgc ctg gtc aat cgt ccg gat ggc agg att ttc aag cag gaa 451
His Pro Arg Leu Val Asn Arg Pro Asp Gly Arg Ile Phe Lys Gln Glu
      105                110                115

tac ctc aag cag act gag gat ttc ttt gag aag cat ggc ccc gtg acg 499
Tyr Leu Lys Gln Thr Glu Asp Phe Phe Glu Lys His Gly Pro Val Thr
      120                125                130

atc att ttg tgc cgt ttc gtg ccc atc gtc cgt act tac gca cct ctg 547
Ile Ile Leu Cys Arg Phe Val Pro Ile Val Arg Thr Tyr Ala Pro Leu
      135                140                145

gtc gca ggt atg gct ggc atg cgt tac cgc acg ttc att att tac aac 595
Val Ala Gly Met Ala Gly Met Arg Tyr Arg Thr Phe Ile Ile Tyr Asn
      150                155                160                165

atg atc ggt ggc att ttg tgg ggt tcc ggc gtg gtg gct ttg ggt gct 643
Met Ile Gly Gly Ile Leu Trp Gly Ser Gly Val Val Ala Leu Gly Ala
      170                175                180

gcg ttg ggt cag ttc gat ttc gtc cgc aac aat att gat ctg att ttc 691
Ala Leu Gly Gln Phe Asp Phe Val Arg Asn Asn Ile Asp Leu Ile Phe
      185                190                195

ttg ctg atc gtg ttc att tcg gtg gtt cct ggt ttg gtc ggc atg gcc 739
Leu Leu Ile Val Phe Ile Ser Val Val Pro Gly Leu Val Gly Met Ala
      200                205                210

cgc aag ctg gct gac ggc cac aag caa gcc aac acc gag cca caa gaa 787
Arg Lys Leu Ala Asp Gly His Lys Gln Ala Asn Thr Glu Pro Gln Glu
      215                220                225

aac ccc gca gtc cag aca gcc cca gta aaa acc cag gaa gcc cag gaa 835
Asn Pro Ala Val Gln Thr Ala Pro Val Lys Thr Gln Glu Ala Gln Glu
      230                235                240                245

gcc ccc cag aac taatctttcc ggtccgccag ttc 870
Ala Pro Gln Asn

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<210> 320

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

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Met Val Phe Thr Leu Ala Asp Ser Val Ser Gln Val Ala Leu Gly Pro
  1              5              10              15

Ser Trp Leu Asp Pro Met Glu Leu Leu Ser Gly Ser Gly Pro Phe Gly
  20              25              30

Ser Phe Ile Leu Pro Ala Met Leu Ala Ile Val Phe Ile Glu Ser Gly
  35              40              45

Leu Leu Phe Pro Leu Leu Pro Gly Asp Ser Leu Leu Phe Thr Gly Gly
  50              55              60

Leu Leu Ala Asn Gln Ala Asp Pro Phe Ala Pro Leu Trp Leu Val Leu
  65              70              75              80

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Ile Leu Cys Pro Ile Ala Ala Ile Leu Gly Asp Gln Val Gly Tyr Trp
 85 90 95
 Ile Gly His Lys Phe His Pro Arg Leu Val Asn Arg Pro Asp Gly Arg
 100 105 110
 Ile Phe Lys Gln Glu Tyr Leu Lys Gln Thr Glu Asp Phe Phe Glu Lys
 115 120 125
 His Gly Pro Val Thr Ile Ile Leu Cys Arg Phe Val Pro Ile Val Arg
 130 135 140
 Thr Tyr Ala Pro Leu Val Ala Gly Met Ala Gly Met Arg Tyr Arg Thr
 145 150 155 160
 Phe Ile Ile Tyr Asn Met Ile Gly Gly Ile Leu Trp Gly Ser Gly Val
 165 170 175
 Val Ala Leu Gly Ala Ala Leu Gly Gln Phe Asp Phe Val Arg Asn Asn
 180 185 190
 Ile Asp Leu Ile Phe Leu Leu Ile Val Phe Ile Ser Val Val Pro Gly
 195 200 205
 Leu Val Gly Met Ala Arg Lys Leu Ala Asp Gly His Lys Gln Ala Asn
 210 215 220
 Thr Glu Pro Gln Glu Asn Pro Ala Val Gln Thr Ala Pro Val Lys Thr
 225 230 235 240
 Gln Glu Ala Gln Glu Ala Pro Gln Asn
 245

<210> 321

<211> 525

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (79)..(525)

<223> FRXA02010

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aagagtactc tgtccacc atg gtt ttt act ctt gcg gac tcc gtc tcc cag 111
 Met Val Phe Thr Leu Ala Asp Ser Val Ser Gln
 1 5 10

gtt gcg cta ggt ccg tcc tgg ctg gac cct atg gaa ctt ctt tcc ggc 159
 Val Ala Leu Gly Pro Ser Trp Leu Asp Pro Met Glu Leu Leu Ser Gly
 15 20 25

tcc ggc ccg ttc ggt agc ttc att ctt ccg gcg atg ctt gcc att gtc 207
 Ser Gly Pro Phe Gly Ser Phe Ile Leu Pro Ala Met Leu Ala Ile Val
 30 35 40

ttt atc gaa tca ggc cta ctt ttc cca ctt cta cca ggt gat tct ctc 255

Phe Ile Glu Ser Gly Leu Leu Phe Pro Leu Leu Pro Gly Asp Ser Leu
 45 50 55
 ctt ttc acc ggt ggt ctc cta gct aac cag gct gac cct ttt gca ccg 303
 Leu Phe Thr Gly Gly Leu Leu Ala Asn Gln Ala Asp Pro Phe Ala Pro
 60 65 70 75
 ctg tgg ctg gtg ctg atc ctc tgc cct atc gcc gca att ctt ggc gat 351
 Leu Trp Leu Val Leu Ile Leu Cys Pro Ile Ala Ala Ile Leu Gly Asp
 80 85 90
 cag gtg ggt tac tgg att ggc cac aag ttc cac cct cgc ctg gtc aat 399
 Gln Val Gly Tyr Trp Ile Gly His Lys Phe His Pro Arg Leu Val Asn
 95 100 105
 cgt ccg gat ggc agg att ttc aag cag gaa tac ctc aag cag act gag 447
 Arg Pro Asp Gly Arg Ile Phe Lys Gln Glu Tyr Leu Lys Gln Thr Glu
 110 115 120
 gat ttc ttt gag aag cat ggc ccc gtg acg atc att ttg tgc cgt ttc 495
 Asp Phe Phe Glu Lys His Gly Pro Val Thr Ile Ile Leu Cys Arg Phe
 125 130 135
 gtg ccc atc gtc cgt act tac gca cct ctg 525
 Val Pro Ile Val Arg Thr Tyr Ala Pro Leu
 140 145

<210> 322

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 322

Met Val Phe Thr Leu Ala Asp Ser Val Ser Gln Val Ala Leu Gly Pro
 1 5 10 15
 Ser Trp Leu Asp Pro Met Glu Leu Leu Ser Gly Ser Gly Pro Phe Gly
 20 25 30
 Ser Phe Ile Leu Pro Ala Met Leu Ala Ile Val Phe Ile Glu Ser Gly
 35 40 45
 Leu Leu Phe Pro Leu Leu Pro Gly Asp Ser Leu Leu Phe Thr Gly Gly
 50 55 60
 Leu Leu Ala Asn Gln Ala Asp Pro Phe Ala Pro Leu Trp Leu Val Leu
 65 70 75 80
 Ile Leu Cys Pro Ile Ala Ala Ile Leu Gly Asp Gln Val Gly Tyr Trp
 85 90 95
 Ile Gly His Lys Phe His Pro Arg Leu Val Asn Arg Pro Asp Gly Arg
 100 105 110
 Ile Phe Lys Gln Glu Tyr Leu Lys Gln Thr Glu Asp Phe Phe Glu Lys
 115 120 125
 His Gly Pro Val Thr Ile Ile Leu Cys Arg Phe Val Pro Ile Val Arg
 130 135 140

Thr Tyr Ala Pro Leu
145

<210> 323
<211> 885
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(862)
<223> RXA02120

<400> 323
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gcaaattagc acaacttcac actttatttta ggagcatgtt atg tct gac ctg aag 115
Met Ser Asp Leu Lys
1 5

tca ctt gcc acg aaa ttt gct agc gat cat gaa tcc gga aag ctg ctg 163
Ser Leu Ala Thr Lys Phe Ala Ser Asp His Glu Ser Gly Lys Leu Leu
10 15 20

gtc ctg cct acc gtc tgg gat acc tgg agc gcg ggg ctc gta gaa gaa 211
Val Leu Pro Thr Val Trp Asp Thr Trp Ser Ala Gly Leu Val Glu Glu
25 30 35

gca gga ttt agt ggc ctg acc att ggt agc cac cca gtc gcg gat gcg 259
Ala Gly Phe Ser Gly Leu Thr Ile Gly Ser His Pro Val Ala Asp Ala
40 45 50

aca gga agc tcc gat ggt gaa aac atg aat ttt gca gat tat atg gcg 307
Thr Gly Ser Ser Asp Gly Glu Asn Met Asn Phe Ala Asp Tyr Met Ala
55 60 65

gtg gtc aag aag atc acc tcg gcg gta tcc atc ccc gta agc gtt gat 355
Val Val Lys Lys Ile Thr Ser Ala Val Ser Ile Pro Val Ser Val Asp
70 75 80 85

gtg gaa tcc ggt tat ggt ctc tcg cct gcg gat ttg atc gca cag att 403
Val Glu Ser Gly Tyr Gly Leu Ser Pro Ala Asp Leu Ile Ala Gln Ile
90 95 100

ttg gaa gct ggc gca gtg ggc atc aat gtg gaa gat gtt gtg cac agc 451
Leu Glu Ala Gly Ala Val Gly Ile Asn Val Glu Asp Val Val His Ser
105 110 115

gag ggt aag cgt gtt cgt gag gcg cag gag cac gct gat tac atc gct 499
Glu Gly Lys Arg Val Arg Glu Ala Gln Glu His Ala Asp Tyr Ile Ala
120 125 130

gcg gca cgt caa gct gcc gat gtg gca ggt gta gat gtg gtg atc aac 547
Ala Ala Arg Gln Ala Ala Asp Val Ala Gly Val Asp Val Val Ile Asn
135 140 145

ggg cgc acg gat gcc gtc aaa ctt ggt gca gac gtt ttt gaa gat ccg 595
Gly Arg Thr Asp Ala Val Lys Leu Gly Ala Asp Val Phe Glu Asp Pro
150 155 160 165

atg gtg gag gcc atc aag cgc atc aag ctc atg gaa cag gca ggc gcg 643
 Met Val Glu Ala Ile Lys Arg Ile Lys Leu Met Glu Gln Ala Gly Ala
 170 175 180

cgt tcg gtg tac ccc gtg ggt ctg agc acc gcc gag cag gtt gag cgc 691
 Arg Ser Val Tyr Pro Val Gly Leu Ser Thr Ala Glu Gln Val Glu Arg
 185 190 195

ctg gtg gac gct gtg tca gtg ccg gtc aac atc acc gcg cac ccg gtt 739
 Leu Val Asp Ala Val Ser Val Pro Val Asn Ile Thr Ala His Pro Val
 200 205 210

gat ggg cac ggc gca ggc gat ctg gcc acc ctc gca ggc ctt ggc gtg 787
 Asp Gly His Gly Ala Gly Asp Leu Ala Thr Leu Ala Gly Leu Gly Val
 215 220 225

cgc cgc gtg acc ttc ggt ccg ctc tgg caa aaa tgg ctg gct gcc acc 835
 Arg Arg Val Thr Phe Gly Pro Leu Trp Gln Lys Trp Leu Ala Ala Thr
 230 235 240 245

tcg gcg cag cag ctt aag ggc tgg gct taaattgctt gtcgacgcct agt 885
 Ser Ala Gln Gln Leu Lys Gly Trp Ala
 250

<210> 324

<211> 254

<212> PRT

<213> Corynebacterium glutamicum.

<400> 324

Met Ser Asp Leu Lys Ser Leu Ala Thr Lys Phe Ala Ser Asp His Glu
 1 5 10 15

Ser Gly Lys Leu Leu Val Leu Pro Thr Val Trp Asp Thr Trp Ser Ala
 20 25 30

Gly Leu Val Glu Glu Ala Gly Phe Ser Gly Leu Thr Ile Gly Ser His
 35 40 45

Pro Val Ala Asp Ala Thr Gly Ser Ser Asp Gly Glu Asn Met Asn Phe
 50 55 60

Ala Asp Tyr Met Ala Val Val Lys Lys Ile Thr Ser Ala Val Ser Ile
 65 70 75 80

Pro Val Ser Val Asp Val Glu Ser Gly Tyr Gly Leu Ser Pro Ala Asp
 85 90 95

Leu Ile Ala Gln Ile Leu Glu Ala Gly Ala Val Gly Ile Asn Val Glu
 100 105 110

Asp Val Val His Ser Glu Gly Lys Arg Val Arg Glu Ala Gln Glu His
 115 120 125

Ala Asp Tyr Ile Ala Ala Ala Arg Gln Ala Ala Asp Val Ala Gly Val
 130 135 140

Asp Val Val Ile Asn Gly Arg Thr Asp Ala Val Lys Leu Gly Ala Asp
 145 150 155 160

Val Phe Glu Asp Pro Met Val Glu Ala Ile Lys Arg Ile Lys Leu Met
 165 170 175

Glu Gln Ala Gly Ala Arg Ser Val Tyr Pro Val Gly Leu Ser Thr Ala
 180 185 190

Glu Gln Val Glu Arg Leu Val Asp Ala Val Ser Val Pro Val Asn Ile
 195 200 205

Thr Ala His Pro Val Asp Gly His Gly Ala Gly Asp Leu Ala Thr Leu
 210 215 220

Ala Gly Leu Gly Val Arg Arg Val Thr Phe Gly Pro Leu Trp Gln Lys
 225 230 235 240

Trp Leu Ala Ala Thr Ser Ala Gln Gln Leu Lys Gly Trp Ala
 245 250

<210> 325

<211> 969

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(946)

<223> RXS01000

<400> 325

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tcattgaagt aatctccaac gcacttcgaa agaggctggt atg agc acc tta acc 115
 Met Ser Thr Leu Thr
 1 5

tct cac cgc aca gta ccg gcc ccc agc tct ccc ccg gcg cgc ccc aac 163
 Ser His Arg Thr Val Pro Ala Pro Ser Ser Pro Pro Ala Arg Pro Asn
 10 15 20

aaa ctg gcg cgc aat atc gtt gca att gtc gct gcg ctg att gtc ctt 211
 Lys Leu Ala Arg Asn Ile Val Ala Ile Val Ala Ala Leu Ile Val Leu
 25 30 35

ata gct acc ggc acg ctc aag atc gag tgg aat gag ctt ccg cag atg 259
 Ile Ala Thr Gly Thr Leu Lys Ile Glu Trp Asn Glu Leu Pro Gln Met
 40 45 50

ccc gcg cag gtg tgg cat tac tta gag ctg atg ttt agc gat ccc gat 307
 Pro Ala Gln Val Trp His Tyr Leu Glu Leu Met Phe Ser Asp Pro Asp
 55 60 65

tgg tcg aag ttt ggc cgc gcc gtc cag gaa atg tgg cgt tcc atc gcc 355
 Trp Ser Lys Phe Gly Arg Ala Val Gln Glu Met Trp Arg Ser Ile Ala
 70 75 80 85

atg gcg tgg ttg ggt gcc att tta tgc gtg gtg gtc tct gtc cct ctg 403
 Met Ala Trp Leu Gly Ala Ile Leu Cys Val Val Val Ser Val Pro Leu
 90 95 100

gga atg ttg gct gcc cgc ggg gtg gga cct tat tgg ctg cgt acc gtt 451

Gly Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val
 105 110 115
 tta cgg ttc gtg ttc gcg gtg att cgt gcg ttc ccc gaa gtg gtt atc 499
 Leu Arg Phe Val Phe Ala Val Ile Arg Ala Phe Pro Glu Val Val Ile
 120 125 130
 gca att att ttg cta act gtc acc ggc cta act cct ttt act ggt gcg 547
 Ala Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala
 135 140 145
 ctc gca ttg ggt atc tcc ggt att gga caa cag gca aag tgg acc tat 595
 Leu Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr
 150 155 160 165
 gaa gcc att gag tcc act ccc acc ggc ccg tca gag gca gtg cgt gca 643
 Glu Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser Glu Ala Val Arg Ala
 170 175 180
 gcg ggt gga act acg ccg gag gtt ctg ccg tgg gcg ttg tgg cca cag 691
 Ala Gly Gly Thr Thr Pro Glu Val Leu Arg Trp Ala Leu Trp Pro Gln
 185 190 195
 gtt gcg cca tcc att gca tct ttt gcc ctg tac cgc ttt gag atc aac 739
 Val Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr Arg Phe Glu Ile Asn
 200 205 210
 atc cgt acc tct gcg gta ttg ggc atc gtt ggt gca ggt ggt atc ggt 787
 Ile Arg Thr Ser Ala Val Leu Gly Ile Val Gly Ala Gly Gly Ile Gly
 215 220 225
 agt atg ctt gcc aat tac acc aac tac agg cag tgg gac acc gtg ggc 835
 Ser Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln Trp Asp Thr Val Gly
 230 235 240 245
 atg ctg ctc atc gtc gtg gtt gtc gca acg atg atc gtc gat ctc atc 883
 Met Leu Leu Ile Val Val Val Val Ala Thr Met Ile Val Asp Leu Ile
 250 255 260
 tcc ggc acc atc cgc cgc cgc atc atg aag ggg gct agt gac cgt gtc 931
 Ser Gly Thr Ile Arg Arg Arg Ile Met Lys Gly Ala Ser Asp Arg Val
 265 270 275
 gtg gca cca agc aac tgacgctcca ccaagcatcc gca 969
 Val Ala Pro Ser Asn
 280

<210> 326

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 326

Met Ser Thr Leu Thr Ser His Arg Thr Val Pro Ala Pro Ser Ser Pro
 1 5 10 15

Pro Ala Arg Pro Asn Lys Leu Ala Arg Asn Ile Val Ala Ile Val Ala
 20 25 30

Ala Leu Ile Val Leu Ile Ala Thr Gly Thr Leu Lys Ile Glu Trp Asn

35					40					45					
Glu	Leu	Pro	Gln	Met	Pro	Ala	Gln	Val	Trp	His	Tyr	Leu	Glu	Leu	Met
50					55					60					
Phe	Ser	Asp	Pro	Asp	Trp	Ser	Lys	Phe	Gly	Arg	Ala	Val	Gln	Glu	Met
65					70					75					80
Trp	Arg	Ser	Ile	Ala	Met	Ala	Trp	Leu	Gly	Ala	Ile	Leu	Cys	Val	Val
				85					90					95	
Val	Ser	Val	Pro	Leu	Gly	Met	Leu	Ala	Ala	Arg	Gly	Val	Gly	Pro	Tyr
			100					105					110		
Trp	Leu	Arg	Thr	Val	Leu	Arg	Phe	Val	Phe	Ala	Val	Ile	Arg	Ala	Phe
		115					120					125			
Pro	Glu	Val	Val	Ile	Ala	Ile	Ile	Leu	Leu	Thr	Val	Thr	Gly	Leu	Thr
	130					135					140				
Pro	Phe	Thr	Gly	Ala	Leu	Ala	Leu	Gly	Ile	Ser	Gly	Ile	Gly	Gln	Gln
145					150					155					160
Ala	Lys	Trp	Thr	Tyr	Glu	Ala	Ile	Glu	Ser	Thr	Pro	Thr	Gly	Pro	Ser
				165					170					175	
Glu	Ala	Val	Arg	Ala	Ala	Gly	Gly	Thr	Thr	Pro	Glu	Val	Leu	Arg	Trp
			180					185					190		
Ala	Leu	Trp	Pro	Gln	Val	Ala	Pro	Ser	Ile	Ala	Ser	Phe	Ala	Leu	Tyr
	195						200					205			
Arg	Phe	Glu	Ile	Asn	Ile	Arg	Thr	Ser	Ala	Val	Leu	Gly	Ile	Val	Gly
	210					215					220				
Ala	Gly	Gly	Ile	Gly	Ser	Met	Leu	Ala	Asn	Tyr	Thr	Asn	Tyr	Arg	Gln
225					230					235					240
Trp	Asp	Thr	Val	Gly	Met	Leu	Leu	Ile	Val	Val	Val	Val	Ala	Thr	Met
				245					250					255	
Ile	Val	Asp	Leu	Ile	Ser	Gly	Thr	Ile	Arg	Arg	Arg	Ile	Met	Lys	Gly
			260					265					270		
Ala	Ser	Asp	Arg	Val	Val	Ala	Pro	Ser	Asn						
	275					280									

<210> 327

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXS01002

<400> 327

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caactaattt ccctgtttcc aataactcaag gtgtgcgcat	atg aat tct gat gct	115
	Met Asn Ser Asp Ala	
	1 5	
tcg gct acc acc aac tcc tgg gct atc aac ttc gac cat gtg tcg gtg		163
Ser Ala Thr Thr Asn Ser Trp Ala Ile Asn Phe Asp His Val Ser Val		
	10 15 20	
acg tat ccc aat ggg acg aaa gcc ctc gat gat gtt tcc ctc acc atc		211
Thr Tyr Pro Asn Gly Thr Lys Ala Leu Asp Asp Val Ser Leu Thr Ile		
	25 30 35	
aat ccc ggt gag atg gtt gcc atc gtg ggt ctg tca gga tcg ggt aaa		259
Asn Pro Gly Glu Met Val Ala Ile Val Gly Leu Ser Gly Ser Gly Lys		
	40 45 50	
tcc acg ctg att cgc acg atc aac ggt ctt gtc cgc gct acg gaa ggc		307
Ser Thr Leu Ile Arg Thr Ile Asn Gly Leu Val Arg Ala Thr Glu Gly		
	55 60 65	
acc gtg acg gtg ggg ccg cat cag atc aac acc ttg aag ggg aaa gca		355
Thr Val Thr Val Gly Pro His Gln Ile Asn Thr Leu Lys Gly Lys Ala		
	70 75 80 85	
ctg cgt gat gcc cgt ggg cag atc ggc atg att ttc cag ggg ttc aac		403
Leu Arg Asp Ala Arg Gly Gln Ile Gly Met Ile Phe Gln Gly Phe Asn		
	90 95 100	
ctg tcg gaa cgc agc agt gtg ttc cag aat gtt ttg gtg ggc cgc ttc		451
Leu Ser Glu Arg Ser Ser Val Phe Gln Asn Val Leu Val Gly Arg Phe		
	105 110 115	
gcg cac aca gcg tgg tgg cgt aac ctc ctc ggg ttt ccc acg gag cac		499
Ala His Thr Ala Trp Trp Arg Asn Leu Leu Gly Phe Pro Thr Glu His		
	120 125 130	
gac aag cag att gct ttt cac gcg ttg gag tcc gtg ggc att ttg cac		547
Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser Val Gly Ile Leu His		
	135 140 145	
aaa gtg tgg acc cga gct ggt gct ttg tcg ggt gga cag aaa cag cgc		595
Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly Gly Gln Lys Gln Arg		
	150 155 160 165	
gtt gct att gcg cgc gcc tta tcg caa gat ccg tct gtc atg ctg gca		643
Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro Ser Val Met Leu Ala		
	170 175 180	
gat gag cct gtg gca agc ctt gat ccg cca acc gcg cat tcc gtg atg		691
Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr Ala His Ser Val Met		
	185 190 195	
cgc gat cta gaa aac atc aac aac gtg gaa ggc ctc acc gtg ttg gtg		739
Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly Leu Thr Val Leu Val		
	200 205 210	
aac ttg cac ttg att gat ttg gct cgt caa tac acc aca agg ctt gtg		787
Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr Thr Thr Arg Leu Val		
	215 220 225	
ggt ttg cgt gcc ggc aag ctg gtc tat gac ggt cct atc tct gag gcc		835

Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly Pro Ile Ser Glu Ala
 230 235 240 245

acc gat aaa gac ttt gaa gct atc tat ggt cgc ccc atc cag gct aaa 883
 Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg Pro Ile Gln Ala Lys
 250 255 260

gac ctg cta ggt gat cgc gca tgaccacgcc ttcttctaca ctt 927
 Asp Leu Leu Gly Asp Arg Ala
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<210> 328

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 328

Met Asn Ser Asp Ala Ser Ala Thr Thr Asn Ser Trp Ala Ile Asn Phe
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Asp His Val Ser Val Thr Tyr Pro Asn Gly Thr Lys Ala Leu Asp Asp
 20 25 30

Val Ser Leu Thr Ile Asn Pro Gly Glu Met Val Ala Ile Val Gly Leu
 35 40 45

Ser Gly Ser Gly Lys Ser Thr Leu Ile Arg Thr Ile Asn Gly Leu Val
 50 55 60

Arg Ala Thr Glu Gly Thr Val Thr Val Gly Pro His Gln Ile Asn Thr
 65 70 75 80

Leu Lys Gly Lys Ala Leu Arg Asp Ala Arg Gly Gln Ile Gly Met Ile
 85 90 95

Phe Gln Gly Phe Asn Leu Ser Glu Arg Ser Ser Val Phe Gln Asn Val
 100 105 110

Leu Val Gly Arg Phe Ala His Thr Ala Trp Trp Arg Asn Leu Leu Gly
 115 120 125

Phe Pro Thr Glu His Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser
 130 135 140

Val Gly Ile Leu His Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly
 145 150 155 160

Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro
 165 170 175

Ser Val Met Leu Ala Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr
 180 185 190

Ala His Ser Val Met Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly
 195 200 205

Leu Thr Val Leu Val Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr
 210 215 220

Thr Thr Arg Leu Val Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly

225	230	235	240
Pro Ile Ser Glu	Ala Thr Asp Lys Asp	Phe Glu Ala Ile Tyr	Gly Arg
	245	250	255
Pro Ile Gln Ala	Lys Asp Leu Leu Gly	Asp Arg Ala	
	260	265	

<210> 329

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXS01003

<400> 329

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gtcgcccat	ccaggctaaa	gacctgctag	gtgatcgcg	atg acc acg cct tct	115
				Met Thr Thr Pro Ser	
				1 5	

tct aca ctt atc	cca caa aag cct	cgg gct ggg gta	aag acc tat ctc	163
Ser Thr Leu Ile	Pro Gln Lys Pro	Arg Ala Gly Val	Lys Thr Tyr Leu	
	10	15	20	

atc atc ggc gcc	atc gtt gtc ttc	acc gtg gca aca	gca acc cca gcg	211
Ile Ile Gly Ala	Ile Val Val Phe	Thr Val Ala Thr	Ala Thr Pro Ala	
	25	30	35	

cta ggt ggc att	gag ctt gat ttc	gct tcc att gct	gcg aat tgg cgc	259
Leu Gly Gly Ile	Glu Leu Asp Phe	Ala Ser Ile Ala	Ala Asn Trp Arg	
	40	45	50	

aat ggt gcc aac	aaa ctc ctg caa	atg ctg cag ccc	aac ttt gcg ttc	307
Asn Gly Ala Asn	Lys Leu Leu Gln	Met Leu Gln Pro	Asn Phe Ala Phe	
	55	60	65	

ttg cct cgt acg	tgg ctt ccc atg	ttg gaa acc ctg	cag atg gcg ctt	355
Leu Pro Arg Thr	Trp Leu Pro Met	Leu Glu Thr Leu	Gln Met Ala Leu	
	70	75	80 85	

gtt gga gct gtc	ttg tct gct gcc	gta tcg gtg cct	ttg acg ttg tgg	403
Val Gly Ala Val	Leu Ser Ala Ala	Val Ser Val Pro	Leu Thr Leu Trp	
	90	95	100	

gca gcg cag gca	acc aac acc agt	gcg att ggt cgt	ggc att gtc cgc	451
Ala Ala Gln Ala	Thr Asn Thr Ser	Ala Ile Gly Arg	Gly Ile Val Arg	
	105	110	115	

acc atc att aac	gtg gtg cgc tct	gtc ccc gac ttg	gtg tat gcc acc	499
Thr Ile Ile Asn	Val Val Arg Ser	Val Pro Asp Leu	Val Tyr Ala Thr	
	120	125	130	

atc ttg gtc gcc	atg gtt ggt gtc	ggc gca tta cct	ggc att ttg acg	547
Ile Leu Val Ala	Met Val Gly Val	Gly Ala Leu Pro	Gly Ile Leu Thr	
	135	140	145	

ctg ttt ctg ttc aac ctg ggc atc gtg gtc aag ctt gtc tct gag gcc 595
 Leu Phe Leu Phe Asn Leu Gly Ile Val Val Lys Leu Val Ser Glu Ala
 150 155 160 165
 att gat tcc act gag cat ccc tat atg gaa gca gga cgc gca gca ggt 643
 Ile Asp Ser Thr Glu His Pro Tyr Met Glu Ala Gly Arg Ala Ala Gly
 170 175 180
 gga tca cag ttc caa atc aac cga gtc tcc gcg ctt cct gaa gtc atg 691
 Gly Ser Gln Phe Gln Ile Asn Arg Val Ser Ala Leu Pro Glu Val Met
 185 190 195
 ccg ctc ttt gcc aac caa tgg ctc tac acc cta gag ctg aat gta cgc 739
 Pro Leu Phe Ala Asn Gln Trp Leu Tyr Thr Leu Glu Leu Asn Val Arg
 200 205 210
 atc tcc gcc atc ctt ggc atc gtg ggc gca ggt ggc atc ggc agg ctg 787
 Ile Ser Ala Ile Leu Gly Ile Val Gly Ala Gly Gly Ile Gly Arg Leu
 215 220 225
 ctt gat gaa cgc cga gct ttc tat gcc tac gcg gat gtt tcc gtg atc 835
 Leu Asp Glu Arg Arg Ala Phe Tyr Ala Tyr Ala Asp Val Ser Val Ile
 230 235 240 245
 att ctg gaa atc ctc atc gtg gtg att gtc att gaa gta atc tcc aac 883
 Ile Leu Glu Ile Leu Ile Val Val Ile Val Ile Glu Val Ile Ser Asn
 250 255 260
 gca ctt cga aag agg ctg gta tgagcacctt aacctctcac cgc 927
 Ala Leu Arg Lys Arg Leu Val
 265

<210> 330

<211> 268

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 330

Met Thr Thr Pro Ser Ser Thr Leu Ile Pro Gln Lys Pro Arg Ala Gly
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 Val Lys Thr Tyr Leu Ile Ile Gly Ala Ile Val Val Phe Thr Val Ala
 20 25 30
 Thr Ala Thr Pro Ala Leu Gly Gly Ile Glu Leu Asp Phe Ala Ser Ile
 35 40 45
 Ala Ala Asn Trp Arg Asn Gly Ala Asn Lys Leu Leu Gln Met Leu Gln
 50 55 60
 Pro Asn Phe Ala Phe Leu Pro Arg Thr Trp Leu Pro Met Leu Glu Thr
 65 70 75 80
 Leu Gln Met Ala Leu Val Gly Ala Val Leu Ser Ala Ala Val Ser Val
 85 90 95
 Pro Leu Thr Leu Trp Ala Ala Gln Ala Thr Asn Thr Ser Ala Ile Gly
 100 105 110

Arg Gly Ile Val Arg Thr Ile Ile Asn Val Val Arg Ser Val Pro Asp
 115 120 125
 Leu Val Tyr Ala Thr Ile Leu Val Ala Met Val Gly Val Gly Ala Leu
 130 135 140
 Pro Gly Ile Leu Thr Leu Phe Leu Phe Asn Leu Gly Ile Val Val Lys
 145 150 155 160
 Leu Val Ser Glu Ala Ile Asp Ser Thr Glu His Pro Tyr Met Glu Ala
 165 170 175
 Gly Arg Ala Ala Gly Gly Ser Gln Phe Gln Ile Asn Arg Val Ser Ala
 180 185 190
 Leu Pro Glu Val Met Pro Leu Phe Ala Asn Gln Trp Leu Tyr Thr Leu
 195 200 205
 Glu Leu Asn Val Arg Ile Ser Ala Ile Leu Gly Ile Val Gly Ala Gly
 210 215 220
 Gly Ile Gly Arg Leu Leu Asp Glu Arg Arg Ala Phe Tyr Ala Tyr Ala
 225 230 235 240
 Asp Val Ser Val Ile Ile Leu Glu Ile Leu Ile Val Val Ile Val Ile
 245 250 255
 Glu Val Ile Ser Asn Ala Leu Arg Lys Arg Leu Val
 260 265

<210> 331
 <211> 1182
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1159)
 <223> RXS01902

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 ttcttcggcg acaccagct gtacaacacc cactccaacc gtg cag aag aag tcc 115
 Val Gln Lys Lys Ser
 1 5
 aga act ggg caa aca acc tgg aac ggc ggc cca cca atc gaa aac cca 163
 Arg Thr Gly Gln Thr Thr Trp Asn Gly Gly Pro Pro Ile Glu Asn Pro
 10 15 20
 gga acc tcc ttc atc ctc tcc gcg ggt gat cag gca aac cac tcc agc 211
 Gly Thr Ser Phe Ile Leu Ser Ala Gly Asp Gln Ala Asn His Ser Ser
 25 30 35
 tgg gac gag cac tcc gca tac atc tcc cca gaa acc ctg cgc aac tac 259
 Trp Asp Glu His Ser Ala Tyr Ile Ser Pro Glu Thr Leu Arg Asn Tyr
 40 45 50
 cgt ctg gcc gtg aac aat gga aac cac gac cag tac aac tac gac gcc 307

Arg	Leu	Ala	Val	Asn	Asn	Gly	Asn	His	Asp	Gln	Tyr	Asn	Tyr	Asp	Ala		
	55					60					65						
tac	aac	gcg	atg	tac	cca	cgc	cct	aac	cag	gtc	gat	gag	aac	tac	ttc	355	
Tyr	Asn	Ala	Met	Tyr	Pro	Arg	Pro	Asn	Gln	Val	Asp	Glu	Asn	Tyr	Phe		
	70				75					80					85		
ttc	gag	tac	aac	aat	gca	ctc	ttc	ctg	tcc	ctg	gac	tcc	aac	gac	tac	403	
Phe	Glu	Tyr	Asn	Asn	Ala	Leu	Phe	Leu	Ser	Leu	Asp	Ser	Asn	Asp	Tyr		
				90					95					100			
ttg	gac	atc	gac	gac	gac	atc	gca	ttc	ctt	cgc	gac	acc	gtc	gca	gca	451	
Leu	Asp	Ile	Asp	Asp	Asp	Ile	Ala	Phe	Leu	Arg	Asp	Thr	Val	Ala	Ala		
			105					110					115				
cac	ggt	gac	gac	aag	gac	tgg	atc	gtc	ctg	acc	tac	cac	cat	tcc	act	499	
His	Gly	Asp	Asp	Lys	Asp	Trp	Ile	Val	Leu	Thr	Tyr	His	His	Ser	Thr		
		120					125					130					
ttc	tcc	cag	gcc	tac	cac	atg	gat	gac	gct	cgc	att	aag	tac	cag	cgc	547	
Phe	Ser	Gln	Ala	Tyr	His	Met	Asp	Asp	Ala	Arg	Ile	Lys	Tyr	Gln	Arg		
	135					140					145						
gaa	cgc	ctc	acc	cca	gtg	atc	tct	gaa	ctg	aac	gtt	gac	ttg	gtt	ctc	595	
Glu	Arg	Leu	Thr	Pro	Val	Ile	Ser	Glu	Leu	Asn	Val	Asp	Leu	Val	Leu		
	150				155					160					165		
ggt	gga	cac	gac	cac	atc	tac	acc	cgc	tcc	cac	ctg	atg	aac	ggc	ttc	643	
Gly	Gly	His	Asp	His	Ile	Tyr	Thr	Arg	Ser	His	Leu	Met	Asn	Gly	Phe		
				170					175					180			
acc	cca	gtc	gat	gca	ggc	cgc	gaa	gca	gtt	gtc	ggt	gaa	act	ctg	aac	691	
Thr	Pro	Val	Asp	Ala	Gly	Arg	Glu	Ala	Val	Val	Gly	Glu	Thr	Leu	Asn		
			185					190					195				
cct	aag	gcc	ggc	gaa	gtt	gtt	tac	ctt	gca	acc	aac	tct	tcc	tca	ggc	739	
Pro	Lys	Ala	Gly	Glu	Val	Val	Tyr	Leu	Ala	Thr	Asn	Ser	Ser	Ser	Gly		
		200					205					210					
tcc	aag	ttc	tac	gac	ttc	tac	gac	ttc	cag	ctc	ggc	cag	cgT	tac	gac	787	
Ser	Lys	Phe	Tyr	Asp	Phe	Tyr	Asp	Phe	Gln	Leu	Gly	Gln	Arg	Tyr	Asp		
	215					220					225						
acc	gga	ctg	gat	ttc	cag	gaa	acc	gtc	gat	cag	aag	aag	atc	cgC	acc	835	
Thr	Gly	Leu	Asp	Phe	Gln	Glu	Thr	Val	Asp	Gln	Lys	Lys	Ile	Arg	Thr		
	230				235					240					245		
tac	acc	gca	gtc	tgg	aac	cag	gac	cag	gtt	cag	gac	tac	acc	aac	gtt	883	
Tyr	Thr	Ala	Val	Trp	Asn	Gln	Asp	Gln	Val	Gln	Asp	Tyr	Thr	Asn	Val		
				250					255					260			
gaa	ctg	acc	cca	gaa	ggc	ctg	act	gtg	acc	act	aag	gac	gca	gtc	tcc	931	
Glu	Leu	Thr	Pro	Glu	Gly	Leu	Thr	Val	Thr	Thr	Lys	Asp	Ala	Val	Ser		
			265					270					275				
ggc	gag	ctg	gtt	gac	cag	ttc	acc	ctg	agc	aag	cag	gac	cgC	gac	gaa	979	
Gly	Glu	Leu	Val	Asp	Gln	Phe	Thr	Leu	Ser	Lys	Gln	Asp	Arg	Asp	Glu		
		280					285					290					
gaa	tct	gaa	gtc	cca	gtt	gaa	gat	gac	aag	gac	gga	gac	aac	gcg	acc	1027	
Glu	Ser	Glu	Val	Pro	Val	Glu	Asp	Asp	Lys	Asp	Gly	Asp	Asn	Ala	Thr		

295	300	305	
ggc tcc tcc aac ctt ggt cta gct gct atc ttg gct cca gtt ctg gcc			1075
Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu Ala Pro Val Leu Ala			
310	315	320	325
atc ttc ggt ttc gtc ggt gga ctc ttt gtt ggc ggc ggc tcc ctc gct			1123
Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly Gly Gly Ser Leu Ala			
	330	335	340
gag ttc ttt gcc aac ctc ggc gtg aag atg cct ttc taatactgtc			1169
Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro Phe			
	345	350	
tgagattcaa gca			1182
<210> 332			
<211> 353			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 332			
Val Gln Lys Lys Ser Arg Thr Gly Gln Thr Thr Trp Asn Gly Gly Pro			
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Pro Ile Glu Asn Pro Gly Thr Ser Phe Ile Leu Ser Ala Gly Asp Gln			
	20	25	30
Ala Asn His Ser Ser Trp Asp Glu His Ser Ala Tyr Ile Ser Pro Glu			
	35	40	45
Thr Leu Arg Asn Tyr Arg Leu Ala Val Asn Asn Gly Asn His Asp Gln			
	50	55	60
Tyr Asn Tyr Asp Ala Tyr Asn Ala Met Tyr Pro Arg Pro Asn Gln Val			
	65	70	75
Asp Glu Asn Tyr Phe Phe Glu Tyr Asn Asn Ala Leu Phe Leu Ser Leu			
	85	90	95
Asp Ser Asn Asp Tyr Leu Asp Ile Asp Asp Asp Ile Ala Phe Leu Arg			
	100	105	110
Asp Thr Val Ala Ala His Gly Asp Asp Lys Asp Trp Ile Val Leu Thr			
	115	120	125
Tyr His His Ser Thr Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg			
	130	135	140
Ile Lys Tyr Gln Arg Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn			
	145	150	155
Val Asp Leu Val Leu Gly Gly His Asp His Ile Tyr Thr Arg Ser His			
	165	170	175
Leu Met Asn Gly Phe Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val			
	180	185	190
Gly Glu Thr Leu Asn Pro Lys Ala Gly Glu Val Val Tyr Leu Ala Thr			
	195	200	205

Asn Ser Ser Ser Gly Ser Lys Phe Tyr Asp Phe Tyr Asp Phe Gln Leu
 210 215 220
 Gly Gln Arg Tyr Asp Thr Gly Leu Asp Phe Gln Glu Thr Val Asp Gln
 225 230 235 240
 Lys Lys Ile Arg Thr Tyr Thr Ala Val Trp Asn Gln Asp Gln Val Gln
 245 250 255
 Asp Tyr Thr Asn Val Glu Leu Thr Pro Glu Gly Leu Thr Val Thr Thr
 260 265 270
 Lys Asp Ala Val Ser Gly Glu Leu Val Asp Gln Phe Thr Leu Ser Lys
 275 280 285
 Gln Asp Arg Asp Glu Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp
 290 295 300
 Gly Asp Asn Ala Thr Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu
 305 310 315 320
 Ala Pro Val Leu Ala Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly
 325 330 335
 Gly Gly Ser Leu Ala Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro
 340 345 350
 Phe

<210> 333
 <211> 1266
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1243)
 <223> RXA01967

<400> 333
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 gttgtcgcca accgtgccac cgcaaaccac caaacgtcac atg cgc atc caa agc 115
 Met Arg Ile Gln Ser
 1 5
 ccc atg gaa att tcc tgg agt gaa gcg gtg cgc gaa ggc ggg gag cat 163
 Pro Met Glu Ile Ser Trp Ser Glu Ala Val Arg Glu Gly Gly Glu His
 10 15 20
 tcc gct cgc cgc tgt ggt gac atg gct gtg tcc gcg ttg gct aag ccg 211
 Ser Ala Arg Arg Cys Gly Asp Met Ala Val Ser Ala Leu Ala Lys Pro
 25 30 35
 aat ccc atc att gac gat gat ccg gaa ggc aac ccc gat gtt tgc atg 259
 Asn Pro Ile Ile Asp Asp Asp Pro Glu Gly Asn Pro Asp Val Cys Met
 40 45 50

tat acc tgg atc gtt gag tgt ccc ggc gct acc gca gtg ctg cta tgg	307
Tyr Thr Trp Ile Val Glu Cys Pro Gly Ala Thr Ala Val Leu Leu Trp	
55 60 65	
atc aat ggg gtt ttt gat cac gag cgc att gaa gaa tct gaa atg acc	355
Ile Asn Gly Val Phe Asp His Glu Arg Ile Glu Glu Ser Glu Met Thr	
70 75 80 85	
cgc ctc gag ggc tct gat ctg tgg att ctc agc ttg cgt atg cct tcc	403
Arg Leu Glu Gly Ser Asp Leu Trp Ile Leu Ser Leu Arg Met Pro Ser	
90 95 100	
gat tgg cga gcc agc tac acc gtc aac gcc tgg tct ggc gac ggg gtt	451
Asp Trp Arg Ala Ser Tyr Thr Val Asn Ala Trp Ser Gly Asp Gly Val	
105 110 115	
gcg cca tgg cgt gag gcg ggc gat cgg atg cat atc cgc aaa gcc gcg	499
Ala Pro Trp Arg Glu Ala Gly Asp Arg Met His Ile Arg Lys Ala Ala	
120 125 130	
atg tcg ggt ggg cgt ccg gat tcc cgc gcg atg ggt cat atc atg gat	547
Met Ser Gly Gly Arg Pro Asp Ser Arg Ala Met Gly His Ile Met Asp	
135 140 145	
tcc tcg ctc gtt gaa ggc cct gat gcg ttg ccg gac tgc tgg gtt gcg	595
Ser Ser Leu Val Glu Gly Pro Asp Ala Leu Pro Asp Cys Trp Val Ala	
150 155 160 165	
gcg tcg aca agc gta aaa gtc gtg gaa gaa acc gtc gcc ggc gag cat	643
Ala Ser Thr Ser Val Lys Val Val Glu Glu Thr Val Ala Gly Glu His	
170 175 180	
ttc tgg ttc tat gag gcg ccg gtc aag gcg ccg ctg ctg gtg ctg ttt	691
Phe Trp Phe Tyr Glu Ala Pro Val Lys Ala Pro Leu Leu Val Leu Phe	
185 190 195	
gat ggc caa cac tgg aac aac agc atg aat ctg cct gcg cag gtc gat	739
Asp Gly Gln His Trp Asn Asn Ser Met Asn Leu Pro Ala Gln Val Asp	
200 205 210	
gcg gcc atc gcc atc ggc ttg ctg ccg ccg gtc agc ctg ctc atg atc	787
Ala Ala Ile Ala Ile Gly Leu Leu Pro Pro Val Ser Leu Leu Met Ile	
215 220 225	
gat tcc gtc aac acc gaa cgc cgc tgg gat agt gtc ggc gtg cca ggt	835
Asp Ser Val Asn Thr Glu Arg Arg Trp Asp Ser Val Gly Val Pro Gly	
230 235 240 245	
ggg cag gtt gat gtg ctt atc gac gcc ctc ctc ccg cac gtc cgc gaa	883
Gly Gln Val Asp Val Leu Ile Asp Ala Leu Leu Pro His Val Arg Glu	
250 255 260	
acc tac aac gtt tcc gcg cgc ggc gaa gac acc att gtc acc ggt gca	931
Thr Tyr Asn Val Ser Ala Arg Gly Glu Asp Thr Ile Val Thr Gly Ala	
265 270 275	
agc ttc ggc ggc ctg gcg tcc ctg tgg gct ctt gcg ctt tcc gac ggc	979
Ser Phe Gly Gly Leu Ala Ser Leu Trp Ala Leu Ala Leu Ser Asp Gly	
280 285 290	
gaa gtc ggc cac gca atc gcg caa tcg cca agc ctg tgg cgc ttc aac	1027

Glu Val Gly His Ala Ile Ala Gln Ser Pro Ser Leu Trp Arg Phe Asn
 295 300 305
 gtt gcc gac gcg ctt tct gca gca gag cag tgg agc tca atc cac ctg 1075
 Val Ala Asp Ala Leu Ser Ala Ala Glu Gln Trp Ser Ser Ile His Leu
 310 315 320 325
 caa gct gga aaa tac gaa ggt gaa atg ctg cgc ctg tcg cat cag ctc 1123
 Gln Ala Gly Lys Tyr Glu Gly Glu Met Leu Arg Leu Ser His Gln Leu
 330 335 340
 gcc gaa gat ctc tcc ggc gac atc cgc gag gtt cgt gtg cgc ggc gtg 1171
 Ala Glu Asp Leu Ser Gly Asp Ile Arg Glu Val Arg Val Arg Gly Val
 345 350 355
 cat ggc ggc cac gat tgg gcc tgg tgg cgg gtg cat atg ctc acc gaa 1219
 His Gly Gly His Asp Trp Ala Trp Trp Arg Val His Met Leu Thr Glu
 360 365 370
 ctc acc agg ctg ctt aaa acc ctc taatcaaagt aggggtgcaaa acg 1266
 Leu Thr Arg Leu Leu Lys Thr Leu
 375 380
 <210> 334
 <211> 381
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 334
 Met Arg Ile Gln Ser Pro Met Glu Ile Ser Trp Ser Glu Ala Val Arg
 1 5 10 15
 Glu Gly Gly Glu His Ser Ala Arg Arg Cys Gly Asp Met Ala Val Ser
 20 25 30
 Ala Leu Ala Lys Pro Asn Pro Ile Ile Asp Asp Asp Pro Glu Gly Asn
 35 40 45
 Pro Asp Val Cys Met Tyr Thr Trp Ile Val Glu Cys Pro Gly Ala Thr
 50 55 60
 Ala Val Leu Leu Trp Ile Asn Gly Val Phe Asp His Glu Arg Ile Glu
 65 70 75 80
 Glu Ser Glu Met Thr Arg Leu Glu Gly Ser Asp Leu Trp Ile Leu Ser
 85 90 95
 Leu Arg Met Pro Ser Asp Trp Arg Ala Ser Tyr Thr Val Asn Ala Trp
 100 105 110
 Ser Gly Asp Gly Val Ala Pro Trp Arg Glu Ala Gly Asp Arg Met His
 115 120 125
 Ile Arg Lys Ala Ala Met Ser Gly Gly Arg Pro Asp Ser Arg Ala Met
 130 135 140
 Gly His Ile Met Asp Ser Ser Leu Val Glu Gly Pro Asp Ala Leu Pro
 145 150 155 160
 Asp Cys Trp Val Ala Ala Ser Thr Ser Val Lys Val Val Glu Glu Thr

165										170					175				
Val	Ala	Gly	Glu	His	Phe	Trp	Phe	Tyr	Glu	Ala	Pro	Val	Lys	Ala	Pro				
			180					185					190						
Leu	Leu	Val	Leu	Phe	Asp	Gly	Gln	His	Trp	Asn	Asn	Ser	Met	Asn	Leu				
		195					200					205							
Pro	Ala	Gln	Val	Asp	Ala	Ala	Ile	Ala	Ile	Gly	Leu	Leu	Pro	Pro	Val				
	210					215					220								
Ser	Leu	Leu	Met	Ile	Asp	Ser	Val	Asn	Thr	Glu	Arg	Arg	Trp	Asp	Ser				
225					230					235					240				
Val	Gly	Val	Pro	Gly	Gly	Gln	Val	Asp	Val	Leu	Ile	Asp	Ala	Leu	Leu				
				245					250					255					
Pro	His	Val	Arg	Glu	Thr	Tyr	Asn	Val	Ser	Ala	Arg	Gly	Glu	Asp	Thr				
			260					265					270						
Ile	Val	Thr	Gly	Ala	Ser	Phe	Gly	Gly	Leu	Ala	Ser	Leu	Trp	Ala	Leu				
		275					280					285							
Ala	Leu	Ser	Asp	Gly	Glu	Val	Gly	His	Ala	Ile	Ala	Gln	Ser	Pro	Ser				
	290					295					300								
Leu	Trp	Arg	Phe	Asn	Val	Ala	Asp	Ala	Leu	Ser	Ala	Ala	Glu	Gln	Trp				
305					310					315				320					
Ser	Ser	Ile	His	Leu	Gln	Ala	Gly	Lys	Tyr	Glu	Gly	Glu	Met	Leu	Arg				
				325					330					335					
Leu	Ser	His	Gln	Leu	Ala	Glu	Asp	Leu	Ser	Gly	Asp	Ile	Arg	Glu	Val				
			340					345					350						
Arg	Val	Arg	Gly	Val	His	Gly	Gly	His	Asp	Trp	Ala	Trp	Trp	Arg	Val				
		355					360					365							
His	Met	Leu	Thr	Glu	Leu	Thr	Arg	Leu	Leu	Lys	Thr	Leu							
	370					375					380								

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<211> 555

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(532)

<223> RXA00070

<400> 335

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actatcgaag	tacattttgt	gtcattgagg	aggatcaacg	gtg	ggt	atc	aat	cgc	115
				Val	Gly	Ile	Asn	Arg	
				1				5	

atc	agc	caa	ggc	tct	gcc	ccg	aag	ctg	gga	gtg	cga	agc	acc	aga	cag	163
Ile	Ser	Gln	Gly	Ser	Ala	Pro	Lys	Leu	Gly	Val	Arg	Ser	Thr	Arg	Gln	

	10	15	20	
cga aaa gcc gta att gac gtt ctt gag gaa atc gat aac ttc gct tcc				211
Arg Lys Ala Val Ile Asp Val Leu Glu Glu Ile Asp Asn Phe Ala Ser				
	25	30	35	
gcc aaa gaa atc cat cac gag cta tcc acc agg gaa cac aac gtc ggc				259
Ala Lys Glu Ile His His Glu Leu Ser Thr Arg Glu His Asn Val Gly				
	40	45	50	
ctc aca acc gtc tac cga acc ctc caa tcc ctc gcc gac atc gga gca				307
Leu Thr Thr Val Tyr Arg Thr Leu Gln Ser Leu Ala Asp Ile Gly Ala				
	55	60	65	
gtc gac gta ctt acc gtc acg ggt gga gaa act ctg tac cgc caa tgc				355
Val Asp Val Leu Thr Val Thr Gly Gly Glu Thr Leu Tyr Arg Gln Cys				
	70	75	80	85
cac gac gag gga cac cac cat cac ctg gtc tgc acc aat tgc ggt cgc				403
His Asp Glu Gly His His His His Leu Val Cys Thr Asn Cys Gly Arg				
	90	95	100	
aca gtc gaa atc gat ggc ggt cca gta gag aca tgg gca cag gaa att				451
Thr Val Glu Ile Asp Gly Gly Pro Val Glu Thr Trp Ala Gln Glu Ile				
	105	110	115	
gcc act aaa aac ggc ttt gct ctc agt agt cac gag gct gaa atc ttt				499
Ala Thr Lys Asn Gly Phe Ala Leu Ser Ser His Glu Ala Glu Ile Phe				
	120	125	130	
gga ctt tgc gct gat tgt aag gaa aaa gtt acg tagttcaagg acatatgaag				552
Gly Leu Cys Ala Asp Cys Lys Glu Lys Val Thr				
	135	140		
ctg				555
<210> 336				
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<400> 336				
Val Gly Ile Asn Arg Ile Ser Gln Gly Ser Ala Pro Lys Leu Gly Val				
1	5	10	15	
Arg Ser Thr Arg Gln Arg Lys Ala Val Ile Asp Val Leu Glu Glu Ile				
	20	25	30	
Asp Asn Phe Ala Ser Ala Lys Glu Ile His His Glu Leu Ser Thr Arg				
	35	40	45	
Glu His Asn Val Gly Leu Thr Thr Val Tyr Arg Thr Leu Gln Ser Leu				
	50	55	60	
Ala Asp Ile Gly Ala Val Asp Val Leu Thr Val Thr Gly Gly Glu Thr				
	65	70	75	80
Leu Tyr Arg Gln Cys His Asp Glu Gly His His His His Leu Val Cys				
	85	90	95	

<400> 337																
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acttcactgg cttagattcc ttaaaagaaa gcattcagga atg aca cct caa cca 115																
Met Thr Pro Gln Pro 1 5																
ctg att.ttg cct ttc ggc gat aaa gtt ccg cgg atc cat gaa agc gca 163																
Leu Ile Leu Pro Phe Gly Asp Lys Val Pro Arg Ile His Glu Ser Ala 10 15 20																
tgg att gcc ccg aat gcc acg att atc ggg gat gtc gag att ggc ccg 211																
Trp Ile Ala Pro Asn Ala Thr Ile Ile Gly Asp Val Glu Ile Gly Pro 25 30 35																
gat gcg tcc att ttt tat ggc gtt gtc ctg cgc ggt gac gtc aac aaa 259																
Asp Ala Ser Ile Phe Tyr Gly Val Val Leu Arg Gly Asp Val Asn Lys 40 45 50																
atc acc atc ggc gcc cgc acc aac gtc cag gac aat tgt gtt ctc cac 307																
Ile Thr Ile Gly Ala Arg Thr Asn Val Gln Asp Asn Cys Val Leu His 55 60 65																
gtc gat ggc gat gcg ccg tgc acc ctc ggc gac gat gtc acg gtc ggc 355																
Val Asp Gly Asp Ala Pro Cys Thr Leu Gly Asp Asp Val Thr Val Gly 70 75 80 85																
cac atg gcg ctt gtt cac ggc gcg acg gtg ggc aac ggc acg ctt gtc 403																
His Met Ala Leu Val His Gly Ala Thr Val Gly Asn Gly Thr Leu Val 90 95 100																
ggc atg aaa tct gcg ctg ctt tcc ggc agc cac gtc ggc gcc ggc gca 451																
Gly Met Lys Ser Ala Leu Leu Ser Gly Ser His Val Gly Ala Gly Ala 105 110 115																
ctc att gcc gct ggt gcg gtg gtg ctg gag ggc cat gaa atc ccg gcg 499																
Leu Ile Ala Ala Gly Ala Val Val Leu Glu Gly His Glu Ile Pro Ala 120 125 130																
aaa gct ttagcg gcc ggg gtt ccg gcc aaa gtg cgc aga ttg ctt gac 547																
Lys Ala Leu Ala Ala Gly Val Pro Ala Lys Val Arg Arg Leu Leu Asp																

135	140	145	
gac gcc cag tcc cag tca ttt atc ccc cac gcg ggc cgc tat gta gaa			595
Asp Ala Gln Ser Gln Ser Phe Ile Pro His Ala Gly Arg Tyr Val Glu			
150	155	160	165
aca tca aaa gcc cag gct tcc atc gcg gaa gca ctg agc tta gat gag			643
Thr Ser Lys Ala Gln Ala Ser Ile Ala Glu Ala Leu Ser Leu Asp Glu			
	170	175	180
gtt agg gta cga gag taagtggctc gttgagtagt cga			681
Val Arg Val Arg Glu			
	185		

<210> 338
 <211> 186
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 338
 Met Thr Pro Gln Pro Leu Ile Leu Pro Phe Gly Asp Lys Val Pro Arg
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 20 25 30
 Val Glu Ile Gly Pro Asp Ala Ser Ile Phe Tyr Gly Val Val Leu Arg
 35 40 45
 Gly Asp Val Asn Lys Ile Thr Ile Gly Ala Arg Thr Asn Val Gln Asp
 50 55 60
 Asn Cys Val Leu His Val Asp Gly Asp Ala Pro Cys Thr Leu Gly Asp
 65 70 75 80
 Asp Val Thr Val Gly His Met Ala Leu Val His Gly Ala Thr Val Gly
 85 90 95
 Asn Gly Thr Leu Val Gly Met Lys Ser Ala Leu Leu Ser Gly Ser His
 100 105 110
 Val Gly Ala Gly Ala Leu Ile Ala Ala Gly Ala Val Val Leu Glu Gly
 115 120 125
 His Glu Ile Pro Ala Lys Ala Leu Ala Ala Gly Val Pro Ala Lys Val
 130 135 140
 Arg Arg Leu Leu Asp Asp Ala Gln Ser Gln Ser Phe Ile Pro His Ala
 145 150 155 160
 Gly Arg Tyr Val Glu Thr Ser Lys Ala Gln Ala Ser Ile Ala Glu Ala
 165 170 175
 Leu Ser Leu Asp Glu Val Arg Val Arg Glu
 180 185

<210> 339
 <211> 609
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) ..(586)

<223> RXN01997

<400> 339

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				Met	Thr	Ile	Asn	Glu	
				1				5	

aag	atc	gca	tca	gct	ttc	aac	aac	caa	gtg	act	gca	gag	ctt	gaa	gct	163
Lys	Ile	Ala	Ser	Ala	Phe	Asn	Asn	Gln	Val	Thr	Ala	Glu	Leu	Glu	Ala	
				10				15						20		

tca	atg	gtg	tac	ctt	cag	ctc	tcc	tac	gtt	cta	gac	gat	ctg	ggc	ctc	211
Ser	Met	Val	Tyr	Leu	Gln	Leu	Ser	Tyr	Val	Leu	Asp	Asp	Leu	Gly	Leu	
			25					30					35			

acc	ggc	atg	cgc	gac	tgg	atg	aag	gca	cag	agc	aaa	gaa	gag	ctc	gaa	259
Thr	Gly	Met	Arg	Asp	Trp	Met	Lys	Ala	Gln	Ser	Lys	Glu	Glu	Leu	Glu	
		40					45					50				

cac	gca	cag	aag	ttc	gct	cag	cac	ctt	ctt	gac	cgt	gac	tac	acc	cca	307
His	Ala	Gln	Lys	Phe	Ala	Gln	His	Leu	Leu	Asp	Arg	Asp	Tyr	Thr	Pro	
	55					60					65					

cag	atc	ggg	gac	att	gca	cca	cca	aag	ctt	gat	gtc	acc	tcc	gct	atc	355
Gln	Ile	Gly	Asp	Ile	Ala	Pro	Pro	Lys	Leu	Asp	Val	Thr	Ser	Ala	Ile	
70					75					80					85	

gag	gct	ttc	gag	gct	tcc	ctg	gca	cac	gag	cag	aag	atc	tcc	ggc	ctg	403
Glu	Ala	Phe	Glu	Ala	Ser	Leu	Ala	His	Glu	Gln	Lys	Ile	Ser	Gly	Leu	
				90					95					100		

atc	cgc	gag	ctc	gct	gcc	atc	cag	gac	gct	gag	aag	gac	tac	gat	tcc	451
Ile	Arg	Glu	Leu	Ala	Ala	Ile	Gln	Asp	Ala	Glu	Lys	Asp	Tyr	Asp	Ser	
			105					110					115			

cgc	gca	ctg	atc	gac	tgg	ttc	ctc	aac	gag	cag	atc	gaa	gaa	gaa	gca	499
Arg	Ala	Leu	Ile	Asp	Trp	Phe	Leu	Asn	Glu	Gln	Ile	Glu	Glu	Glu	Ala	
		120					125					130				

acc	gtc	ggc	gag	atc	atc	gac	cgc	ctc	cgt	atc	gct	ggg	gat	tcc	ggg	547
Thr	Val	Gly	Glu	Ile	Ile	Asp	Arg	Leu	Arg	Ile	Ala	Gly	Asp	Ser	Gly	
	135					140					145					

tcc	gga	atc	ctg	cgc	atc	gac	ggc	gaa	ctc	ggc	tcc	cgc	taaattcccc	596
Ser	Gly	Ile	Leu	Arg	Ile	Asp	Gly	Glu	Leu	Gly	Ser	Arg		
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gcagttttta	atg	609
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<210> 340

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 340

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Ala Glu Leu Glu Ala Ser Met Val Tyr Leu Gln Leu Ser Tyr Val Leu
      20           25           30

Asp Asp Leu Gly Leu Thr Gly Met Arg Asp Trp Met Lys Ala Gln Ser
 35           40           45

Lys Glu Glu Leu Glu His Ala Gln Lys Phe Ala Gln His Leu Leu Asp
 50           55           60

Arg Asp Tyr Thr Pro Gln Ile Gly Asp Ile Ala Pro Pro Lys Leu Asp
 65           70           75           80

Val Thr Ser Ala Ile Glu Ala Phe Glu Ala Ser Leu Ala His Glu Gln
      85           90           95

Lys Ile Ser Gly Leu Ile Arg Glu Leu Ala Ala Ile Gln Asp Ala Glu
 100          105          110

Lys Asp Tyr Asp Ser Arg Ala Leu Ile Asp Trp Phe Leu Asn Glu Gln
 115          120          125

Ile Glu Glu Glu Ala Thr Val Gly Glu Ile Ile Asp Arg Leu Arg Ile
 130          135          140

Ala Gly Asp Ser Gly Ser Gly Ile Leu Arg Ile Asp Gly Glu Leu Gly
145          150          155          160

Ser Arg

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<210> 341

<211> 490

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(490)

<223> FRXA01997

<400> 341

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                                   Met Thr Ile Asn Glu
                                   1           5

aag atc gca tca gct ttc aac aac caa gtg act gca gag ctt gaa gct 163
Lys Ile Ala Ser Ala Phe Asn Asn Gln Val Thr Ala Glu Leu Glu Ala
      10           15           20

tca atg gtg tac ctt cag ctc tcc tac gtt cta gac gat ctg ggc ctc 211
Ser Met Val Tyr Leu Gln Leu Ser Tyr Val Leu Asp Asp Leu Gly Leu
      25           30           35

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acc ggc atg cgc gac tgg atg aag gca cag agc aaa gaa gag ctc gaa 259
 Thr Gly Met Arg Asp Trp Met Lys Ala Gln Ser Lys Glu Glu Leu Glu
 40 45 50

cac gca cag aag ttc gct cag cac ctt ctt gac cgt gac tac acc cca 307
 His Ala Gln Lys Phe Ala Gln His Leu Leu Asp Arg Asp Tyr Thr Pro
 55 60 65

cag atc ggt gac att gca cca cca aag ctt gat gtc acc tcc gct atc 355
 Gln Ile Gly Asp Ile Ala Pro Pro Lys Leu Asp Val Thr Ser Ala Ile
 70 75 80 85

gag gct ttc gag gct tcc ctg gca cac gag cag aag atc tcc ggc ctg 403
 Glu Ala Phe Glu Ala Ser Leu Ala His Glu Gln Lys Ile Ser Gly Leu
 90 95 100

atc cgc gag ctc gct gcc atc cag gac gct gag aag gac tac gat tcc 451
 Ile Arg Glu Leu Ala Ala Ile Gln Asp Ala Glu Lys Asp Tyr Asp Ser
 105 110 115

cgc gca ctg atc gac tgg ttc ctc aac gag cag atc gaa 490
 Arg Ala Leu Ile Asp Trp Phe Leu Asn Glu Gln Ile Glu
 120 125 130

<210> 342

<211> 130

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

Met Thr Ile Asn Glu Lys Ile Ala Ser Ala Phe Asn Asn Gln Val Thr
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Ala Glu Leu Glu Ala Ser Met Val Tyr Leu Gln Leu Ser Tyr Val Leu
 20 25 30

Asp Asp Leu Gly Leu Thr Gly Met Arg Asp Trp Met Lys Ala Gln Ser
 35 40 45

Lys Glu Glu Leu Glu His Ala Gln Lys Phe Ala Gln His Leu Leu Asp
 50 55 60

Arg Asp Tyr Thr Pro Gln Ile Gly Asp Ile Ala Pro Pro Lys Leu Asp
 65 70 75 80

Val Thr Ser Ala Ile Glu Ala Phe Glu Ala Ser Leu Ala His Glu Gln
 85 90 95

Lys Ile Ser Gly Leu Ile Arg Glu Leu Ala Ala Ile Gln Asp Ala Glu
 100 105 110

Lys Asp Tyr Asp Ser Arg Ala Leu Ile Asp Trp Phe Leu Asn Glu Gln
 115 120 125

Ile Glu
 130

<210> 343

<211> 783

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(760)

<223> RXA01082

<400> 343

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cacttatcaa acatcggcgg cgaattaaga aggtgaacag ttg acg cag tgg ggt 115
Leu Thr Gln Trp Gly
1 5

aat tcg aat gtt gtg gag gac tat ctc aca gca ctt ttc cgt gca gaa 163
Asn Ser Asn Val Val Glu Asp Tyr Leu Thr Ala Leu Phe Arg Ala Glu
10 15 20

gaa tgg gat gag gaa cca aca aca gga aaa ctc gct gaa gta att gga 211
Glu Trp Asp Glu Glu Pro Thr Thr Gly Lys Leu Ala Glu Val Ile Gly
25 30 35

gtt acc gca tca acg gtg tcg gcg acg ctc aaa aaa ctc aac cct gag 259
Val Thr Ala Ser Thr Val Ser Ala Thr Leu Lys Lys Leu Asn Pro Glu
40 45 50

ggc ttc gtc aat tac cgt ccc tac ggg gac atc gag ctg acg ccc gca 307
Gly Phe Val Asn Tyr Arg Pro Tyr Gly Asp Ile Glu Leu Thr Pro Ala
55 60 65

ggg cga gac atc gcc atc aac gtg atc agg cgg cgc cgg atc att gag 355
Gly Arg Asp Ile Ala Ile Asn Val Ile Arg Arg Arg Arg Ile Ile Glu
70 75 80 85

acc tat ctg tct gag aag ctt gga tta ggc gct cat gaa cta cac ggc 403
Thr Tyr Leu Ser Glu Lys Leu Gly Leu Gly Ala His Glu Leu His Gly
90 95 100

gag gca gat tta tta gag cac gca gtg tct cca ctg gtg ttg gag aag 451
Glu Ala Asp Leu Leu Glu His Ala Val Ser Pro Leu Val Leu Glu Lys
105 110 115

atg ttt cag gca gtg ggc tat cca acg ttg gat cct cac ggg gat ccc 499
Met Phe Gln Ala Val Gly Tyr Pro Thr Leu Asp Pro His Gly Asp Pro
120 125 130

atc ccc acc gaa tct ggg gag atg acc atc aat gat gga ctc atg ctt 547
Ile Pro Thr Glu Ser Gly Glu Met Thr Ile Asn Asp Gly Leu Met Leu
135 140 145

ttg gga cta aaa gct ggc gca tct gcc acg gtt aca cgt gtt agg gac 595
Leu Gly Leu Lys Ala Gly Ala Ser Ala Thr Val Thr Arg Val Arg Asp
150 155 160 165

gga aac cca tca gtg gtt cgg tac ctc act gga gtg gga att acc gtg 643
Gly Asn Pro Ser Val Val Arg Tyr Leu Thr Gly Val Gly Ile Thr Val
170 175 180

ggc aca acg gtc acg gtc gtt gaa gct ctt agc gat att gcc aca ctg 691
Gly Thr Thr Val Thr Val Val Glu Ala Leu Ser Asp Ile Ala Thr Leu

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	185		190		195	
cgc ctg cag atc ggg gaa atg ttt caa gac att ccc ctt gca gtg gca						739
Arg Leu Gln Ile Gly Glu Met Phe Gln Asp Ile Pro Leu Ala Val Ala						
	200		205		210	
aac gca gtg cgc gta tca cgt tagttcagcg tgcccagcgc gct						783
Asn Ala Val Arg Val Ser Arg						
	215		220			

<210> 344
 <211> 220
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 344
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 Leu Phe Arg Ala Glu Glu Trp Asp Glu Glu Pro Thr Thr Gly Lys Leu
 20 25 30
 Ala Glu Val Ile Gly Val Thr Ala Ser Thr Val Ser Ala Thr Leu Lys
 35 40 45
 Lys Leu Asn Pro Glu Gly Phe Val Asn Tyr Arg Pro Tyr Gly Asp Ile
 50 55 60
 Glu Leu Thr Pro Ala Gly Arg Asp Ile Ala Ile Asn Val Ile Arg Arg
 65 70 75 80
 Arg Arg Ile Ile Glu Thr Tyr Leu Ser Glu Lys Leu Gly Leu Gly Ala
 85 90 95
 His Glu Leu His Gly Glu Ala Asp Leu Leu Glu His Ala Val Ser Pro
 100 105 110
 Leu Val Leu Glu Lys Met Phe Gln Ala Val Gly Tyr Pro Thr Leu Asp
 115 120 125
 Pro His Gly Asp Pro Ile Pro Thr Glu Ser Gly Glu Met Thr Ile Asn
 130 135 140
 Asp Gly Leu Met Leu Leu Gly Leu Lys Ala Gly Ala Ser Ala Thr Val
 145 150 155 160
 Thr Arg Val Arg Asp Gly Asn Pro Ser Val Val Arg Tyr Leu Thr Gly
 165 170 175
 Val Gly Ile Thr Val Gly Thr Thr Val Thr Val Val Glu Ala Leu Ser
 180 185 190
 Asp Ile Ala Thr Leu Arg Leu Gln Ile Gly Glu Met Phe Gln Asp Ile
 195 200 205
 Pro Leu Ala Val Ala Asn Ala Val Arg Val Ser Arg
 210 215 220

<210> 345

<211> 1068

<212> DNA.

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1045)

<223> RXA01236

<400> 345

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ggtttcaacc acaacatctc gctcaatcgc tggactgtca  gtg ctt gtg gca aca  115
                                         Val Leu Val Ala Thr
                                         1                               5

gca cta atc gct ggc tgt agt tcc gca gag gat ggg acg gtt gac tcg  163
Ala Leu Ile Ala Gly Cys Ser Ser Ala Glu Asp Gly Thr Val Asp Ser
                        10                        15                        20

ggg agc agc aca gag gtc acc aca acc caa agc aag gaa ggt ttt cct  211
Gly Ser Ser Thr Glu Val Thr Thr Thr Gln Ser Lys Glu Gly Phe Pro
                        25                        30                        35

gtc acc gtc acg ttt gcc cca gaa gca cct gtg acc att gag gat caa  259
Val Thr Val Thr Phe Ala Pro Glu Ala Pro Val Thr Ile Glu Asp Gln
                        40                        45                        50

cca gag cgc atc gtc agt ttg tcc cca gcg att aca gaa acc ttg ttc  307
Pro Glu Arg Ile Val Ser Leu Ser Pro Ala Ile Thr Glu Thr Leu Phe
                        55                        60                        65

gct gtc ggg gca ggg gat cat gtc gtc gca gtg gat gaa tac tca aac  355
Ala Val Gly Ala Gly Asp His Val Val Ala Val Asp Glu Tyr Ser Asn
                        70                        75                        80                        85

tac cca gag gac gca ccg ctg gtg cag ggt ctg tct ggt ttt act ccc  403
Tyr Pro Glu Asp Ala Pro Leu Val Gln Gly Leu Ser Gly Phe Thr Pro
                        90                        95                        100

aat gtg gag tcc atc ttg gat tac gat cct gac ctg gtc gtg ttg atg  451
Asn Val Glu Ser Ile Leu Asp Tyr Asp Pro Asp Leu Val Val Leu Met
                        105                        110                        115

tct gca gat gat tcc att ttg acc ggc ctg gat gct gca gga gtg gat  499
Ser Ala Asp Asp Ser Ile Leu Thr Gly Leu Asp Ala Ala Gly Val Asp
                        120                        125                        130

act tta gtg atc ccc gca gca gag aac ttg gat gag acc tac tcc cag  547
Thr Leu Val Ile Pro Ala Ala Glu Asn Leu Asp Glu Thr Tyr Ser Gln
                        135                        140                        145

att gaa caa gta ggt cga gcc acc gga ttt gaa gat caa gca aca acg  595
Ile Glu Gln Val Gly Arg Ala Thr Gly Phe Glu Asp Gln Ala Thr Thr
                        150                        155                        160                        165

gtt gtt gat cag atg aaa acc gcc att gat gct gca gtt gcc aca gtt  643
Val Val Asp Gln Met Lys Thr Ala Ile Asp Ala Ala Val Ala Thr Val
                        170                        175                        180

cct gaa gag gta aaa gag cag ggc tta acc tac ttc cac gag ctg ggc  691

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Pro Glu Glu Val Lys Glu Gln Gly Leu Thr Tyr Phe His Glu Leu Gly
 185 190 195

agt gat ttg ttc act gtg tca gag caa acc tac atc ggt cag att tac 739
 Ser Asp Leu Phe Thr Val Ser Glu Gln Thr Tyr Ile Gly Gln Ile Tyr
 200 205 210

gac atg ttt ggt ctc acc tct att gct gac ggt ggc gac gct tac tcg 787
 Asp Met Phe Gly Leu Thr Ser Ile Ala Asp Gly Gly Asp Ala Tyr Ser
 215 220 225

cag cta tcc aac gaa gca atc att gcg gca aac cct gat ctg att ttc 835
 Gln Leu Ser Asn Glu Ala Ile Ile Ala Ala Asn Pro Asp Leu Ile Phe
 230 235 240 245

ctc agc gat gcc aag gcc gaa aac ctc act gca gaa gat att gcg gcg 883
 Leu Ser Asp Ala Lys Ala Glu Asn Leu Thr Ala Glu Asp Ile Ala Ala
 250 255 260

cgt cca ggc tgg gac acc att gat gca gta gcc aat gga cgt atc tac 931
 Arg Pro Gly Trp Asp Thr Ile Asp Ala Val Ala Asn Gly Arg Ile Tyr
 265 270 275

att ttg gac gat gat att gct tcc agg tgg gga cct cgc gta tcc cag 979
 Ile Leu Asp Asp Asp Ile Ala Ser Arg Trp Gly Pro Arg Val Ser Gln
 280 285 290

ctg gtg gaa gaa atc gca gcg cag ttg aat cag ctt gct tct tct gaa 1027
 Leu Val Glu Glu Ile Ala Ala Gln Leu Asn Gln Leu Ala Ser Ser Glu
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gct gtg ccg gcc gct gct taagtttttcg tgctgaagag aat 1068
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<210> 346

<211> 315

<212> PRT

<213> Corynebacterium glutamicum

<400> 346

Val Leu Val Ala Thr Ala Leu Ile Ala Gly Cys Ser Ser Ala Glu Asp
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Gly Thr Val Asp Ser Gly Ser Ser Thr Glu Val Thr Thr Thr Gln Ser
 20 25 30

Lys Glu Gly Phe Pro Val Thr Val Thr Phe Ala Pro Glu Ala Pro Val
 35 40 45

Thr Ile Glu Asp Gln Pro Glu Arg Ile Val Ser Leu Ser Pro Ala Ile
 50 55 60

Thr Glu Thr Leu Phe Ala Val Gly Ala Gly Asp His Val Val Ala Val
 65 70 75 80

Asp Glu Tyr Ser Asn Tyr Pro Glu Asp Ala Pro Leu Val Gln Gly Leu
 85 90 95

Ser Gly Phe Thr Pro Asn Val Glu Ser Ile Leu Asp Tyr Asp Pro Asp

100					105					110						
Leu	Val	Val	Leu	Met	Ser	Ala	Asp	Asp	Ser	Ile	Leu	Thr	Gly	Leu	Asp	
115					120					125						
Ala	Ala	Gly	Val	Asp	Thr	Leu	Val	Ile	Pro	Ala	Ala	Glu	Asn	Leu	Asp	
130					135					140						
Glu	Thr	Tyr	Ser	Gln	Ile	Glu	Gln	Val	Gly	Arg	Ala	Thr	Gly	Phe	Glu	
145					150					155					160	
Asp	Gln	Ala	Thr	Thr	Val	Val	Asp	Gln	Met	Lys	Thr	Ala	Ile	Asp	Ala	
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Ala	Val	Ala	Thr	Val	Pro	Glu	Glu	Val	Lys	Glu	Gln	Gly	Leu	Thr	Tyr	
180					185					190						
Phe	His	Glu	Leu	Gly	Ser	Asp	Leu	Phe	Thr	Val	Ser	Glu	Gln	Thr	Tyr	
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Ile	Gly	Gln	Ile	Tyr	Asp	Met	Phe	Gly	Leu	Thr	Ser	Ile	Ala	Asp	Gly	
210					215					220						
Gly	Asp	Ala	Tyr	Ser	Gln	Leu	Ser	Asn	Glu	Ala	Ile	Ile	Ala	Ala	Asn	
225					230					235					240	
Pro	Asp	Leu	Ile	Phe	Leu	Ser	Asp	Ala	Lys	Ala	Glu	Asn	Leu	Thr	Ala	
245					250					255						
Glu	Asp	Ile	Ala	Ala	Arg	Pro	Gly	Trp	Asp	Thr	Ile	Asp	Ala	Val	Ala	
260					265					270						
Asn	Gly	Arg	Ile	Tyr	Ile	Leu	Asp	Asp	Asp	Ile	Ala	Ser	Arg	Trp	Gly	
275					280					285						
Pro	Arg	Val	Ser	Gln	Leu	Val	Glu	Glu	Ile	Ala	Ala	Gln	Leu	Asn	Gln	
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<211> 1059

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1036)

<223> RXA01354

<400> 347

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				Met	Lys	Ile	Ser	Arg	
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cgc	gca	ttc	ctc	ggc	aca	ctg	ctc	ggc	gcc	acc	acc	ctt	gct	gta	act	163
Arg	Ala	Phe	Leu	Gly	Thr	Leu	Leu	Gly	Ala	Thr	Thr	Leu	Ala	Val	Thr	

				10				15				20				
gcc	tgc	gcg	caa	tcc	tct	caa	aac	caa	aac	tcc	tcc	gct	tcc	tca	tct	211
Ala	Cys	Ala	Gln	Ser	Ser	Gln	Asn	Gln	Asn	Ser	Ser	Ala	Ser	Ser	Ser	
25				30				35								
tct	tca	tcc	tca	gcg	gaa	tca	agc	acc	tct	tca	tcc	tcc	tcc	gat	gaa	259
Ser	Ser	Ser	Ser	Ala	Glu	Ser	Ser	Thr	Ser	Ser	Ser	Ser	Ser	Asp	Glu	
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cag	cgc	atc	gtc	gcc	ctc	aac	acc	ggc	cag	ttg	gac	aac	ctc	ctc	ctt	307
Gln	Arg	Ile	Val	Ala	Leu	Asn	Thr	Gly	Gln	Leu	Asp	Asn	Leu	Leu	Leu	
55				60				65								
ctc	ggc	atc	acc	cca	gtg	ggc	gtc	gcc	gct	gca	aaa	aac	tct	gac	ctg	355
Leu	Gly	Ile	Thr	Pro	Val	Gly	Val	Ala	Ala	Ala	Lys	Asn	Ser	Asp	Leu	
70				75				80				85				
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Ile	Pro	Gln	Phe	Leu	Lys	Asp	Arg	Phe	Gly	Ala	Asp	Met	Asp	Leu	Asp	
90				95				100								
agc	atc	gcc	gac	tgc	ggc	ctc	cgc	caa	tct	cca	gac	atc	gaa	gcc	atc	451
Ser	Ile	Ala	Asp	Cys	Gly	Leu	Arg	Gln	Ser	Pro	Asp	Ile	Glu	Ala	Ile	
105				110				115								
gcg	aac	ctc	aac	ccc	acc	ctg	atc	tgc	gca	aac	tcc	cgc	gcc	gac	gaa	499
Ala	Asn	Leu	Asn	Pro	Thr	Leu	Ile	Cys	Ala	Asn	Ser	Arg	Ala	Asp	Glu	
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gag	gtc	ctc	aac	aaa	ctc	cgc	acg	atc	gcc	ccc	gtg	gtc	acc	ggc	gaa	547
Glu	Val	Leu	Asn	Lys	Leu	Arg	Thr	Ile	Ala	Pro	Val	Val	Thr	Gly	Glu	
135				140				145								
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Gly	Gly	Gly	Glu	Asn	Trp	Lys	Gln	Asp	Leu	Leu	Thr	Ile	Ala	Glu	Ala	
150				155				160				165				
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Ala	Gly	Gln	Lys	Glu	Lys	Ala	Glu	Thr	Leu	Leu	Lys	Ser	Tyr	Glu	Asp	
170				175				180								
tca	gca	gcc	gaa	atc	gcc	gca	aac	cag	cct	gcg	aac	cca	cca	acc	gtt	691
Ser	Ala	Ala	Glu	Ile	Ala	Ala	Asn	Gln	Pro	Ala	Asn	Pro	Pro	Thr	Val	
185				190				195								
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Ser	Phe	Leu	Arg	Thr	Lys	Asp	Gln	Glu	Phe	Gln	Met	Tyr	Gly	Ala	Gln	
200				205				210								
tcc	atg	gcc	gga	acg	gtt	gct	gcc	gat	tgc	ggc	tac	gcc	cgc	cca	gaa	787
Ser	Met	Ala	Gly	Thr	Val	Ala	Ala	Asp	Cys	Gly	Tyr	Ala	Arg	Pro	Glu	
215				220				225								
aac	cag	cag	ttc	acc	gac	acg	gca	ggc	caa	gac	ctc	tcc	gct	gag	ctc	835
Asn	Gln	Gln	Phe	Thr	Asp	Thr	Ala	Gly	Gln	Asp	Leu	Ser	Ala	Glu	Leu	
230				235				240				245				
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aac atc aac cct gaa gac acc cca ttg tgg act tca ctc aaa gcg gtt 931
 Asn Ile Asn Pro Glu Asp Thr Pro Leu Trp Thr Ser Leu Lys Ala Val
 265 270 275

 cag tcc aac caa gca atc cca gtt gac ggc gat tcc tgg tac ctc aac 979
 Gln Ser Asn Gln Ala Ile Pro Val Asp Gly Asp Ser Trp Tyr Leu Asn
 280 285 290

 gca tcc ctc gtg tgg gct gaa atc atc ctc caa ggc ctc aaa gac aac 1027
 Ala Ser Leu Val Ser Ala Glu Ile Ile Leu Gln Gly Leu Lys Asp Asn
 295 300 305

 gtc acc gtc taagccgat't taagggcctc aaa 1059
 Val Thr Val
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<210> 348
 <211> 312
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 348
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 Ser Ala Ser Ser Ser Ser Ser Ser Ala Glu Ser Ser Thr Ser Ser
 35 40 45

 Ser Ser Ser Asp Glu Gln Arg Ile Val Ala Leu Asn Thr Gly Gln Leu
 50 55 60

 Asp Asn Leu Leu Leu Leu Gly Ile Thr Pro Val Gly Val Ala Ala Ala
 65 70 75 80

 Lys Asn Ser Asp Leu Ile Pro Gln Phe Leu Lys Asp Arg Phe Gly Ala
 85 90 95

 Asp Met Asp Leu Asp Ser Ile Ala Asp Cys Gly Leu Arg Gln Ser Pro
 100 105 110

 Asp Ile Glu Ala Ile Ala Asn Leu Asn Pro Thr Leu Ile Cys Ala Asn
 115 120 125

 Ser Arg Ala Asp Glu Glu Val Leu Asn Lys Leu Arg Thr Ile Ala Pro
 130 135 140

 Val Val Thr Gly Glu Gly Gly Gly Glu Asn Trp Lys Gln Asp Leu Leu
 145 150 155 160

 Thr Ile Ala Glu Ala Ala Gly Gln Lys Glu Lys Ala Glu Thr Leu Leu
 165 170 175

 Lys Ser Tyr Glu Asp Ser Ala Ala Glu Ile Ala Ala Asn Gln Pro Ala
 180 185 190

 Asn Pro Pro Thr Val Ser Phe Leu Arg Thr Lys Asp Gln Glu Phe Gln

195					200					205					
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Tyr	Ala	Arg	Pro	Glu	Asn	Gln	Gln	Phe	Thr	Asp	Thr	Ala	Gly	Gln	Asp
225					230					235				240	
Leu	Ser	Ala	Glu	Leu	Ile	Ala	Gln	Ala	Asp	Ala	Asp	Trp	Leu	Phe	Tyr
				245					250					255	
Gly	Ile	Lys	Glu	Gly	Asn	Ile	Asn	Pro	Glu	Asp	Thr	Pro	Leu	Trp	Thr
			260				265						270		
Ser	Leu	Lys	Ala	Val	Gln	Ser	Asn	Gln	Ala	Ile	Pro	Val	Asp	Gly	Asp
		275					280					285			
Ser	Trp	Tyr	Leu	Asn	Ala	Ser	Leu	Val	Ser	Ala	Glu	Ile	Ile	Leu	Gln
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<211> 1071

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1048)

<223> RXA01620

<400> 349

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agactggcaa taggttaaga acttgcgtta ggatagccta atg caa tct att cga 115
                                     Met Gln Ser Ile Arg
                                     1 5
acg acc ttc agg tcg ctt tca cgc agc gca gtt atc gtg ggt acc gtt 163
Thr Thr Phe Arg Ser Leu Ser Arg Ser Ala Val Ile Val Gly Thr Val
                                     10 15 20
ttg gct ttg ggt atc gca gga tgt tcc acg gcc agt gat gaa gcc aca 211
Leu Ala Leu Gly Ile Ala Gly Cys Ser Thr Ala Ser Asp Glu Ala Thr
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agc acc agc gac gat gta gct gtc ggc ggc cgc cta ttt tct aca gcg 259
Ser Thr Ser Asp Asp Val Ala Val Gly Gly Arg Leu Phe Ser Thr Ala
                                     40 45 50
gat tcc gcc acc gcc gct ctg gga agc gac gcc gaa cca ggc caa ttc 307
Asp Ser Ala Thr Ala Ala Leu Gly Ser Asp Ala Glu Pro Gly Gln Phe
                                     55 60 65
ccc cgc acc gtt gtg cat tca cgc ggc gaa act acc ctt gag cag cag 355
Pro Arg Thr Val Val His Ser Arg Gly Glu Thr Thr Leu Glu Gln Gln
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cca caa cga gtc gtc gtt ctc gac agc ggt gaa atc gac cag gtt ttg	403
Pro Gln Arg Val Val Val Leu Asp Ser Gly Glu Ile Asp Gln Val Leu	
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agc ctc ggc gtc act ccc gtc ggc atc gcc agc ccg aaa gac gcc tcc	451
Ser Leu Gly Val Thr Pro Val Gly Ile Ala Ser Pro Lys Asp Ala Ser	
105 110 115	
agc cag ccc gct tac ctc gaa aat cag ctg gca gat gta caa act gtg	499
Ser Gln Pro Ala Tyr Leu Glu Asn Gln Leu Ala Asp Val Gln Thr Val	
120 125 130	
ggc acc acg agt gag ctc aat ttc gaa gcc atc gcc gcc ctc aag cct	547
Gly Thr Thr Ser Glu Leu Asn Phe Glu Ala Ile Ala Ala Leu Lys Pro	
135 140 145	
gac ctg att ctg ggc agc aag ctg cgc gtc gac gaa tcc tac gat cag	595
Asp Leu Ile Leu Gly Ser Lys Leu Arg Val Asp Glu Ser Tyr Asp Gln	
150 155 160 165	
ctc tcc caa atc gca cca acc gtg ctg agt att cgc ccc gga ttc ccc	643
Leu Ser Gln Ile Ala Pro Thr Val Leu Ser Ile Arg Pro Gly Phe Pro	
170 175 180	
tgg aag gaa aac ttc ctc ctc acc gcc gac gcg ctc ggt ctc gag ggc	691
Trp Lys Glu Asn Phe Leu Leu Thr Ala Asp Ala Leu Gly Leu Glu Gly	
185 190 195	
aaa gcc gtc gag gtt ctc aac gag tac caa acc cat gtc gat gca gtc	739
Lys Ala Val Glu Val Leu Asn Glu Tyr Gln Thr His Val Asp Ala Val	
200 205 210	
cgc gag acc atc gac ggc agc cca gaa atc tca ctc gtc cgc ttc atg	787
Arg Glu Thr Ile Asp Gly Ser Pro Glu Ile Ser Leu Val Arg Phe Met	
215 220 225	
cct ggt cgc acc cgc ctg tac gga aac ctc tct ttc atc ggt gca atc	835
Pro Gly Arg Thr Arg Leu Tyr Gly Asn Leu Ser Phe Ile Gly Ala Ile	
230 235 240 245	
ctt aag gac ctg ggg ctt tct cgc cca gag atc caa aat atc gac gat	883
Leu Lys Asp Leu Gly Leu Ser Arg Pro Glu Ile Gln Asn Ile Asp Asp	
250 255 260	
ctt gcc gtg gag atc tcc ccc gaa aac atc acc gat gcc aac ggc gac	931
Leu Ala Val Glu Ile Ser Pro Glu Asn Ile Thr Asp Ala Asn Gly Asp	
265 270 275	
tgg att ttc tac tcc acc tac ggc aag ccc gag gcc acc gag cag gac	979
Trp Ile Phe Tyr Ser Thr Tyr Gly Lys Pro Glu Ala Thr Glu Gln Asp	
280 285 290	
aac att ttg tcc aac gag ctg tgg cac aac ctt ccc cgc cgt cca aga	1027
Asn Ile Leu Ser Asn Glu Leu Trp His Asn Leu Pro Arg Arg Pro Arg	
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agg tca tgc cct gga ggt caa tgacgagagc tgggttcattgg ggt	1071
Arg Ser Cys Pro Gly Gly Gln	
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<210> 350

<211> 316

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 350

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Ile Val Gly Thr Val Leu Ala Leu Gly Ile Ala Gly Cys Ser Thr Ala
 20 25 30

Ser Asp Glu Ala Thr Ser Thr Ser Asp Asp Val Ala Val Gly Gly Arg
 35 40 45

Leu Phe Ser Thr Ala Asp Ser Ala Thr Ala Ala Leu Gly Ser Asp Ala
 50 55 60

Glu Pro Gly Gln Phe Pro Arg Thr Val Val His Ser Arg Gly Glu Thr
 65 70 75 80

Thr Leu Glu Gln Gln Pro Gln Arg Val Val Val Leu Asp Ser Gly Glu
 85 90 95

Ile Asp Gln Val Leu Ser Leu Gly Val Thr Pro Val Gly Ile Ala Ser
 100 105 110

Pro Lys Asp Ala Ser Ser Gln Pro Ala Tyr Leu Glu Asn Gln Leu Ala
 115 120 125

Asp Val Gln Thr Val Gly Thr Thr Ser Glu Leu Asn Phe Glu Ala Ile
 130 135 140

Ala Ala Leu Lys Pro Asp Leu Ile Leu Gly Ser Lys Leu Arg Val Asp
 145 150 155 160

Glu Ser Tyr Asp Gln Leu Ser Gln Ile Ala Pro Thr Val Leu Ser Ile
 165 170 175

Arg Pro Gly Phe Pro Trp Lys Glu Asn Phe Leu Leu Thr Ala Asp Ala
 180 185 190

Leu Gly Leu Glu Gly Lys Ala Val Glu Val Leu Asn Glu Tyr Gln Thr
 195 200 205

His Val Asp Ala Val Arg Glu Thr Ile Asp Gly Ser Pro Glu Ile Ser
 210 215 220

Leu Val Arg Phe Met Pro Gly Arg Thr Arg Leu Tyr Gly Asn Leu Ser
 225 230 235 240

Phe Ile Gly Ala Ile Leu Lys Asp Leu Gly Leu Ser Arg Pro Glu Ile
 245 250 255

Gln Asn Ile Asp Asp Leu Ala Val Glu Ile Ser Pro Glu Asn Ile Thr
 260 265 270

Asp Ala Asn Gly Asp Trp Ile Phe Tyr Ser Thr Tyr Gly Lys Pro Glu
 275 280 285

Ala Thr Glu Gln Asp Asn Ile Leu Ser Asn Glu Leu Trp His Asn Leu

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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(892)
<223> RXA02052

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Met Gly Thr Thr Glu
1 5

atc cct gaa acc cca acg cgt gtg gtc gtc att gat tcc cca cac ctc 163
Ile Pro Glu Thr Pro Thr Arg Val Val Val Ile Asp Ser Pro His Leu
10 15 20

gac gca ctt ttg gct ttg gga att act cca gtc gga gct acg gaa tct 211
Asp Ala Leu Leu Ala Leu Gly Ile Thr Pro Val Gly Ala Thr Glu Ser
25 30 35

gga tcc gaa aat ggt ttc ccc gcc tac ttg gct gac gag cta aaa gac 259
Gly Ser Glu Asn Gly Phe Pro Ala Tyr Leu Ala Asp Glu Leu Lys Asp
40 45 50

acc gaa tct gtt ggg ctg aca tct gag cca aat ttg gaa aag atc gcc 307
Thr Glu Ser Val Gly Leu Thr Ser Glu Pro Asn Leu Glu Lys Ile Ala
55 60 65

gca ctg gat ccg gat ttg atc att ggc gca aag gtc cgc cac gag gct 355
Ala Leu Asp Pro Asp Leu Ile Ile Gly Ala Lys Val Arg His Glu Ala
70 75 80 85

att tat gat cag ctt tca gac atc gca cca acc gtg atg tcc gaa ggt 403
Ile Tyr Asp Gln Leu Ser Asp Ile Ala Pro Thr Val Met Ser Glu Gly
90 95 100

tcc ggc aca aac tgg aat gaa cag gca gaa atc act gcg gca gca gta 451
Ser Gly Thr Asn Trp Asn Glu Gln Ala Glu Ile Thr Ala Ala Ala Val
105 110 115

aac aag tct gat gag atg gac aaa ctg atc tca gac ttg gac acc cgt 499
Asn Lys Ser Asp Glu Met Asp Lys Leu Ile Ser Asp Leu Asp Thr Arg
120 125 130

gcc aca gag ctt ggt gaa gag atc ggt gct gac gga caa acc gct tca 547
Ala Thr Glu Leu Gly Glu Glu Ile Gly Ala Asp Gly Gln Thr Ala Ser
135 140 145

atg gtt cga ttc cgc acg gac aac ttc agg ctc tat ggt ccc gag acc 595
Met Val Arg Phe Arg Thr Asp Asn Phe Arg Leu Tyr Gly Pro Glu Thr

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ttc tct ggt tca gtt ctg gaa caa gtt gga ttt gac ctg ggg gaa cgt				643
Phe Ser Gly Ser Val Leu Glu Gln Val Gly Phe Asp Leu Gly Glu Arg	170	175	180	
gat tgg aat gag tac tcc atg atg gag cta tcc tca gaa aac ttt ggg				691
Asp Trp Asn Glu Tyr Ser Met Met Glu Leu Ser Ser Glu Asn Phe Gly	185	190	195	
cag atc gat gga gac ctt att ttc tac acc atc cca gga tcc cct gaa				739
Gln Ile Asp Gly Asp Leu Ile Phe Tyr Thr Ile Pro Gly Ser Pro Glu	200	205	210	
gca acc act tat cca aag att tcc gaa ctg tgg gtt gat tca cca gca				787
Ala Thr Thr Tyr Pro Lys Ile Ser Glu Leu Trp Val Asp Ser Pro Ala	215	220	225	
gtt cgg caa ggt aga act tac gag ttt gaa gac gaa acc tgg atg gtc				835
Val Arg Gln Gly Arg Thr Tyr Glu Phe Glu Asp Glu Thr Trp Met Val	230	235	240	245
ggc atc ggt gta tta ggt gcc aat gaa atc ttg gat gac ctg gaa gaa				883
Gly Ile Gly Val Leu Gly Ala Asn Glu Ile Leu Asp Asp Leu Glu Glu	250	255	260	
act ctg agc tagtttcctt taggcccaagc aac				915
Thr Leu Ser				

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<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 352

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Gly Ala Thr Glu Ser Gly Ser Glu Asn Gly Phe Pro Ala Tyr Leu Ala	35	40	45	
Asp Glu Leu Lys Asp Thr Glu Ser Val Gly Leu Thr Ser Glu Pro Asn	50	55	60	
Leu Glu Lys Ile Ala Ala Leu Asp Pro Asp Leu Ile Ile Gly Ala Lys	65	70	75	80
Val Arg His Glu Ala Ile Tyr Asp Gln Leu Ser Asp Ile Ala Pro Thr	85	90	95	
Val Met Ser Glu Gly Ser Gly Thr Asn Trp Asn Glu Gln Ala Glu Ile	100	105	110	
Thr Ala Ala Ala Val Asn Lys Ser Asp Glu Met Asp Lys Leu Ile Ser	115	120	125	

Asp Leu Asp Thr Arg Ala Thr Glu Leu Gly Glu Glu Ile Gly Ala Asp
 130 135 140
 Gly Gln Thr Ala Ser Met Val Arg Phe Arg Thr Asp Asn Phe Arg Leu
 145 150 155 160
 Tyr Gly Pro Glu Thr Phe Ser Gly Ser Val Leu Glu Gln Val Gly Phe
 165 170 175
 Asp Leu Gly Glu Arg Asp Trp Asn Glu Tyr Ser Met Met Glu Leu Ser
 180 185 190
 Ser Glu Asn Phe Gly Gln Ile Asp Gly Asp Leu Ile Phe Tyr Thr Ile
 195 200 205
 Pro Gly Ser Pro Glu Ala Thr Thr Tyr Pro Lys Ile Ser Glu Leu Trp
 210 215 220
 Val Asp Ser Pro Ala Val Arg Gln Gly Arg Thr Tyr Glu Phe Glu Asp
 225 230 235 240
 Glu Thr Trp Met Val Gly Ile Gly Val Leu Gly Ala Asn Glu Ile Leu
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 Asp Asp Leu Glu Glu Thr Leu Ser
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<210> 353

<211> 1200

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1177)

<223> RXA00372

<400> 353

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 Met Ser Ser Lys His
 1 5
 cct ttg aag cgc act gcc gtt act gtt ttt gca ctc ggc gct tcc gct 163
 Pro Leu Lys Arg Thr Ala Val Thr Val Phe Ala Leu Gly Ala Ser Ala
 10 15 20
 gct ctc ctc gtg gct tgc tct gaa cct tct gag gac gtt tcc acc gca 211
 Ala Leu Leu Val Ala Cys Ser Glu Pro Ser Glu Asp Val Ser Thr Ala
 25 30 35
 gag acc acc act gca agc tct tcc gct aac gca tcc gat gca gcc ggt 259
 Glu Thr Thr Thr Ala Ser Ser Ser Ala Asn Ala Ser Asp Ala Ala Gly
 40 45 50
 gaa aaa gta acc atc acc gtc tac acc tct gag cct gag gaa aag gtc 307
 Glu Lys Val Thr Ile Thr Val Tyr Thr Ser Glu Pro Glu Glu Lys Val
 55 60 65

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Asp Glu Ile Asn Lys Ala Phe Met Glu Ala Asn Pro Asp Ile Glu Val	
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gag gtg tac cgc gct ggt act ggc gat ctg act gct cgc att gaa gct	403
Glu Val Tyr Arg Ala Gly Thr Gly Asp Leu Thr Ala Arg Ile Glu Ala	
90 95 100	
gaa aag gca tcc ggt tct atc gag gct gat gtg ttg tgg gct gcg gat	451
Glu Lys Ala Ser Gly Ser Ile Glu Ala Asp Val Leu Trp Ala Ala Asp	
105 110 115	
gct gca acc ttt gaa act tat gca gca cag ggc gac ctt gca gag ctg	499
Ala Ala Thr Phe Glu Thr Tyr Ala Ala Gln Gly Asp Leu Ala Glu Leu	
120 125 130	
gaa gat gtt gag act tcc gac atc att gaa gag gct ctg gat gct gag	547
Glu Asp Val Glu Thr Ser Asp Ile Ile Glu Glu Ala Leu Asp Ala Glu	
135 140 145	
aac ttt tat gta ggc acc cgc atc atc cca acc gtg att gca tac aac	595
Asn Phe Tyr Val Gly Thr Arg Ile Ile Pro Thr Val Ile Ala Tyr Asn	
150 155 160 165	
act gaa gtt gtt gat cag gct gag ctt cct acg tct tgg gct gat ctg	643
Thr Glu Val Val Asp Gln Ala Glu Leu Pro Thr Ser Trp Ala Asp Leu	
170 175 180	
act gat cct aag tat gca ggc caa ctg gtc atg ccg gat cca gct gtg	691
Thr Asp Pro Lys Tyr Ala Gly Gln Leu Val Met Pro Asp Pro Ala Val	
185 190 195	
tct ggt gct gca gcc ttc aat gct tct gtg tgg aag aac gac cct gcg	739
Ser Gly Ala Ala Ala Phe Asn Ala Ser Val Trp Lys Asn Asp Pro Ala	
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ctt ggc gaa gcc tgg atc acc gcc ttg ggt gaa aac caa cca atg atc	787
Leu Gly Glu Ala Trp Ile Thr Ala Leu Gly Glu Asn Gln Pro Met Ile	
215 220 225	
gct cag tcc aac ggc cca acc tcc cag gag atc gct ggc ggt ggc cac	835
Ala Gln Ser Asn Gly Pro Thr Ser Gln Glu Ile Ala Gly Gly Gly His	
230 235 240 245	
cca gtg ggc atc gtg gtg gac tac ttg gtg cgc gac ttg gct gct gct	883
Pro Val Gly Ile Val Val Asp Tyr Leu Val Arg Asp Leu Ala Ala Ala	
250 255 260	
gga tct cca atc gac acc atc tac gca tcg gag ggt tct cct tac atc	931
Gly Ser Pro Ile Asp Thr Ile Tyr Ala Ser Glu Gly Ser Pro Tyr Ile	
265 270 275	
act gag cct gca ggt gtg ttc gct gat tct gaa aag aag gaa gca gcc	979
Thr Glu Pro Ala Gly Val Phe Ala Asp Ser Glu Lys Lys Glu Ala Ala	
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Glu Arg Tyr Ile Asn Phe Leu Leu Ser Val Glu Gly Gln Glu Ile Ala	
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Val Glu Gln Ala Tyr Leu Pro Val Arg Glu Asp Val Gly Thr Pro Glu
 310 315 320 325
 ggc acc ccc gag ttg gct gac atc gag ctc atg acc cct gac ctg gag 1123
 Gly Thr Pro Glu Leu Ala Asp Ile Glu Leu Met Thr Pro Asp Leu Glu
 330 335 340
 gtt gta acc gct gat aag gcg gct gct gtt gag ttc ttc caa aac gca 1171
 Val Val Thr Ala Asp Lys Ala Ala Val Glu Phe Phe Gln Asn Ala
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 Met Asn

<210> 354

<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 354

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 35 40 45
 Ser Asp Ala Ala Gly Glu Lys Val Thr Ile Thr Val Tyr Thr Ser Glu
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 Pro Glu Glu Lys Val Asp Glu Ile Asn Lys Ala Phe Met Glu Ala Asn
 65 70 75 80
 Pro Asp Ile Glu Val Glu Val Tyr Arg Ala Gly Thr Gly Asp Leu Thr
 85 90 95
 Ala Arg Ile Glu Ala Glu Lys Ala Ser Gly Ser Ile Glu Ala Asp Val
 100 105 110
 Leu Trp Ala Ala Asp Ala Ala Thr Phe Glu Thr Tyr Ala Ala Gln Gly
 115 120 125
 Asp Leu Ala Glu Leu Glu Asp Val Glu Thr Ser Asp Ile Ile Glu Glu
 130 135 140
 Ala Leu Asp Ala Glu Asn Phe Tyr Val Gly Thr Arg Ile Ile Pro Thr
 145 150 155 160
 Val Ile Ala Tyr Asn Thr Glu Val Val Asp Gln Ala Glu Leu Pro Thr
 165 170 175
 Ser Trp Ala Asp Leu Thr Asp Pro Lys Tyr Ala Gly Gln Leu Val Met
 180 185 190
 Pro Asp Pro Ala Val Ser Gly Ala Ala Ala Phe Asn Ala Ser Val Trp
 195 200 205

Lys Asn Asp Pro Ala Leu Gly Glu Ala Trp Ile Thr Ala Leu Gly Glu
 210 215 220
 Asn Gln Pro Met Ile Ala Gln Ser Asn Gly Pro Thr Ser Gln Glu Ile
 225 230 235 240
 Ala Gly Gly Gly His Pro Val Gly Ile Val Val Asp Tyr Leu Val Arg
 245 250 255
 Asp Leu Ala Ala Ala Gly Ser Pro Ile Asp Thr Ile Tyr Ala Ser Glu
 260 265 270
 Gly Ser Pro Tyr Ile Thr Glu Pro Ala Gly Val Phe Ala Asp Ser Glu
 275 280 285
 Lys Lys Glu Ala Ala Glu Arg Tyr Ile Asn Phe Leu Leu Ser Val Glu
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 Gly Gln Glu Ile Ala Val Glu Gln Ala Tyr Leu Pro Val Arg Glu Asp
 305 310 315 320
 Val Gly Thr Pro Glu Gly Thr Pro Glu Leu Ala Asp Ile Glu Leu Met
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 <223> RXA00088

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 Met Val Lys Asn Arg
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 Phe Lys Leu Val Ser Ile Ala Thr Val Ala Ala Leu Ala Leu Val Gly
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 Cys Ser Ser Thr Asp Ser Thr Ser Ser Glu Ser Ser Ser Ala Ala Glu
 25 30 35
 tca acc gct gca gct agc acc ctg act atc gaa gac aac cac ggc acc 259
 Ser Thr Ala Ala Ala Ser Thr Leu Thr Ile Glu Asp Asn His Gly Thr
 40 45 50
 gaa ggg atc tcc ctg cca atc gag ggc gtc gct gcg acc gac aac cgc 307

Glu	Gly	Ile	Ser	Leu	Pro	Ile	Glu	Gly	Val	Ala	Ala	Thr	Asp	Asn	Arg		
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Ala	Phe	Glu	Leu	Leu	Asp	Arg	Trp	Gly	Val	Glu	Leu	Val	Ala	Ala	Pro	85	
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Leu	Gln	Leu	Val	Pro	Phe	Thr	Val	Thr	Gly	Tyr	Thr	Glu	Glu	Gly	Gly	100	
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gtc	gct	aac	ctt	ggc	tcc	cac	cgc	gag	cca	gac	ctg	gaa	gca	ctt	gct	451	
Val	Ala	Asn	Leu	Gly	Ser	His	Arg	Glu	Pro	Asp	Leu	Glu	Ala	Leu	Ala	115	
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Ala	Ala	Gln	Pro	Ser	Leu	Ile	Ile	Asn	Gly	Gln	Arg	Phe	Ala	Gln	Tyr	130	
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Tyr	Asp	Asp	Ile	Ile	Ala	Leu	Asn	Pro	Asp	Ala	Thr	Val	Val	Glu	Leu	145	
	135					140											
gac	cca	cgc	gat	ggc	gag	cca	ctt	gac	cag	gag	ctt	atc	cgc	cag	gct	595	
Asp	Pro	Arg	Asp	Gly	Glu	Pro	Leu	Asp	Gln	Glu	Leu	Ile	Arg	Gln	Ala	165	
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gaa	acc	ctc	ggg	gag	atc	ttc	ggc	gaa	gaa	gaa	gat	gct	gca	aag	atc	643	
Glu	Thr	Leu	Gly	Glu	Ile	Phe	Gly	Glu	Glu	Glu	Asp	Ala	Ala	Lys	Ile	180	
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Val	Ala	Asp	Phe	Glu	Ser	Ala	Leu	Glu	Arg	Ala	Lys	Thr	Ala	Tyr	Ala	195	
			185					190									
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Ala	Ile	Ser	Asp	Gln	Thr	Val	Met	Ala	Val	Asn	Val	Ser	Gly	Gly	Asn	210	
		200					205										
att	ggc	tac	atc	gct	cct	tcc	gtt	gga	cgc	acc	tac	ggg	cca	atc	ttc	787	
Ile	Gly	Tyr	Ile	Ala	Pro	Ser	Val	Gly	Arg	Thr	Tyr	Gly	Pro	Ile	Phe	225	
	215						220										
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Asp	Leu	Val	Gly	Leu	Thr	Pro	Ala	Leu	Glu	Val	Gly	Asn	Ala	Ser	Ser	245	
230					235					240							
gac	cac	gag	ggc	gac	gac	att	aac	gtc	gaa	gca	atc	gca	gct	gca	aac	883	
Asp	His	Glu	Gly	Asp	Asp	Ile	Asn	Val	Glu	Ala	Ile	Ala	Ala	Ala	Asn	260	
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cca	gac	ctg	atc	ctg	gtc	atg	gac	cgc	gat	ggg	ggc	acc	agc	acc	cgc	931	
Pro	Asp	Leu	Ile	Leu	Val	Met	Asp	Arg	Asp	Gly	Gly	Thr	Ser	Thr	Arg	275	
			265					270									
aac	gaa	gct	gat	tac	gtt	cca	gca	gag	cag	atc	gtc	tcc	gac	aat	gaa	979	
Asn	Glu	Ala	Asp	Tyr	Val	Pro	Ala	Glu	Gln	Ile	Val	Ser	Asp	Asn	Glu	290	
		280					285										
gca	ctg	gca	aac	gtc	aag	gct	gtc	acc	gac	gga	tac	gtt	tac	tac	gca	1027	
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cct gca gat acc tac acc aac gaa aac atc atc acc tac acc gag atc 1075
Pro Ala Asp Thr Tyr Thr Asn Glu Asn Ile Ile Thr Tyr Thr Glu Ile
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ctc aac ggc atg gca gat atg ttc gag aag gca gct cag taggggatcg 1124
Leu Asn Gly Met Ala Asp Met Phe Glu Lys Ala Ala Gln
330          335

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<213> Corynebacterium glutamicum

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35          40          45

Asp Asn His Gly Thr Glu Gly Ile Ser Leu Pro Ile Glu Gly Val Ala
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Ala Thr Asp Asn Arg Ala Phe Glu Leu Leu Asp Arg Trp Gly Val Glu
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Leu Val Ala Ala Pro Leu Gln Leu Val Pro Phe Thr Val Thr Gly Tyr
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Thr Glu Glu Gly Gly Val Ala Asn Leu Gly Ser His Arg Glu Pro Asp
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Leu Glu Ala Leu Ala Ala Ala Gln Pro Ser Leu Ile Ile Asn Gly Gln
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Arg Phe Ala Gln Tyr Tyr Asp Asp Ile Ile Ala Leu Asn Pro Asp Ala
130         135         140

Thr Val Val Glu Leu Asp Pro Arg Asp Gly Glu Pro Leu Asp Gln Glu
145         150         155         160

Leu Ile Arg Gln Ala Glu Thr Leu Gly Glu Ile Phe Gly Glu Glu Glu
165         170         175

Asp Ala Ala Lys Ile Val Ala Asp Phe Glu Ser Ala Leu Glu Arg Ala
180         185         190

Lys Thr Ala Tyr Ala Ala Ile Ser Asp Gln Thr Val Met Ala Val Asn
195         200         205

Val Ser Gly Gly Asn Ile Gly Tyr Ile Ala Pro Ser Val Gly Arg Thr
210         215         220

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Tyr Gly Pro Ile Phe Asp Leu Val Gly Leu Thr Pro Ala Leu Glu Val
 225 230 235 240
 Gly Asn Ala Ser Ser Asp His Glu Gly Asp Asp Ile Asn Val Glu Ala
 245 250 255
 Ile Ala Ala Ala Asn Pro Asp Leu Ile Leu Val Met Asp Arg Asp Gly
 260 265 270
 Gly Thr Ser Thr Arg Asn Glu Ala Asp Tyr Val Pro Ala Glu Gln Ile
 275 280 285
 Val Ser Asp Asn Glu Ala Leu Ala Asn Val Lys Ala Val Thr Asp Gly
 290 295 300
 Tyr Val Tyr Tyr Ala Pro Ala Asp Thr Tyr Thr Asn Glu Asn Ile Ile
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 Thr Tyr Thr Glu Ile Leu Asn Gly Met Ala Asp Met Phe Glu Lys Ala
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Ala Gln

<210> 357

<211> 1233

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1210)

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 Met Asn Glu Arg Thr
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 tcg gat gca ttt gac gcc ctc ctt gtg ctc tcc ttc ggt ggt ccc gaa 163
 Ser Asp Ala Phe Asp Ala Leu Leu Val Leu Ser Phe Gly Gly Pro Glu
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 ggg cac gag gag gtt cgt ccg ttt ttg gag aat gtc act cac gga agg 211
 Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn Val Thr His Gly Arg
 25 30 35
 ggg att ccg ccg gaa cgt cta gat gaa gtg gcg gtt cat tac cac cac 259
 Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala Val His Tyr His His
 40 45 50
 ttc ggt ggt atc agc ccc atc aat gcg ctg aac agg gaa att atc gcc 307
 Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn Arg Glu Ile Ile Ala
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 aat gtg gaa aaa gaa ttg gcg tct cgc gat cac aag ctg cct gtt tat 355
 Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His Lys Leu Pro Val Tyr
 70 75 80 85

ttt ggt aac cgc aac tgg aag ccg ttt gat aat gag gcc gct gaa caa	403
Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn Glu Ala Ala Glu Gln	
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Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val Leu Ala Thr Ser Ala	
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Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln Glu Asp Ile Gln Gly	
120 125 130	
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Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser Ile Thr Phe Thr Lys	
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ctg cgt cag ttc tac gat cac cct cgt ttt gtc tcc acc atg gct caa	595
Leu Arg Gln Phe Tyr Asp His Pro Arg Phe Val Ser Thr Met Ala Gln	
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Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp Glu Leu Arg Asp Glu	
170 175 180	
gcg cgt ctg gtc ttc acc gcg cac tcc att cca ctg act gcg gac aat	691
Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro Leu Thr Ala Asp Asn	
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gct gcg gga acc cct gag gat ggc tcc ttg tat tcc aca cag gtc aag	739
Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr Ser Thr Gln Val Lys	
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Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly Val Ser Asp Phe Asp	
215 220 225	
gtg gtg tgg cag tcc cgc tcg ggt agc ccg cac act ccg tgg ctg gag	835
Val Val Trp Gln Ser Arg Ser Gly Ser Pro His Thr Pro Trp Leu Glu	
230 235 240 245	
cct gac atc gtg gat cac gca gtg gag ctc aac gag aag ggt caa aaa	883
Pro Asp Ile Val Asp His Ala Val Glu Leu Asn Glu Lys Gly Gln Lys	
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gcg ctc gtt gtc tgc cct gta ggc ttt att tct gat cat atg gaa gtc	931
Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser Asp His Met Glu Val	
265 270 275	
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Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu Ala Glu Lys Arg Asn	
280 285 290	
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Met Val Val Glu Arg Val Ala Thr Val Gly Pro Thr Asp Glu Phe Ala	
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gcc ctt gtg gtt gat ctc atc gag gag gca gag ctc aag cgc gtt atc	1075
Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu Leu Lys Arg Val Ile	
310 315 320 325	

gag cgc ctt gga aag ctg cca gca cgc gga agt tcc gtc aac ggc gca 1123
 Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser Ser Val Asn Gly Ala
 330 335 340

ccg tgt ggc gac ggc tgc tgt ggt acc gcc aag cat aaa acc gcg cgg 1171
 Pro Cys Gly Asp Gly Cys Cys Gly Thr Ala Lys His Lys Thr Ala Arg
 345 350 355

gtg aac ccc aac gct cgc tca gcg gcg cca gct gcc aac taggagtgat 1220
 Val Asn Pro Asn Ala Arg Ser Ala Ala Pro Ala Ala Asn
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<210> 358

<211> 370

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

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Val Thr His Gly Arg Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala
 35 40 45

Val His Tyr His His Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn
 50 55 60

Arg Glu Ile Ile Ala Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His
 65 70 75 80

Lys Leu Pro Val Tyr Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn
 85 90 95

Glu Ala Ala Glu Gln Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val
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Leu Ala Thr Ser Ala Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln
 115 120 125

Glu Asp Ile Gln Gly Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser
 130 135 140

Ile Thr Phe Thr Lys Leu Arg Gln Phe Tyr Asp His Pro Arg Phe Val
 145 150 155 160

Ser Thr Met Ala Gln Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp
 165 170 175

Glu Leu Arg Asp Glu Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro
 180 185 190

Leu Thr Ala Asp Asn Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr
 195 200 205

Ser Thr Gln Val Lys Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly

210	215	220
Val Ser Asp Phe Asp 225	Val Val Trp Gln Ser Arg 230	Ser Gly Ser Pro His 240
Thr Pro Trp Leu Glu 245	Pro Asp Ile Val Asp 250	His Ala Val Glu Leu Asn 255
Glu Lys Gly Gln Lys 260	Ala Leu Val Val Cys 265	Pro Val Gly Phe Ile Ser 270
Asp His Met Glu Val 275	Ile Trp Asp Leu Asp 280	Ser Glu Leu Met Glu Glu 285
Ala Glu Lys Arg Asn 290	Met Val Val Glu Arg 295	Val Ala Thr Val Gly Pro 300
Thr Asp Glu Phe Ala 305	Ala Leu Val Val Asp 310	Leu Ile Glu Glu Ala Glu 315
Leu Lys Arg Val Ile 325	Glu Arg Leu Gly Lys 330	Leu Pro Ala Arg Gly Ser 335
Ser Val Asn Gly Ala 340	Pro Cys Gly Asp 345	Gly Cys Cys Gly Thr Ala Lys 350
His Lys Thr Ala Arg 355	Val Asn Pro Asn Ala 360	Arg Ser Ala Ala Pro Ala 365
Ala Asn 370		

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<211> 810

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(787)

<223> RXS00624

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	Met Ser Gly Arg Leu	
	1 5	

ctt gtt tca gtt tct agt att ttc gac cag acc cga tcg gcg gct gac	163
Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr Arg Ser Ala Ala Asp	
10 15 20	

agg ctc att tca gac ctg cga gcc gac ggc atc gag gtc tca tta ctt	211
Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile Glu Val Ser Leu Leu	
25 30 35	

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Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu Ala Lys Asp Lys Gly	
40 45 50	

acc ctc gcg tgg atg gaa caa caa cgc gaa cgc ggc cac gaa ctc atc 307
 Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg Gly His Glu Leu Ile
 55 60 65

ctc aac ggt ttc gac caa gca gtt cag gga cgt cgc tca gaa ttc gcc 355
 Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg Arg Ser Glu Phe Ala
 70 75 80 85

aac ctt gaa cgg cac gaa gca cgt ctt cgc ctt acc ggt gcc att agg 403
 Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu Thr Gly Ala Ile Arg
 90 95 100

caa atg cag aaa att ggc ttc gaa ttc caa atc ttt gcc cca cct cgt 451
 Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile Phe Ala Pro Pro Arg
 105 110 115

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 Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu Pro Glu Phe Asp Phe
 120 125 130

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 Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn Leu Asp Thr Gly Glu
 135 140 145

ttc ttg gcg tgt aga aac ctc tcc gtg ggt gaa ggt ttt ggt gct gca 595
 Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu Gly Phe Gly Ala Ala
 150 155 160 165

aaa tgg tgg cgc aag aat gtc atc aag gct gtc act cgt gga gcg gaa 643
 Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val Thr Arg Gly Ala Glu
 170 175 180

aaa gga aat aca gtg cgc ttg tcc gca tcg gcg cga aat ctc acc aac 691
 Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala Arg Asn Leu Thr Asn
 185 190 195

cct aaa gtc gca gct gac ttc cgg gaa gct gca tta gct gcc ttg gat 739
 Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala Leu Ala Ala Leu Asp
 200 205 210

ttg ggt gct cag gtg caa acc tat tct cag gcg gcc gca caa ctg gcc 787
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tagttgggga ggttcggggc acc 810

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<211> 229

<212> PRT

<213> Corynebacterium glutamicum

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 20 25 30

Glu Val Ser Leu Leu Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu

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<212> DNA
<213> Corynebacterium glutamicum
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                                         Met Glu His Gly Val
                                         1                               5

acc gtt att aaa ggc act gaa ttt gat gtt ttc cca cta aac ctc ggt 163
Thr Val Ile Lys Gly Thr Glu Phe Asp Val Phe Pro Leu Asn Leu Gly
                        10                        15                        20

gga aat acc ttt ggc tgg acc tcg aat agg gaa cag acc ttc gcg gtt 211

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Gly	Asn	Thr	Phe	Gly	Trp	Thr	Ser	Asn	Arg	Glu	Gln	Thr	Phe	Ala	Val	
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ttg	gat	gca	ttc	gtg	gca	gcg	gga	gga	aac	ttt	gtt	gac	acc	gcc	gat	259
Leu	Asp	Ala	Phe	Val	Ala	Ala	Gly	Gly	Asn	Phe	Val	Asp	Thr	Ala	Asp	
		40					45				50					
tct	tat	tct	gca	tgg	gtt	gaa	ggc	aat	gag	ggc	ggc	gag	tcg	gag	cgg	307
Ser	Tyr	Ser	Ala	Trp	Val	Glu	Gly	Asn	Glu	Gly	Gly	Glu	Ser	Glu	Arg	
	55					60					65					
gag	ctc	ggc	gcg	tgg	att	aag	gaa	cgt	ggc	gca	gac	aag	ctg	atc	att	355
Glu	Leu	Gly	Ala	Trp	Ile	Lys	Glu	Arg	Gly	Ala	Asp	Lys	Leu	Ile	Ile	
70					75					80					85	
gct	acc	aag	tct	ggt	gcg	ttg	gag	cct	gtt	gct	ggt	cgt	tcc	cgt	gag	403
Ala	Thr	Lys	Ser	Gly	Ala	Leu	Glu	Pro	Val	Ala	Gly	Arg	Ser	Arg	Glu	
				90					95					100		
gca	act	ttc	aag	gct	gtc	gag	ggt	tcc	ctg	gag	cgt	ttg	ggc	gtg	gaa	451
Ala	Thr	Phe	Lys	Ala	Val	Glu	Gly	Ser	Leu	Glu	Arg	Leu	Gly	Val	Glu	
			105					110					115			
tcg	atc	gat	att	ttt	tac	tac	cac	tac	gac	gat	gag	gca	gtc	agc	att	499
Ser	Ile	Asp	Ile	Phe	Tyr	Tyr	His	Tyr	Asp	Asp	Glu	Ala	Val	Ser	Ile	
		120					125					130				
gat	gag	cag	gtt	gct	atc	gct	aat	gat	ctg	att	gca	cag	ggc	aag	att	547
Asp	Glu	Gln	Val	Ala	Ile	Ala	Asn	Asp	Leu	Ile	Ala	Gln	Gly	Lys	Ile	
	135					140					145					
aag	cac	ctc	gca	ttg	tct	aac	tac	agc	gcg	gag	cgt	tta	gct	gag	ttc	595
Lys	His	Leu	Ala	Leu	Ser	Asn	Tyr	Ser	Ala	Glu	Arg	Leu	Ala	Glu	Phe	
150					155					160					165	
ttt	gag	aag	tct	gta	ggc	act	cca	gcg	cag	ccg	gtt	gct	ctg	caa	ccg	643
Phe	Glu	Lys	Ser	Val	Gly	Thr	Pro	Ala	Gln	Pro	Val	Ala	Leu	Gln	Pro	
				170					175					180		
cac	tac	aac	ctg	gtg	tcg	agg	aag	gat	tat	gag	gag	aac	gtg	cag	cca	691
His	Tyr	Asn	Leu	Val	Ser	Arg	Lys	Asp	Tyr	Glu	Glu	Asn	Val	Gln	Pro	
			185					190					195			
ctc	gcc	gag	aag	cat	ggc	gtt	gca	gtc	ttc	cct	tat	ttc	gcg	ctt	gcc	739
Leu	Ala	Glu	Lys	His	Gly	Val	Ala	Val	Phe	Pro	Tyr	Phe	Ala	Leu	Ala	
		200					205					210				
gcg	ggt	ctt	ttg	acc	gga	aag	tac	acc	tcc	aag	gag	gat	att	tcg	ggt	787
Ala	Gly	Leu	Leu	Thr	Gly	Lys	Tyr	Thr	Ser	Lys	Glu	Asp	Ile	Ser	Gly	
	215					220					225					
aaa	gcg	cgt	gcg	ggg	cag	ttg	gat	cgt	tac	gcc	agc	gat	gag	gcg	ttt	835
Lys	Ala	Arg	Ala	Gly	Gln	Leu	Asp	Arg	Tyr	Ala	Ser	Asp	Glu	Ala	Phe	
230					235					240					245	
gcc	gtg	gtg	aca	gag	ttg	cgt	gct	gtt	gcc	gat	gag	ttg	ggt	gtt	gcg	883
Ala	Val	Val	Thr	Glu	Leu	Arg	Ala	Val	Ala	Asp	Glu	Leu	Gly	Val	Ala	
				250					255					260		
cca	acg	act	gtg	gcg	ctt	gcg	tgg	ttg	gtt	gcg	cat	ggt	gtg	acc	gca	931
Pro	Thr	Thr	Val	Ala	Leu	Ala	Trp	Leu	Val	Ala	His	Gly	Val	Thr	Ala	

265					270					275						
ccg	att	gcg	tcc	gtg	tcc	aag	gta	gag	cag	ttg	aag	gat	ttg	atg	gct	979
Pro	Ile	Ala	Ser	Val	Ser	Lys	Val	Glu	Gln	Leu	Lys	Asp	Leu	Met	Ala	
		280					285					290				
gtg	aag	gat	gtg	gag	ctg	agc	gct	gag	cag	ctt	gca	cgt	ttg	gat	aag	1027
Val	Lys	Asp	Val	Glu	Leu	Ser	Ala	Glu	Gln	Leu	Ala	Arg	Leu	Asp	Lys	
	295					300					305					
ggt	tcc	gag	cct	ttc	gct	taagctctcc	tcaaaagtaa	gtg								1068
Val	Ser	Glu	Pro	Phe	Ala											
310					315											

<210> 362

<211> 315

<212> PRT

<213> Corynebacterium glutamicum

<400> 362

Met	Glu	His	Gly	Val	Thr	Val	Ile	Lys	Gly	Thr	Glu	Phe	Asp	Val	Phe	
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			20					25					30			
Gln	Thr	Phe	Ala	Val	Leu	Asp	Ala	Phe	Val	Ala	Ala	Gly	Gly	Asn	Phe	
		35					40					45				
Val	Asp	Thr	Ala	Asp	Ser	Tyr	Ser	Ala	Trp	Val	Glu	Gly	Asn	Glu	Gly	
	50					55					60					
Gly	Glu	Ser	Glu	Arg	Glu	Leu	Gly	Ala	Trp	Ile	Lys	Glu	Arg	Gly	Ala	
	65				70					75					80	
Asp	Lys	Leu	Ile	Ile	Ala	Thr	Lys	Ser	Gly	Ala	Leu	Glu	Pro	Val	Ala	
			85						90					95		
Gly	Arg	Ser	Arg	Glu	Ala	Thr	Phe	Lys	Ala	Val	Glu	Gly	Ser	Leu	Glu	
		100						105					110			
Arg	Leu	Gly	Val	Glu	Ser	Ile	Asp	Ile	Phe	Tyr	Tyr	His	Tyr	Asp	Asp	
		115					120					125				
Glu	Ala	Val	Ser	Ile	Asp	Glu	Gln	Val	Ala	Ile	Ala	Asn	Asp	Leu	Ile	
	130					135					140					
Ala	Gln	Gly	Lys	Ile	Lys	His	Leu	Ala	Leu	Ser	Asn	Tyr	Ser	Ala	Glu	
	145				150					155					160	
Arg	Leu	Ala	Glu	Phe	Phe	Glu	Lys	Ser	Val	Gly	Thr	Pro	Ala	Gln	Pro	
			165						170					175		
Val	Ala	Leu	Gln	Pro	His	Tyr	Asn	Leu	Val	Ser	Arg	Lys	Asp	Tyr	Glu	
		180						185					190			
Glu	Asn	Val	Gln	Pro	Leu	Ala	Glu	Lys	His	Gly	Val	Ala	Val	Phe	Pro	
	195						200					205				
Tyr	Phe	Ala	Leu	Ala	Ala	Gly	Leu	Leu	Thr	Gly	Lys	Tyr	Thr	Ser	Lys	

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      210              215              220
Glu Asp Ile Ser Gly Lys Ala Arg Ala Gly Gln Leu Asp Arg Tyr Ala
225              230              235              240

Ser Asp Glu Ala Phe Ala Val Val Thr Glu Leu Arg Ala Val Ala Asp
                245              250              255

Glu Leu Gly Val Ala Pro Thr Thr Val Ala Leu Ala Trp Leu Val Ala
                260              265              270

His Gly Val Thr Ala Pro Ile Ala Ser Val Ser Lys Val Glu Gln Leu
                275              280              285

Lys Asp Leu Met Ala Val Lys Asp Val Glu Leu Ser Ala Glu Gln Leu
                290              295              300

Ala Arg Leu Asp Lys Val Ser Glu Pro Phe Ala
305              310              315

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<210> 363
<211> 1329
<212> DNA
<213> Corynebacterium glutamicum

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<220>
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<222> (101)..(1306)
<223> RXA02526

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tgccggagaga gcactctcaa ctgctcaagc ccgccatggt gtg atc act gaa gac 115
                Val Ile Thr Glu Asp
                1              5

gat gct gca cag atc aac cag gcg gca gtc ctt tcc aac att gac cgc 163
Asp Ala Ala Gln Ile Asn Gln Ala Ala Val Leu Ser Asn Ile Asp Arg
                10              15              20

gag aag ctg tgg gaa gat gcc aaa aat gtc ggc tac ccc atc ctt ggc 211
Glu Lys Leu Trp Glu Asp Ala Lys Asn Val Gly Tyr Pro Ile Leu Gly
                25              30              35

ttg gta aga caa atc gcc agt cac ctt cca gaa ggc ccc aac ggg cga 259
Leu Val Arg Gln Ile Ala Ser His Leu Pro Glu Gly Pro Asn Gly Arg
                40              45              50

gtc cac tac ggc gcc acg acc caa gtc atc atg gac act gga ctg gtg 307
Val His Tyr Gly Ala Thr Thr Gln Val Ile Met Asp Thr Gly Leu Val
                55              60              65

ttg caa atg act gcc tct ttg aac gcc ctt gat aaa cag atc gtg cgt 355
Leu Gln Met Thr Ala Ser Leu Asn Ala Leu Asp Lys Gln Ile Val Arg
                70              75              80              85

ctg ggg aat gca ctg gca gca cgg gct gaa gag cac aaa gac acc gtg 403
Leu Gly Asn Ala Leu Ala Ala Arg Ala Glu Glu His Lys Asp Thr Val
                90              95              100

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atg ccg gga cgc acc cat gct cag cag gca att ccc act aca ttt gga	451
Met Pro Gly Arg Thr His Ala Gln Gln Ala Ile Pro Thr Thr Phe Gly	
105 110 115	
gca acc ctc gct acc ttt ttg gat caa atc cgc agg cag agg gaa cga	499
Ala Thr Leu Ala Thr Phe Leu Asp Gln Ile Arg Arg Gln Arg Glu Arg	
120 125 130	
ctt gag gaa gca ctc gag cgc gtg cga gtc att tcg ctg ttt ggt gct	547
Leu Glu Glu Ala Leu Glu Arg Val Arg Val Ile Ser Leu Phe Gly Ala	
135 140 145	
ggg gga aac aac gca gca caa ggc gaa caa gcg gca acg gtt cgt gca	595
Gly Gly Asn Asn Ala Ala Gln Gly Glu Gln Ala Ala Thr Val Arg Ala	
150 155 160 165	
gag atg gcc cgc ctg ttg gat ctg aag gac ccg gtg gtg tca tgg cat	643
Glu Met Ala Arg Leu Leu Asp Leu Lys Asp Pro Val Val Ser Trp His	
170 175 180	
gtg gaa cgc gat gtg ctt ggg gac ttc gga tgg gtg tgc tca acg ctg	691
Val Glu Arg Asp Val Leu Gly Asp Phe Gly Trp Val Cys Ser Thr Leu	
185 190 195	
tgt gga tcg atg gca aaa ttt ggc cga aac atc gtg gat ctt tcc cga	739
Cys Gly Ser Met Ala Lys Phe Gly Arg Asn Ile Val Asp Leu Ser Arg	
200 205 210	
act gaa atc gga gaa gtt ttt gag cct tac aac tcc cat cgg ggt gca	787
Thr Glu Ile Gly Glu Val Phe Glu Pro Tyr Asn Ser His Arg Gly Ala	
215 220 225	
tct tcc atg atg cct cag aaa gtc aac ccg att tct tcc gag ctc atg	835
Ser Ser Met Met Pro Gln Lys Val Asn Pro Ile Ser Ser Glu Leu Met	
230 235 240 245	
att ggt att tca gtg gtg gcg ggt gcc ttg acc tcg act ttg cca cgg	883
Ile Gly Ile Ser Val Val Ala Gly Ala Leu Thr Ser Thr Leu Pro Arg	
250 255 260	
ctt cag gaa tcg gga cat gaa cga gca gca gga gag tgg cag gga gaa	931
Leu Gln Glu Ser Gly His Glu Arg Ala Ala Gly Glu Trp Gln Gly Glu	
265 270 275	
tgg ctt gtc att cca acg ttg gcc aat cta gct ggc gct gca ctc gat	979
Trp Leu Val Ile Pro Thr Leu Ala Asn Leu Ala Gly Ala Ala Leu Asp	
280 285 290	
gaa gcc att gtg gtg gct gaa gga atg cga gtg gat aca gat cgt atg	1027
Glu Ala Ile Val Val Ala Glu Gly Met Arg Val Asp Thr Asp Arg Met	
295 300 305	
tcc tcg aac ttg gct ttt gct ggt gga ttg atc atg gcg gaa gct cag	1075
Ser Ser Asn Leu Ala Phe Ala Gly Gly Leu Ile Met Ala Glu Ala Gln	
310 315 320 325	
atg att caa cta gct cca gct ctg ggg cgt gag aaa gct cat gac ttg	1123
Met Ile Gln Leu Ala Pro Ala Leu Gly Arg Glu Lys Ala His Asp Leu	
330 335 340	

gtt tat gaa gca tcc aca aag act cgt gaa gag cac acc acg ctg gca 1171
 Val Tyr Glu Ala Ser Thr Lys Thr Arg Glu Glu His Thr Thr Leu Ala
 345 350 355

gaa gaa ctg ccg ata att gca gtt caa cat ggg gtc gaa gac ctg ttg 1219
 Glu Glu Leu Pro Ile Ile Ala Val Gln His Gly Val Glu Asp Leu Leu
 360 365 370

cct aag aat ttt gcg cag cct gca gac tac gtc ggc gaa gca caa tcc 1267
 Pro Lys Asn Phe Ala Gln Pro Ala Asp Tyr Val Gly Glu Ala Gln Ser
 375 380 385

atg gtg aat gca gct gtc gcc gcc tgg aat gcc caa ctt taacaaccga 1316
 Met Val Asn Ala Ala Val Ala Ala Trp Asn Ala Gln Leu
 390 395 400

aaactttaac aac 1329

<210> 364

<211> 402

<212> PRT

<213> Corynebacterium glutamicum

<400> 364

Val Ile Thr Glu Asp Asp Ala Ala Gln Ile Asn Gln Ala Ala Val Leu
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Ser Asn Ile Asp Arg Glu Lys Leu Trp Glu Asp Ala Lys Asn Val Gly
 20 25 30

Tyr Pro Ile Leu Gly Leu Val Arg Gln Ile Ala Ser His Leu Pro Glu
 35 40 45

Gly Pro Asn Gly Arg Val His Tyr Gly Ala Thr Thr Gln Val Ile Met
 50 55 60

Asp Thr Gly Leu Val Leu Gln Met Thr Ala Ser Leu Asn Ala Leu Asp
 65 70 75 80

Lys Gln Ile Val Arg Leu Gly Asn Ala Leu Ala Ala Arg Ala Glu Glu
 85 90 95

His Lys Asp Thr Val Met Pro Gly Arg Thr His Ala Gln Gln Ala Ile
 100 105 110

Pro Thr Thr Phe Gly Ala Thr Leu Ala Thr Phe Leu Asp Gln Ile Arg
 115 120 125

Arg Gln Arg Glu Arg Leu Glu Glu Ala Leu Glu Arg Val Arg Val Ile
 130 135 140

Ser Leu Phe Gly Ala Gly Gly Asn Asn Ala Ala Gln Gly Glu Gln Ala
 145 150 155 160

Ala Thr Val Arg Ala Glu Met Ala Arg Leu Leu Asp Leu Lys Asp Pro
 165 170 175

Val Val Ser Trp His Val Glu Arg Asp Val Leu Gly Asp Phe Gly Trp
 180 185 190

Val Cys Ser Thr Leu Cys Gly Ser Met Ala Lys Phe Gly Arg Asn Ile
 195 200 205
 Val Asp Leu Ser Arg Thr Glu Ile Gly Glu Val Phe Glu Pro Tyr Asn
 210 215 220
 Ser His Arg Gly Ala Ser Ser Met Met Pro Gln Lys Val Asn Pro Ile
 225 230 235 240
 Ser Ser Glu Leu Met Ile Gly Ile Ser Val Val Ala Gly Ala Leu Thr
 245 250 255
 Ser Thr Leu Pro Arg Leu Gln Glu Ser Gly His Glu Arg Ala Ala Gly
 260 265 270
 Glu Trp Gln Gly Glu Trp Leu Val Ile Pro Thr Leu Ala Asn Leu Ala
 275 280 285
 Gly Ala Ala Leu Asp Glu Ala Ile Val Val Ala Glu Gly Met Arg Val
 290 295 300
 Asp Thr Asp Arg Met Ser Ser Asn Leu Ala Phe Ala Gly Gly Leu Ile
 305 310 315 320
 Met Ala Glu Ala Gln Met Ile Gln Leu Ala Pro Ala Leu Gly Arg Glu
 325 330 335
 Lys Ala His Asp Leu Val Tyr Glu Ala Ser Thr Lys Thr Arg Glu Glu
 340 345 350
 His Thr Thr Leu Ala Glu Glu Leu Pro Ile Ile Ala Val Gln His Gly
 355 360 365
 Val Glu Asp Leu Leu Pro Lys Asn Phe Ala Gln Pro Ala Asp Tyr Val
 370 375 380
 Gly Glu Ala Gln Ser Met Val Asn Ala Ala Val Ala Ala Trp Asn Ala
 385 390 395 400
 Gln Leu

<210> 365

<211> 1108

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1099)

<223> RXN02813

<400> 365

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 Val Glu Ala Ala Leu
 1 5

gcg gtt gca gct gcc ccc gag cac gca gca atg gcg aag gcc acc att 163

Ala	Val	Ala	Ala	Ala	Pro	Glu	His	Ala	Ala	Met	Ala	Lys	Ala	Thr	Ile	
				10					15					20		
gat	tct	tat	cag	ttg	gat	gtg	gag	gag	ctt	tcc	cgt	cgc	gca	gcc	gag	211
Asp	Ser	Tyr	Gln	Leu	Asp	Val	Glu	Glu	Leu	Ser	Arg	Arg	Ala	Ala	Glu	
			25				30						35			
ggc	ggt	aat	ccg	ctc	att	ccg	ctg	gtc	act	gac	ctc	aag	gcc	atc	aat	259
Gly	Gly	Asn	Pro	Leu	Ile	Pro	Leu	Val	Thr	Asp	Leu	Lys	Ala	Ile	Asn	
		40					45					50				
ccg	gca	ggc	atc	cac	att	ggc	gca	acg	agc	cag	gac	atc	att	gat	tct	307
Pro	Ala	Gly	Ile	His	Ile	Gly	Ala	Thr	Ser	Gln	Asp	Ile	Ile	Asp	Ser	
	55					60					65					
gcg	tta	atg	ctg	tgc	atg	aag	gaa	ggg	gtg	ggg	gag	gtc	gtc	gac	aag	355
Ala	Leu	Met	Leu	Cys	Met	Lys	Glu	Gly	Val	Gly	Glu	Val	Val	Asp	Lys	
70					75				80						85	
ctt	aaa	aag	ctt	gcg	cga	gat	ttg	gcc	gag	ctc	acc	gcg	gag	cat	aaa	403
Leu	Lys	Lys	Leu	Ala	Arg	Asp	Leu	Ala	Glu	Leu	Thr	Ala	Glu	His	Lys	
			90						95					100		
gca	acc	ccg	atc	atg	ggg	cgc	acg	ttg	ggg	cag	atc	gcg	acg	ccg	acg	451
Ala	Thr	Pro	Ile	Met	Gly	Arg	Thr	Leu	Gly	Gln	Ile	Ala	Thr	Pro	Thr	
			105					110					115			
acg	ttc	ggc	gcg	ctg	acc	ggc	ggc	tgg	ctg	gtt	gcg	gtg	gac	aat	gcg	499
Thr	Phe	Gly	Ala	Leu	Thr	Gly	Gly	Trp	Leu	Val	Ala	Val	Asp	Asn	Ala	
		120					125					130				
gca	cgc	gcc	ctg	gag	gcg	ctg	gag	ttt	ccg	gtg	tcg	tat	ggc	ggt	gcc	547
Ala	Arg	Ala	Leu	Glu	Ala	Leu	Glu	Phe	Pro	Val	Ser	Tyr	Gly	Gly	Ala	
	135					140					145					
agc	gga	aat	atg	acg	gcg	gtg	cac	ccg	cgt	ggc	ttc	gag	att	cag	gcg	595
Ser	Gly	Asn	Met	Thr	Ala	Val	His	Pro	Arg	Gly	Phe	Glu	Ile	Gln	Ala	
150					155				160					165		
aag	ctg	gcc	gag	gag	ttg	ggc	ctt	ttt	gat	ccg	cag	tgg	gtg	tgg	cat	643
Lys	Leu	Ala	Glu	Glu	Leu	Gly	Leu	Phe	Asp	Pro	Gln	Trp	Val	Trp	His	
			170						175					180		
tcc	gat	cgc	acg	ccg	atc	act	gcg	atc	gcg	tcg	gcg	ctg	gca	acg	gcc	691
Ser	Asp	Arg	Thr	Pro	Ile	Thr	Ala	Ile	Ala	Ser	Ala	Leu	Ala	Thr	Ala	
			185					190					195			
gct	ggt	gtg	gta	cgc	aaa	att	gct	ggt	gac	gtg	gtg	ttt	tac	tca	caa	739
Ala	Gly	Val	Val	Arg	Lys	Ile	Ala	Gly	Asp	Val	Val	Phe	Tyr	Ser	Gln	
		200					205					210				
acc	gag	gtc	ggc	gag	ttg	cgg	gag	aaa	tcc	ccc	ggc	ggc	agc	tcc	gcg	787
Thr	Glu	Val	Gly	Glu	Leu	Arg	Glu	Lys	Ser	Pro	Gly	Gly	Ser	Ser	Ala	
	215					220					225					
atg	ccc	cac	aaa	gcc	aat	ccg	gcc	gct	gcg	att	gcg	tgc	gac	ggt	tac	835
Met	Pro	His	Lys	Ala	Asn	Pro	Ala	Ala	Ala	Ile	Ala	Cys	Asp	Gly	Tyr	
230					235					240				245		
gcg	cgc	cgg	gca	cct	ggc	ctt	ctt	gca	acg	ctt	ttc	gac	gcc	ctc	gac	883
Ala	Arg	Arg	Ala	Pro	Gly	Leu	Leu	Ala	Thr	Leu	Phe	Asp	Ala	Leu	Asp	

250										255					260					
tgc	cgt	ttg	cag	cgc	ggc	acc	ggc	agc	tgg	cac	gcg	gag	tgg	gca	acg	931				
Cys	Arg	Leu	Gln	Arg	Gly	Thr	Gly	Ser	Trp	His	Ala	Glu	Trp	Ala	Thr					
			265				270				275									
ctg	cgc	gag	ttg	gct	gct	gtc	act	cac	tca	gca	gtg	agc	agg	gct	gca	979				
Leu	Arg	Glu	Leu	Ala	Ala	Val	Thr	His	Ser	Ala	Val	Ser	Arg	Ala	Ala					
			280				285				290									
acc	agc	atc	gat	ggc	atc	acc	gtc	aac	gtt	gat	gtg	atg	gca	agt	cgc	1027				
Thr	Ser	Ile	Asp	Gly	Ile	Thr	Val	Asn	Val	Asp	Val	Met	Ala	Ser	Arg					
			295				300				305									
gtc	aat	gga	cca	acc	ggg	cac	gcc	gaa	gat	ttg	gcg	gag	cgg	gca	cta	1075				
Val	Asn	Gly	Pro	Thr	Gly	His	Ala	Glu	Asp	Leu	Ala	Glu	Arg	Ala	Leu					
310				315				320				325								
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Glu Ile Tyr Gly Lys Gly Arg Ser																				
			330																	

<210> 366

<211> 333

<212> PRT

<213> Corynebacterium glutamicum

<400> 366

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			20				25				30				

Arg	Arg	Ala	Ala	Glu	Gly	Gly	Asn	Pro	Leu	Ile	Pro	Leu	Val	Thr	Asp
			35				40				45				

Leu	Lys	Ala	Ile	Asn	Pro	Ala	Gly	Ile	His	Ile	Gly	Ala	Thr	Ser	Gln
			50				55				60				

Asp	Ile	Ile	Asp	Ser	Ala	Leu	Met	Leu	Cys	Met	Lys	Glu	Gly	Val	Gly
			65				70				75				80

Glu	Val	Val	Asp	Lys	Leu	Lys	Lys	Leu	Ala	Arg	Asp	Leu	Ala	Glu	Leu
			85				90				95				

Thr	Ala	Glu	His	Lys	Ala	Thr	Pro	Ile	Met	Gly	Arg	Thr	Leu	Gly	Gln
			100				105				110				

Ile	Ala	Thr	Pro	Thr	Thr	Phe	Gly	Ala	Leu	Thr	Gly	Gly	Trp	Leu	Val
			115				120				125				

Ala	Val	Asp	Asn	Ala	Ala	Arg	Ala	Leu	Glu	Ala	Leu	Glu	Phe	Pro	Val
			130				135				140				

Ser	Tyr	Gly	Gly	Ala	Ser	Gly	Asn	Met	Thr	Ala	Val	His	Pro	Arg	Gly
			145				150				155				160

Phe	Glu	Ile	Gln	Ala	Lys	Leu	Ala	Glu	Glu	Leu	Gly	Leu	Phe	Asp	Pro
			165				170				175				

Gln Trp Val Trp His Ser Asp Arg Thr Pro Ile Thr Ala Ile Ala Ser
 180 185 190
 Ala Leu Ala Thr Ala Ala Gly Val Val Arg Lys Ile Ala Gly Asp Val
 195 200 205
 Val Phe Tyr Ser Gln Thr Glu Val Gly Glu Leu Arg Glu Lys Ser Pro
 210 215 220
 Gly Gly Ser Ser Ala Met Pro His Lys Ala Asn Pro Ala Ala Ala Ile
 225 230 235 240
 Ala Cys Asp Gly Tyr Ala Arg Arg Ala Pro Gly Leu Leu Ala Thr Leu
 245 250 255
 Phe Asp Ala Leu Asp Cys Arg Leu Gln Arg Gly Thr Gly Ser Trp His
 260 265 270
 Ala Glu Trp Ala Thr Leu Arg Glu Leu Ala Ala Val Thr His Ser Ala
 275 280 285
 Val Ser Arg Ala Ala Thr Ser Ile Asp Gly Ile Thr Val Asn Val Asp
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 Ala Glu Arg Ala Leu Glu Ile Tyr Gly Lys Gly Arg Ser
 325 330

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<211> 651

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(642)

<223> FRXA02813

<400> 367

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gcc ctg gag gcg ctg gag ttt ccg gtg tcg tat ggc ggt gcc agc gga	96
Ala Leu Glu Ala Leu Glu Phe Pro Val Ser Tyr Gly Gly Ala Ser Gly	
20 25 30	
aat atg acg gcg gtg cac ccg cgt ggc ttc gag att cag gcg aag ctg	144
Asn Met Thr Ala Val His Pro Arg Gly Phe Glu Ile Gln Ala Lys Leu	
35 40 45	
gcc gag gag ttg ggc ctt ttt gat ccg cag tgg gtg tgg cat tcc gat	192
Ala Glu Glu Leu Gly Leu Phe Asp Pro Gln Trp Val Trp His Ser Asp	
50 55 60	
cgc acg ccg atc act gcg atc gcg tcg gcg ctg gca acg gcc gct ggt	240
Arg Thr Pro Ile Thr Ala Ile Ala Ser Ala Leu Ala Thr Ala Ala Gly	

65	70	75	80	
gtg gta cgc aaa att gct ggt gac gtg gtg ttt tac tca caa acc gag				288
Val Val Arg Lys Ile Ala Gly Asp Val Val Phe Tyr Ser Gln Thr Glu	85	90	95	
gtc ggc gag ttg cgg gag aaa tcc ccc ggc ggc agc tcc gcg atg ccc				336
Val Gly Glu Leu Arg Glu Lys Ser Pro Gly Gly Ser Ser Ala Met Pro	100	105	110	
cac aaa gcc aat ccg gcc gct gcg att gcg tgc gac ggt tac gcg cgc				384
His Lys Ala Asn Pro Ala Ala Ile Ala Cys Asp Gly Tyr Ala Arg	115	120	125	
cgg gca cct ggc ctt ctt gca acg ctt ttc gac gcc ctc gac tgc cgt				432
Arg Ala Pro Gly Leu Leu Ala Thr Leu Phe Asp Ala Leu Asp Cys Arg	130	135	140	
ttg cag cgc ggc acc ggc agc tgg cac gcg gag tgg gca acg ctg cgc				480
Leu Gln Arg Gly Thr Gly Ser Trp His Ala Glu Trp Ala Thr Leu Arg	145	150	155	160
gag ttg gct gct gtc act cac tca gca gtg agc agg gct gca acc agc				528
Glu Leu Ala Ala Val Thr His Ser Ala Val Ser Arg Ala Ala Thr Ser	165	170	175	
atc gat ggc atc acc gtc aac gtt gat gtg atg gca agt cgc gtc aat				576
Ile Asp Gly Ile Thr Val Asn Val Asp Val Met Ala Ser Arg Val Asn	180	185	190	
gga cca acc ggg cac gcc gaa gat ttg gcg gag cgg gca cta gaa att				624
Gly Pro Thr Gly His Ala Glu Asp Leu Ala Glu Arg Ala Leu Glu Ile	195	200	205	
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Tyr Gly Lys Gly Arg Ser	210			
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Asn Met Thr Ala Val His Pro Arg Gly Phe Glu Ile Gln Ala Lys Leu	35	40	45	
Ala Glu Glu Leu Gly Leu Phe Asp Pro Gln Trp Val Trp His Ser Asp	50	55	60	
Arg Thr Pro Ile Thr Ala Ile Ala Ser Ala Leu Ala Thr Ala Ala Gly	65	70	75	80
Val Val Arg Lys Ile Ala Gly Asp Val Val Phe Tyr Ser Gln Thr Glu				

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1				5					10					15		
ctc acc atc gcg att ttg acc gcg gtg ggc aat gac ggc gag ttg gac																96
Leu	Thr	Ile	Ala	Ile	Leu	Thr	Ala	Val	Gly	Asn	Asp	Gly	Glu	Leu	Asp	
			20					25					30			
atg cac att cgt gct gct ctg cgc gct ggc gtg gat cag gaa acc atc																144
Met	His	Ile	Arg	Ala	Ala	Leu	Arg	Ala	Gly	Val	Asp	Gln	Glu	Thr	Ile	
		35					40					45				
ggc gag gtc atc ctg cac act gcg gtg tat gcg ggt gtg ccg aac tcc																192
Gly	Glu	Val	Ile	Leu	His	Thr	Ala	Val	Tyr	Ala	Gly	Val	Pro	Asn	Ser	
	50					55					60					
aac cat ggt ttc aag ctg ctg aac aac gct gtg tca gac ctt cag																237
Asn	His	Gly	Phe	Lys	Leu	Leu	Asn	Asn	Ala	Val	Ser	Asp	Leu	Gln		
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<400> 370

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			20					25					30		
Met	His	Ile	Arg	Ala	Ala	Leu	Arg	Ala	Gly	Val	Asp	Gln	Glu	Thr	Ile
		35					40					45			
Gly	Glu	Val	Ile	Leu	His	Thr	Ala	Val	Tyr	Ala	Gly	Val	Pro	Asn	Ser
	50					55					60				
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acc	gca	ggt	cgt	gac	atc	cta	gga	gag	ttt	gca	cct	aag	tcc	gct	gaa		163	
Thr	Ala	Gly	Arg	Asp	Ile	Leu	Gly	Glu	Phe	Ala	Pro	Lys	Ser	Ala	Glu			
				10					15					20				
ctc	aac	gat	gat	gtc	ctc	ttt	ggc	cag	gtg	tgg	tcg	agg	gaa	tca	gag		211	
Leu	Asn	Asp	Asp	Val	Leu	Phe	Gly	Gln	Val	Trp	Ser	Arg	Glu	Ser	Glu			
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ctt	tcc	cca	cgt	gac	cga	agc	atc	gtg	atc	gtg	aca	atg	ttg	atg	gca		259	
Leu	Ser	Pro	Arg	Asp	Arg	Ser	Ile	Val	Ile	Val	Thr	Met	Leu	Met	Ala			
				40					45					50				
agt	ggc	gtg	ctg	gat	agt	gct	ttt	gaa	agc	cac	gtt	cag	cga	gcc	aaa		307	
Ser	Gly	Val	Leu	Asp	Ser	Ala	Phe	Glu	Ser	His	Val	Gln	Arg	Ala	Lys			
		55					60					65						
gac	aac	ggt	gtc	act	gct	gaa	gaa	atc	gca	gag	atc	atc	acc	cac	gtg		355	
Asp	Asn	Gly	Val	Thr	Ala	Glu	Glu	Ile	Ala	Glu	Ile	Ile	Thr	His	Val			
70					75					80					85			
gcc	ttt	tat	gca	ggt	tgg	cca	aag	gct	tgg	gct	gcg	ttc	cgc	atc	gca		403	
Ala	Phe	Tyr	Ala	Gly	Trp	Pro	Lys	Ala	Trp	Ala	Ala	Phe	Arg	Ile	Ala			

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Lys Asp Ile Tyr Thr Lys
105

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<212> PRT
<213> Corynebacterium glutamicum

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35 40 45
Thr Met Leu Met Ala Ser Gly Val Leu Asp Ser Ala Phe Glu Ser His
50 55 60
Val Gln Arg Ala Lys Asp Asn Gly Val Thr Ala Glu Glu Ile Ala Glu
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Ile Ile Thr His Val Ala Phe Tyr Ala Gly Trp Pro Lys Ala Trp Ala
85 90 95
Ala Phe Arg Ile Ala Lys Asp Ile Tyr Thr Lys
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<222> (101)..(1261)
<223> RXA01465

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Val Ala Gly Leu Phe
1 5
cca ctt aac cag aaa gcc ata gaa aaa ttg tct gat tta acc atc caa 163
Pro Leu Asn Gln Lys Ala Ile Glu Lys Leu Ser Asp Leu Thr Ile Gln
10 15 20
aaa gtc gaa tcc cgt atc ctc gac gtt ccc ctc att cgc cca cac ggc 211
Lys Val Glu Ser Arg Ile Leu Asp Val Pro Leu Ile Arg Pro His Gly
25 30 35
ttc gca act acc acc tcc act gag cag cac att ctg ctg gtc agc gtg 259

Phe	Ala	Thr	Thr	Thr	Ser	Thr	Glu	Gln	His	Ile	Leu	Leu	Val	Ser	Val		
		40					45					50					
cac	tta	gaa	aac	ggt	gtc	atc	ggc	tac	ggt	gag	ggc	gtt	gtg	ccc	ggc	307	
His	Leu	Glu	Asn	Gly	Val	Ile	Gly	Tyr	Gly	Glu	Gly	Val	Val	Pro	Gly		
	55					60					65						
ggt	cca	tgg	tgg	ggc	ggc	gag	tcg	gtt	gag	acc	atg	aag	gcg	ctt	gtc	355	
Gly	Pro	Trp	Trp	Gly	Gly	Glu	Ser	Val	Glu	Thr	Met	Lys	Ala	Leu	Val		
70					75					80					85		
gac	ggc	tac	ctc	gcc	cca	gtg	ctc	atc	ggc	cgt	gct	gtc	tcc	gag	ctt	403	
Asp	Gly	Tyr	Leu	Ala	Pro	Val	Leu	Ile	Gly	Arg	Ala	Val	Ser	Glu	Leu		
				90					95					100			
gca	gga	att	atg	gca	gac	ctt	gag	cgt	gtt	gtt	gca	cgt	gcg	cgt	tat	451	
Ala	Gly	Ile	Met	Ala	Asp	Leu	Glu	Arg	Val	Val	Ala	Arg	Ala	Arg	Tyr		
			105					110					115				
gcc	aag	gcg	gct	gtt	gac	gtc	gca	atg	cat	gat	gcc	tgg	gca	cgc	agc	499	
Ala	Lys	Ala	Ala	Val	Asp	Val	Ala	Met	His	Asp	Ala	Trp	Ala	Arg	Ser		
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ctc	aat	gtg	ccc	gtc	cgc	gac	ctg	ctt	ggt	ggc	acc	gtg	cgc	gac	aag	547	
Leu	Asn	Val	Pro	Val	Arg	Asp	Leu	Leu	Gly	Gly	Thr	Val	Arg	Asp	Lys		
	135					140					145						
gtg	gat	gtc	acc	tgg	gcg	ctg	ggc	gtt	ttg	ccg	ctt	gat	gtt	gcg	gtg	595	
Val	Asp	Val	Thr	Trp	Ala	Leu	Gly	Val	Leu	Pro	Leu	Asp	Val	Ala	Val		
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Ala	Glu	Ile	Glu	Glu	Arg	Ile	Glu	Glu	Phe	Gly	Asn	Arg	Ser	Phe	Lys		
				170					175					180			
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Leu	Lys	Met	Gly	Ala	Gly	Asp	Pro	Ala	Glu	Asp	Thr	Arg	Arg	Val	Ala		
			185					190					195				
gaa	ttg	gcg	cgc	gaa	gtt	ggc	gac	cgc	gtt	tct	ctg	cgc	att	gat	att	739	
Glu	Leu	Ala	Arg	Glu	Val	Gly	Asp	Arg	Val	Ser	Leu	Arg	Ile	Asp	Ile		
	200						205					210					
aac	gca	cgt	tgg	gat	cgc	cgc	acc	gct	ctg	cat	tac	ttg	ccg	att	ctc	787	
Asn	Ala	Arg	Trp	Asp	Arg	Arg	Thr	Ala	Leu	His	Tyr	Leu	Pro	Ile	Leu		
	215					220					225						
gcg	gag	gct	ggc	gtc	gag	ctg	ttc	gag	cag	ccc	acc	ccg	gcc	gac	gac	835	
Ala	Glu	Ala	Gly	Val	Glu	Leu	Phe	Glu	Gln	Pro	Thr	Pro	Ala	Asp	Asp		
230					235					240					245		
ctg	gaa	acc	ctg	cgc	gaa	atc	acc	cgc	cgc	acc	aac	gtt	tcg	gtc	atg	883	
Leu	Glu	Thr	Leu	Arg	Glu	Ile	Thr	Arg	Arg	Thr	Asn	Val	Ser	Val	Met		
				250					255					260			
gca	gat	gaa	tcc	gtg	tgg	acc	cca	gct	gaa	gct	ctc	gcg	gtg	gtg	aaa	931	
Ala	Asp	Glu	Ser	Val	Trp	Thr	Pro	Ala	Glu	Ala	Leu	Ala	Val	Val	Lys		
			265					270					275				
gcc	cag	gct	gcg	gat	gtt	atc	gca	ctg	aaa	acc	act	aag	cac	ggt	ggt	979	
Ala	Gln	Ala	Ala	Asp	Val	Ile	Ala	Leu	Lys	Thr	Thr	Lys	His	Gly	Gly		

280	285	290	
ctg ctg gaa tcc aag aag atc gcc gct atc gcc gaa gcc ggc ggg ctg			1027
Leu Leu Glu Ser Lys Lys Ile Ala Ala Ile Ala Glu Ala Gly Gly Leu			
295	300	305	
gcc tgc cat ggt gca acc agt ctg gaa ggt cca atc ggc acc gca gca			1075
Ala Cys His Gly Ala Thr Ser Leu Glu Gly Pro Ile Gly Thr Ala Ala			
310	315	320	325
tcc ctg cag ttt gcg gca tcc acc aag gcg atc tcc tac ggt aca gaa			1123
Ser Leu Gln Phe Ala Ala Ser Thr Lys Ala Ile Ser Tyr Gly Thr Glu			
	330	335	340
ctg ttc gga ccg cag ttg ctc aaa gat acc tat att gtc caa gaa ttt			1171
Leu Phe Gly Pro Gln Leu Leu Lys Asp Thr Tyr Ile Val Gln Glu Phe			
	345	350	355
gag tac aag gac ggc cag gtt gct att cca caa ggc cca ggt ttg ggc			1219
Glu Tyr Lys Asp Gly Gln Val Ala Ile Pro Gln Gly Pro Gly Leu Gly			
	360	365	370
gtc gat gtg gac atg gac aaa gtc aac ttc tac acc cgt aaa			1261
Val Asp Val Asp Met Asp Lys Val Asn Phe Tyr Thr Arg Lys			
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<213> Corynebacterium glutamicum			
<400> 374			
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	20	25	30
Ile Arg Pro His Gly Phe Ala Thr Thr Thr Ser Thr Glu Gln His Ile			
	35	40	45
Leu Leu Val Ser Val His Leu Glu Asn Gly Val Ile Gly Tyr Gly Glu			
	50	55	60
Gly Val Val Pro Gly Gly Pro Trp Trp Gly Gly Glu Ser Val Glu Thr			
	65	70	75
Met Lys Ala Leu Val Asp Gly Tyr Leu Ala Pro Val Leu Ile Gly Arg			
	85	90	95
Ala Val Ser Glu Leu Ala Gly Ile Met Ala Asp Leu Glu Arg Val Val			
	100	105	110
Ala Arg Ala Arg Tyr Ala Lys Ala Ala Val Asp Val Ala Met His Asp			
	115	120	125
Ala Trp Ala Arg Ser Leu Asn Val Pro Val Arg Asp Leu Leu Gly Gly			
	130	135	140

Thr Val Arg Asp Lys Val Asp Val Thr Trp Ala Leu Gly Val Leu Pro
 145 150 155 160
 Leu Asp Val Ala Val Ala Glu Ile Glu Glu Arg Ile Glu Glu Phe Gly
 165 170 175
 Asn Arg Ser Phe Lys Leu Lys Met Gly Ala Gly Asp Pro Ala Glu Asp
 180 185 190
 Thr Arg Arg Val Ala Glu Leu Ala Arg Glu Val Gly Asp Arg Val Ser
 195 200 205
 Leu Arg Ile Asp Ile Asn Ala Arg Trp Asp Arg Arg Thr Ala Leu His
 210 215 220
 Tyr Leu Pro Ile Leu Ala Glu Ala Gly Val Glu Leu Phe Glu Gln Pro
 225 230 235 240
 Thr Pro Ala Asp Asp Leu Glu Thr Leu Arg Glu Ile Thr Arg Arg Thr
 245 250 255
 Asn Val Ser Val Met Ala Asp Glu Ser Val Trp Thr Pro Ala Glu Ala
 260 265 270
 Leu Ala Val Val Lys Ala Gln Ala Ala Asp Val Ile Ala Leu Lys Thr
 275 280 285
 Thr Lys His Gly Gly Leu Leu Glu Ser Lys Lys Ile Ala Ala Ile Ala
 290 295 300
 Glu Ala Gly Gly Leu Ala Cys His Gly Ala Thr Ser Leu Glu Gly Pro
 305 310 315 320
 Ile Gly Thr Ala Ala Ser Leu Gln Phe Ala Ala Ser Thr Lys Ala Ile
 325 330 335
 Ser Tyr Gly Thr Glu Leu Phe Gly Pro Gln Leu Leu Lys Asp Thr Tyr
 340 345 350
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 Thr Arg Lys
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 <223> RXA02316

<400> 375

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cct gct ggt tgg gga gag ttc gcg ccc ttc ctt gag tat gac ccg caa Pro Ala Gly Trp Gly Glu Phe Ala Pro Phe Leu Glu Tyr Asp Pro Gln 40 45 50															259
gaa tcg gcc agt tgg cta aag tcc ggc att gaa gca gcg tgg gag ggt Glu Ser Ala Ser Trp Leu Lys Ser Gly Ile Glu Ala Ala Trp Glu Gly 55 60 65															307
ttt ccg gcg ccg ttg cgt gat cgc gtg gaa gtc aat gcc acc atc cca Phe Pro Ala Pro Leu Arg Asp Arg Val Glu Val Asn Ala Thr Ile Pro 70 75 80 85															355
gct gtt ccg gcc gat caa gtg gca gaa gtt ttg gac cgt ttc cca ggc Ala Val Pro Ala Asp Gln Val Ala Glu Val Leu Asp Arg Phe Pro Gly 90 95 100															403
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 His Leu Arg Ala Arg Thr Met Asp Ile Thr Val Ala Ser Ala Leu Asp
 230 235 240 245
 acg gtt gtg ggg atg aat gct ggg ttg gct gcg gtg gcg gcg ttg ccg 883
 Thr Val Val Gly Met Asn Ala Gly Leu Ala Ala Val Ala Ala Leu Pro
 250 255 260
 aag ttg gat gat gac gat ctc att gat gtg cca cca gcg gcg gcg ggt 931
 Lys Leu Asp Asp Asp Asp Leu Ile Asp Val Pro Pro Ala Ala Ala Gly
 265 270 275
 ctt gcg act tcg cag ttg ttc ctg gag gat gtc gcg acc ccg cac gca 979
 Leu Ala Thr Ser Gln Leu Phe Leu Glu Asp Val Ala Thr Pro His Ala
 280 285 290
 atc act gat ggg ttc atg gaa acg cgt gta att gcc ccg gaa atg gat 1027
 Ile Thr Asp Gly Phe Met Glu Thr Arg Val Ile Ala Pro Glu Met Asp
 295 300 305
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 Arg Leu Glu Thr Leu Ala Ala Ser Lys Asp Arg Arg Asp Trp Trp Phe
 310 315 320 325
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<210> 376

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 376

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 35 40 45
 Glu Tyr Asp Pro Gln Glu Ser Ala Ser Trp Leu Lys Ser Gly Ile Glu
 50 55 60
 Ala Ala Trp Glu Gly Phe Pro Ala Pro Leu Arg Asp Arg Val Glu Val
 65 70 75 80
 Asn Ala Thr Ile Pro Ala Val Pro Ala Asp Gln Val Ala Glu Val Leu
 85 90 95
 Asp Arg Phe Pro Gly Cys Arg Thr Ile Lys Val Lys Val Ala Glu Pro
 100 105 110
 Gly Gln Thr Leu Ala Asp Asp Ile Ala Arg Val Ala Ala Ala Arg Glu
 115 120 125

Ala Arg Pro Gly Ala Ile Ile Arg Val Asp Ala Asn Cys Gly Trp Ser
 130 135 140
 Val Glu Gln Ala Val Glu Ala Ala Gln Ala Leu Ala Pro Leu Asp Tyr
 145 150 155 160
 Leu Glu Gln Pro Cys Ala Thr Val Glu Glu Leu Ala Glu Val Arg Met
 165 170 175
 Thr Val Gln Arg Arg Gly Leu Phe Val Arg Val Ala Ala Asp Glu Ser
 180 185 190
 Ile Arg Lys Ser Asp Asp Pro Tyr Arg Val Ala Asp Leu Arg Ala Ala
 195 200 205
 Asp Val Ala Val Val Lys Val Ala Pro Leu Gly Gly Val Lys Arg Val
 210 215 220
 Leu Glu Val Val Gln His Leu Arg Ala Arg Thr Met Asp Ile Thr Val
 225 230 235 240
 Ala Ser Ala Leu Asp Thr Val Val Gly Met Asn Ala Gly Leu Ala Ala
 245 250 255
 Val Ala Ala Leu Pro Lys Leu Asp Asp Asp Asp Leu Ile Asp Val Pro
 260 265 270
 Pro Ala Ala Ala Gly Leu Ala Thr Ser Gln Leu Phe Leu Glu Asp Val
 275 280 285
 Ala Thr Pro His Ala Ile Thr Asp Gly Phe Met Glu Thr Arg Val Ile
 290 295 300
 Ala Pro Glu Met Asp Arg Leu Glu Thr Leu Ala Ala Ser Lys Asp Arg
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 Arg Asp Trp Trp Phe Glu Arg Val Arg Glu Ser Tyr Pro Tyr Leu Glu
 325 330 335

Thr Ile

<210> 377
 <211> 414
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(391)
 <223> RXA01464

<400> 377
 caaggacggc caggttgcta ttccacaagg cccaggtttg ggcgtcgatg tggacatgga 60

caaagtcaac ttctacaccc gtaaataagg agaattatcg atg ctg ttt cta gca 115
 Met Leu Phe Leu Ala
 1 5

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cgc atg gac gtc gtc ttc cct gat tcc atg gac gcc gat gtg atg gca 163
Arg Met Asp Val Val Phe Pro Asp Ser Met Asp Ala Asp Val Met Ala
      10      15      20

gat ttc cag gct aag gaa aag gcc tac tcc gga gac ctg caa tcc cgt 211
Asp Phe Gln Ala Lys Glu Lys Ala Tyr Ser Gly Asp Leu Gln Ser Arg
      25      30      35

gga atc atg aaa gca atc tgg cga gtc gtc ggc gag tat gca aac tac 259
Gly Ile Met Lys Ala Ile Trp Arg Val Val Gly Glu Tyr Ala Asn Tyr
      40      45      50

tcc att ttc gat gtc gat gac cac gac gag ctg cat gca att ctt agt 307
Ser Ile Phe Asp Val Asp Asp His Asp Glu Leu His Ala Ile Leu Ser
      55      60      65

ggc ttt ccg atg ttc aaa tac atg aat gtc aag atc act cca ctg gca 355
Gly Phe Pro Met Phe Lys Tyr Met Asn Val Lys Ile Thr Pro Leu Ala
      70      75      80      85

aaa cac ccc aat gct ctg gag tat tac ctc aag gga tagttgaggt 401
Lys His Pro Asn Ala Leu Glu Tyr Tyr Leu Lys Gly
      90      95

tctaaccgct cta 414

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<210> 378

<211> 97

<212> PRT

<213> Corynebacterium glutamicum

<400> 378

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Met Leu Phe Leu Ala Arg Met Asp Val Val Phe Pro Asp Ser Met Asp
 1      5      10      15

Ala Asp Val Met Ala Asp Phe Gln Ala Lys Glu Lys Ala Tyr Ser Gly
      20      25      30

Asp Leu Gln Ser Arg Gly Ile Met Lys Ala Ile Trp Arg Val Val Gly
      35      40      45

Glu Tyr Ala Asn Tyr Ser Ile Phe Asp Val Asp Asp His Asp Glu Leu
      50      55      60

His Ala Ile Leu Ser Gly Phe Pro Met Phe Lys Tyr Met Asn Val Lys
      65      70      75      80

Ile Thr Pro Leu Ala Lys His Pro Asn Ala Leu Glu Tyr Tyr Leu Lys
      85      90      95

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Gly

<210> 379

<211> 1119

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1096)

<223> RXA02603

<400> 379

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gcacgggtgct tggcgtgcat tacccaaccg atgtgctagc cggcgcgttg ttgggagcag 60
cgaccgcaga ggccgtccat aagatcgaaa gggctacgaa gtg agc gaa cac gcc 115
Val Ser Glu His Ala
1 5

gct gaa cat cac cgc gat acc caa aat ttc tta acc tcc gaa ccg cac 163
Ala Glu His His Arg Asp Thr Gln Asn Phe Leu Thr Ser Glu Pro His
10 15 20

acc acg gca atc gaa gac aac aag aag cgc caa ccg ccg aaa aac ctt 211
Thr Thr Ala Ile Glu Asp Asn Lys Lys Arg Gln Pro Pro Lys Asn Leu
25 30 35

gct gac ggc atg atc aag gcg ctg cgc ccc aag cag tgg gtc aag aac 259
Ala Asp Gly Met Ile Lys Ala Leu Arg Pro Lys Gln Trp Val Lys Asn
40 45 50

gtt ctt gtg cta gca gca cca ctt gct gct ggt gca gat gcg atc ttc 307
Val Leu Val Leu Ala Ala Pro Leu Ala Ala Gly Ala Asp Ala Ile Phe
55 60 65

aac cag cgc acg atc atc gac gtt gct atc gca ttc gta gtg ttc tgc 355
Asn Gln Arg Thr Ile Ile Asp Val Ala Ile Ala Phe Val Val Phe Cys
70 75 80 85

ttc ggt gca tca gcc att tac ttg gtt aat gat gcc cgt gac gtg gaa 403
Phe Gly Ala Ser Ala Ile Tyr Leu Val Asn Asp Ala Arg Asp Val Glu
90 95 100

gct gac cgc gag cac cca acc aag cgt ttc cgc ccc atc gct gca gga 451
Ala Asp Arg Glu His Pro Thr Lys Arg Phe Arg Pro Ile Ala Ala Gly
105 110 115

gtc ctg cca gta gga atg gca tac ggc atg gcc gtg gcg ctc att gca 499
Val Leu Pro Val Gly Met Ala Tyr Gly Met Ala Val Ala Leu Ile Ala
120 125 130

cta tcc atc gga ctg tct ttc ctc gcc acc gac ggc gtg gca ctt gcc 547
Leu Ser Ile Gly Leu Ser Phe Leu Ala Thr Asp Gly Val Ala Leu Ala
135 140 145

tgc gtg att ggc gtg tac att gcg ctg cag ctg gga tac tgc ttc ggt 595
Cys Val Ile Gly Val Tyr Ile Ala Leu Gln Leu Gly Tyr Cys Phe Gly
150 155 160 165

tgg aag cac atg cca gtg atc gat att gcg ctt gtc tcc tcc gga ttc 643
Trp Lys His Met Pro Val Ile Asp Ile Ala Leu Val Ser Ser Gly Phe
170 175 180

atg ctc cgc gca atg gca ggt ggt gtc gca gca ggc atc gag cta tcc 691
Met Leu Arg Ala Met Ala Gly Gly Val Ala Ala Gly Ile Glu Leu Ser
185 190 195

cag tgg ttc ctg cta gtc gct gcg ttt ggt tcc ctg ttc atg gca tct 739
Gln Trp Phe Leu Leu Val Ala Ala Phe Gly Ser Leu Phe Met Ala Ser

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200					205					210					
gga aag cgc tac gca gaa atc ctt ctg cac gag cgc acc ggc gct aag	787														
Gly Lys Arg Tyr Ala Glu Ile Leu Leu His Glu Arg Thr Gly Ala Lys															
215 220 225															
atc cgc aag tcc ctg gaa agc tac acc ccc acc tac ctg cgc ttc gtt	835														
Ile Arg Lys Ser Leu Glu Ser Tyr Thr Pro Thr Tyr Leu Arg Phe Val															
230 235 240 245															
tgg acc atg gca gca aca gca gtg gtc atg tcc tac gca ctg tgg ggc	883														
Trp Thr Met Ala Ala Thr Ala Val Val Met Ser Tyr Ala Leu Trp Gly															
250 255 260															
ttc gac ctt tcc caa cac tcc acc gac gca ggt ccg tgg tac caa atc	931														
Phe Asp Leu Ser Gln His Ser Thr Asp Ala Gly Pro Trp Tyr Gln Ile															
265 270 275															
tcc atg gtt cca ttc acc atc gcc atc ctg cgc tac gca gcc ggc gta	979														
Ser Met Val Pro Phe Thr Ile Ala Ile Leu Arg Tyr Ala Ala Gly Val															
280 285 290															
gac acc ggc gac ggc ggt gcc cct gac gaa gtg gca ctc agc gac aaa	1027														
Asp Thr Gly Asp Gly Gly Ala Pro Asp Glu Val Ala Leu Ser Asp Lys															
295 300 305															
gtt ctg cag gta cta gcc cta gca tgg gtt ttc tgc atc gtg atg gct	1075														
Val Leu Gln Val Leu Ala Leu Ala Trp Val Phe Cys Ile Val Met Ala															
310 315 320 325															
gtg tac atc atg ccg atg ttt tgaatatatta ccaatgaaca tgc	1119														
Val Tyr Ile Met Pro Met Phe															
330															

<210> 380

<211> 332

<212> PRT

<213> Corynebacterium glutamicum

<400> 380

Val Ser Glu His Ala Ala Glu His His Arg Asp Thr Gln Asn Phe Leu
1 5 10 15

Thr Ser Glu Pro His Thr Thr Ala Ile Glu Asp Asn Lys Lys Arg Gln
20 25 30

Pro Pro Lys Asn Leu Ala Asp Gly Met Ile Lys Ala Leu Arg Pro Lys
35 40 45

Gln Trp Val Lys Asn Val Leu Val Leu Ala Ala Pro Leu Ala Ala Gly
50 55 60

Ala Asp Ala Ile Phe Asn Gln Arg Thr Ile Ile Asp Val Ala Ile Ala
65 70 75 80

Phe Val Val Phe Cys Phe Gly Ala Ser Ala Ile Tyr Leu Val Asn Asp
85 90 95

Ala Arg Asp Val Glu Ala Asp Arg Glu His Pro Thr Lys Arg Phe Arg
100 105 110

Pro Ile Ala Ala Gly Val Leu Pro Val Gly Met Ala Tyr Gly Met Ala
 115 120 125
 Val Ala Leu Ile Ala Leu Ser Ile Gly Leu Ser Phe Leu Ala Thr Asp
 130 135 140
 Gly Val Ala Leu Ala Cys Val Ile Gly Val Tyr Ile Ala Leu Gln Leu
 145 150 155 160
 Gly Tyr Cys Phe Gly Trp Lys His Met Pro Val Ile Asp Ile Ala Leu
 165 170 175
 Val Ser Ser Gly Phe Met Leu Arg Ala Met Ala Gly Gly Val Ala Ala
 180 185 190
 Gly Ile Glu Leu Ser Gln Trp Phe Leu Leu Val Ala Ala Phe Gly Ser
 195 200 205
 Leu Phe Met Ala Ser Gly Lys Arg Tyr Ala Glu Ile Leu Leu His Glu
 210 215 220
 Arg Thr Gly Ala Lys Ile Arg Lys Ser Leu Glu Ser Tyr Thr Pro Thr
 225 230 235 240
 Tyr Leu Arg Phe Val Trp Thr Met Ala Ala Thr Ala Val Val Met Ser
 245 250 255
 Tyr Ala Leu Trp Gly Phe Asp Leu Ser Gln His Ser Thr Asp Ala Gly
 260 265 270
 Pro Trp Tyr Gln Ile Ser Met Val Pro Phe Thr Ile Ala Ile Leu Arg
 275 280 285
 Tyr Ala Ala Gly Val Asp Thr Gly Asp Gly Gly Ala Pro Asp Glu Val
 290 295 300
 Ala Leu Ser Asp Lys Val Leu Gln Val Leu Ala Leu Ala Trp Val Phe
 305 310 315 320
 Cys Ile Val Met Ala Val Tyr Ile Met Pro Met Phe
 325 330

<210> 381

<211> 470

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(447)

<223> RXN02839

<400> 381

tgt gtg gtg aat gat tat gct gac cgc aag ttt gat ggt cat gtt aag 48
 Cys Val Val Asn Asp Tyr Ala Asp Arg Lys Phe Asp Gly His Val Lys
 1 5 10 15

cgc acg gcg aac cga cca ctt ccc agc ggc gcg gta aca gag aaa gag 96
 Arg Thr Ala Asn Arg Pro Leu Pro Ser Gly Ala Val Thr Glu Lys Glu

20	25	30	
gcg cgc gcg ctg ttt gtc gtg ctg gta ctg att tcg ttt tta ctg gtg			144
Ala Arg Ala Leu Phe Val Val Leu Val Leu Ile Ser Phe Leu Leu Val			
35	40	45	
ctg acg ctg aat acg atg acc att ctg ttg tcg att gcc gcg cta gcg			192
Leu Thr Leu Asn Thr Met Thr Ile Leu Leu Ser Ile Ala Ala Leu Ala			
50	55	60	
ctg gcg tgg gtg tac ccg ttt atg aag cgg tat acc cat cta ccg caa			240
Leu Ala Trp Val Tyr Pro Phe Met Lys Arg Tyr Thr His Leu Pro Gln			
65	70	75	80
gtg gtg ctg ggc gcg gcg ttt ggc tgg tcg att cca atg gct ttt gcc			288
Val Val Leu Gly Ala Ala Phe Gly Trp Ser Ile Pro Met Ala Phe Ala			
85	90	95	
gct gtg agt gag tcg gtg cca ttg agt tgc tgg tta atg ttc ctc gcc			336
Ala Val Ser Glu Ser Val Pro Leu Ser Cys Trp Leu Met Phe Leu Ala			
100	105	110	
aat att ctc tgg gcg gtg gct tac gac acg cag tat gcg atg gtt gac			384
Asn Ile Leu Trp Ala Val Ala Tyr Asp Thr Gln Tyr Ala Met Val Asp			
115	120	125	
cgc gat gat gat gtg aag att ggc att aaa tcc acg gca atc ctg ttg			432
Arg Asp Asp Asp Val Lys Ile Gly Ile Lys Ser Thr Ala Ile Leu Leu			
130	135	140	
gcc aat acg ata aat tgatattggg attttgcaga ttg			470
Ala Asn Thr Ile Asn			
145			

<210> 382

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 382

Cys	Val	Val	Asn	Asp	Tyr	Ala	Asp	Arg	Lys	Phe	Asp	Gly	His	Val	Lys
1				5					10					15	

Arg	Thr	Ala	Asn	Arg	Pro	Leu	Pro	Ser	Gly	Ala	Val	Thr	Glu	Lys	Glu
			20					25					30		

Ala	Arg	Ala	Leu	Phe	Val	Val	Leu	Val	Leu	Ile	Ser	Phe	Leu	Leu	Val
			35				40					45			

Leu	Thr	Leu	Asn	Thr	Met	Thr	Ile	Leu	Leu	Ser	Ile	Ala	Ala	Leu	Ala
	50					55					60				

Leu	Ala	Trp	Val	Tyr	Pro	Phe	Met	Lys	Arg	Tyr	Thr	His	Leu	Pro	Gln
	65				70					75				80	

Val	Val	Leu	Gly	Ala	Ala	Phe	Gly	Trp	Ser	Ile	Pro	Met	Ala	Phe	Ala
				85					90					95	

Ala	Val	Ser	Glu	Ser	Val	Pro	Leu	Ser	Cys	Trp	Leu	Met	Phe	Leu	Ala
			100					105					110		

Asn Ile Leu Trp Ala Val Ala Tyr Asp Thr Gln Tyr Ala Met Val Asp
 115 120 125

Arg Asp Asp Asp Val Lys Ile Gly Ile Lys Ser Thr Ala Ile Leu Leu
 130 135 140

Ala Asn Thr Ile Asn
 145

<210> 383

<211> 417

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1) .. (417)

<223> FRXA02839

<400> 383

tgt gtg gtg aat gat tat gct gac cgc aag ttt gat ggt cat gtt aag 48
 Cys Val Val Asn Asp Tyr Ala Asp Arg Lys Phe Asp Gly His Val Lys
 1 5 10 15

cgc acg gcg aac cga cca ctt ccc agc ggc gcg gta aca gag aaa gag 96
 Arg Thr Ala Asn Arg Pro Leu Pro Ser Gly Ala Val Thr Glu Lys Glu
 20 25 30

gcg cgc gcg ctg ttt gtc gtg ctg gta ctg att tcg ttt tta ctg gtg 144
 Ala Arg Ala Leu Phe Val Val Leu Val Leu Ile Ser Phe Leu Leu Val
 35 40 45

ctg acg ctg aat acg atg acc att ctg ttg tcg att gcc gcg cta gcg 192
 Leu Thr Leu Asn Thr Met Thr Ile Leu Leu Ser Ile Ala Ala Leu Ala
 50 55 60

ctg gcg tgg gtg tac ccg ttt atg aag cgg tat acc cat cta ccg caa 240
 Leu Ala Trp Val Tyr Pro Phe Met Lys Arg Tyr Thr His Leu Pro Gln
 65 70 75 80

gtg gtg ctg ggc gcg gcg ttt ggc tgg tcg att cca atg gct ttt gcc 288
 Val Val Leu Gly Ala Ala Phe Gly Trp Ser Ile Pro Met Ala Phe Ala
 85 90 95

gct gtg agt gag tcg gtg cca ttg agt tgc tgg tta atg ttc ctc gcc 336
 Ala Val Ser Glu Ser Val Pro Leu Ser Cys Trp Leu Met Phe Leu Ala
 100 105 110

aat att ctc tgg gcg gtg gct tac gac acg cag tat gcg atg gtt gac 384
 Asn Ile Leu Trp Ala Val Ala Tyr Asp Thr Gln Tyr Ala Met Val Asp
 115 120 125

cgc gat gat gat gtg aag att ggc att aaa tcc 417
 Arg Asp Asp Asp Val Lys Ile Gly Ile Lys Ser
 130 135

<210> 384

<211> 139

<212> PRT

<213> Corynebacterium glutamicum

<400> 384

Cys Val Val Asn Asp Tyr Ala Asp Arg Lys Phe Asp Gly His Val Lys
 1 5 10 15

Arg Thr Ala Asn Arg Pro Leu Pro Ser Gly Ala Val Thr Glu Lys Glu
 20 25 30

Ala Arg Ala Leu Phe Val Val Leu Val Leu Ile Ser Phe Leu Leu Val
 35 40 45

Leu Thr Leu Asn Thr Met Thr Ile Leu Leu Ser Ile Ala Ala Leu Ala
 50 55 60

Leu Ala Trp Val Tyr Pro Phe Met Lys Arg Tyr Thr His Leu Pro Gln
 65 70 75 80

Val Val Leu Gly Ala Ala Phe Gly Trp Ser Ile Pro Met Ala Phe Ala
 85 90 95

Ala Val Ser Glu Ser Val Pro Leu Ser Cys Trp Leu Met Phe Leu Ala
 100 105 110

Asn Ile Leu Trp Ala Val Ala Tyr Asp Thr Gln Tyr Ala Met Val Asp
 115 120 125

Arg Asp Asp Asp Val Lys Ile Gly Ile Lys Ser
 130 135

<210> 385

<211> 1356

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1333)

<223> RXA01502

<400> 385

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gcgcctgacc gtccactttt ttagggacta ggagtacagc atg agc aca cca caa 115
 Met Ser Thr Pro Gln
 1 5

agc atc gtc att atc ggc ggc ggt tta gcc gga gcg aaa acc gca gag 163
 Ser Ile Val Ile Ile Gly Gly Gly Leu Ala Gly Ala Lys Thr Ala Glu
 10 15 20

gca cta cgt gta aac ggg tat gaa ggc tcc atc acg ctc atc gca gca 211
 Ala Leu Arg Val Asn Gly Tyr Glu Gly Ser Ile Thr Leu Ile Ala Ala
 25 30 35

gag gat tat ctg cca tat gag cgc cca ccg ctg tca aag gag tac atg 259
 Glu Asp Tyr Leu Pro Tyr Glu Arg Pro Pro Leu Ser Lys Glu Tyr Met
 40 45 50

gct gga aaa gtg ggc ttt gac aag gcg att gtt cac ccg gcg gag tgg	307
Ala Gly Lys Val Gly Phe Asp Lys Ala Ile Val His Pro Ala Glu Trp	
55 60 65	
tac aaa gaa aac aat gtc acg ctg cgt caa ggt gtg cgt gca acg gca	355
Tyr Lys Glu Asn Asn Val Thr Leu Arg Gln Gly Val Arg Ala Thr Ala	
70 75 80 85	
att gat gcg ggt tca cgc caa gtc acc gtt gat gat ggc gga aac act	403
Ile Asp Ala Gly Ser Arg Gln Val Thr Val Asp Asp Gly Gly Asn Thr	
90 95 100	
gag acc att aac tac gac aaa cta gtt ctt gct act gga tca gca gtg	451
Glu Thr Ile Asn Tyr Asp Lys Leu Val Leu Ala Thr Gly Ser Ala Val	
105 110 115	
cgc aaa ctt cca att ccg gga gcc gac gcc tct aat gtg cac tac ctg	499
Arg Lys Leu Pro Ile Pro Gly Ala Asp Ala Ser Asn Val His Tyr Leu	
120 125 130	
cgc acc gtg gaa gac tct gac gcg atc aag gca acc ttc ggt gaa ggt	547
Arg Thr Val Glu Asp Ser Asp Ala Ile Lys Ala Thr Phe Gly Glu Gly	
135 140 145	
aaa aag ctg gtc ctc atc ggt ggt ggc tgg atc gga ctc gaa gtc gca	595
Lys Lys Leu Val Leu Ile Gly Gly Gly Trp Ile Gly Leu Glu Val Ala	
150 155 160 165	
tca gcg gca cga gga gct ggc act gac gtc act gtt ttg gaa ggt gga	643
Ser Ala Ala Arg Gly Ala Gly Thr Asp Val Thr Val Leu Glu Gly Gly	
170 175 180	
aag ctc cca ctt ttg aaa gtc ctt ggt gaa acg gtc gcg caa gtc ttt	691
Lys Leu Pro Leu Leu Lys Val Leu Gly Glu Thr Val Ala Gln Val Phe	
185 190 195	
gcc gat ctg cat gtg gca aac ggc gtt gac ctg cgc acc gaa gtg aaa	739
Ala Asp Leu His Val Ala Asn Gly Val Asp Leu Arg Thr Glu Val Lys	
200 205 210	
att acg gac atc gtc acc gaa gat gga cgt gca gtt ggc gtg cga ctt	787
Ile Thr Asp Ile Val Thr Glu Asp Gly Arg Ala Val Gly Val Arg Leu	
215 220 225	
gat gac ggc gaa gtg gtt ccc gca gac gca gta gtc att ggc atc ggt	835
Asp Asp Gly Glu Val Val Pro Ala Asp Ala Val Val Ile Gly Ile Gly	
230 235 240 245	
gtc acc cca gtg att gac cta gcg gaa act gct gga ctg gaa atc gac	883
Val Thr Pro Val Ile Asp Leu Ala Glu Thr Ala Gly Leu Glu Ile Asp	
250 255 260	
aat ggt gtt ttg gtg gac gca gca ctg cgt acc agc gac ccg gat atc	931
Asn Gly Val Leu Val Asp Ala Ala Leu Arg Thr Ser Asp Pro Asp Ile	
265 270 275	
tac gca gtt gga gac att gcg aac cac gat cac cca gtt cta gga cac	979
Tyr Ala Val Gly Asp Ile Ala Asn His Asp His Pro Val Leu Gly His	
280 285 290	
cgc atc cgc gtg gag cac tgg gcc acc gcg ttg aat caa cct gcg gct	1027

Arg Ile Arg Val Glu His Trp Ala Thr Ala Leu Asn Gln Pro Ala Ala
 295 300 305
 gcg gtg aaa tcc cta ctt ggc aaa gac gcc gag ttt acc aac ctt ccg 1075
 Ala Val Lys Ser Leu Leu Gly Lys Asp Ala Glu Phe Thr Asn Leu Pro
 310 315 320 325
 tac ttc ttt aca gat caa ttc gat ctg ggt tgt gaa tac gtc ggc cac 1123
 Tyr Phe Phe Thr Asp Gln Phe Asp Leu Gly Cys Glu Tyr Val Gly His
 330 335 340
 gcc acc ggt tgc cag gag aag gta ttc atc cgt gga aac ctt gaa aca 1171
 Ala Thr Gly Ser Gln Glu Lys Val Phe Ile Arg Gly Asn Leu Glu Thr
 345 350 355
 cga gaa ttt gtc gcc ttc tgg gtt gat act gaa aac cga att ctc gcc 1219
 Arg Glu Phe Val Ala Phe Trp Val Asp Thr Glu Asn Arg Ile Leu Ala
 360 365 370
 gca atg aac gtg aat gtg tgg gat gtt cct gat caa atc aag cct ctc 1267
 Ala Met Asn Val Asn Val Trp Asp Val Pro Asp Gln Ile Lys Pro Leu
 375 380 385
 atc gca tca gga aag agc gtt gac acc gag aag cta gtg gat cca gaa 1315
 Ile Ala Ser Gly Lys Ser Val Asp Thr Glu Lys Leu Val Asp Pro Glu
 390 395 400 405
 gtt ccg tat tca gag ctc taagcagtgt gtttgatggc cgc 1356
 Val-Pro Tyr Ser Glu Leu
 410

<210> 386

<211> 411

<212> PRT

<213> Corynebacterium glutamicum

<400> 386

Met Ser Thr Pro Gln Ser Ile Val Ile Ile Gly Gly Gly Leu Ala Gly
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 Ala Lys Thr Ala Glu Ala Leu Arg Val Asn Gly Tyr Glu Gly Ser Ile
 20 25 30
 Thr Leu Ile Ala Ala Glu Asp Tyr Leu Pro Tyr Glu Arg Pro Pro Leu
 35 40 45
 Ser Lys Glu Tyr Met Ala Gly Lys Val Gly Phe Asp Lys Ala Ile Val
 50 55 60
 His Pro Ala Glu Trp Tyr Lys Glu Asn Asn Val Thr Leu Arg Gln Gly
 65 70 75 80
 Val Arg Ala Thr Ala Ile Asp Ala Gly Ser Arg Gln Val Thr Val Asp
 85 90 95
 Asp Gly Gly Asn Thr Glu Thr Ile Asn Tyr Asp Lys Leu Val Leu Ala
 100 105 110
 Thr Gly Ser Ala Val Arg Lys Leu Pro Ile Pro Gly Ala Asp Ala Ser
 115 120 125

Asn Val His Tyr Leu Arg Thr Val Glu Asp Ser Asp Ala Ile Lys Ala
 130 135 140
 Thr Phe Gly Glu Gly Lys Lys Leu Val Leu Ile Gly Gly Gly Trp Ile
 145 150 155 160
 Gly Leu Glu Val Ala Ser Ala Ala Arg Gly Ala Gly Thr Asp Val Thr
 165 170 175
 Val Leu Glu Gly Gly Lys Leu Pro Leu Leu Lys Val Leu Gly Glu Thr
 180 185 190
 Val Ala Gln Val Phe Ala Asp Leu His Val Ala Asn Gly Val Asp Leu
 195 200 205
 Arg Thr Glu Val Lys Ile Thr Asp Ile Val Thr Glu Asp Gly Arg Ala
 210 215 220
 Val Gly Val Arg Leu Asp Asp Gly Glu Val Val Pro Ala Asp Ala Val
 225 230 235 240
 Val Ile Gly Ile Gly Val Thr Pro Val Ile Asp Leu Ala Glu Thr Ala
 245 250 255
 Gly Leu Glu Ile Asp Asn Gly Val Leu Val Asp Ala Ala Leu Arg Thr
 260 265 270
 Ser Asp Pro Asp Ile Tyr Ala Val Gly Asp Ile Ala Asn His Asp His
 275 280 285
 Pro Val Leu Gly His Arg Ile Arg Val Glu His Trp Ala Thr Ala Leu
 290 295 300
 Asn Gln Pro Ala Ala Ala Val Lys Ser Leu Leu Gly Lys Asp Ala Glu
 305 310 315 320
 Phe Thr Asn Leu Pro Tyr Phe Phe Thr Asp Gln Phe Asp Leu Gly Cys
 325 330 335
 Glu Tyr Val Gly His Ala Thr Gly Ser Gln Glu Lys Val Phe Ile Arg
 340 345 350
 Gly Asn Leu Glu Thr Arg Glu Phe Val Ala Phe Trp Val Asp Thr Glu
 355 360 365
 Asn Arg Ile Leu Ala Ala Met Asn Val Asn Val Trp Asp Val Pro Asp
 370 375 380
 Gln Ile Lys Pro Leu Ile Ala Ser Gly Lys Ser Val Asp Thr Glu Lys
 385 390 395 400
 Leu Val Asp Pro Glu Val Pro Tyr Ser Glu Leu
 405 410

<210> 387

<211> 572

<212> DNA

<213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (15)..(572)
 <223> RXA02828

<220>
 <221> misc_feature
 <222> (71)
 <223> n=a,c,g, or t

<400> 387

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          Met Lys Arg Arg Asp Phe Leu Ser Ala Leu Ser Ala
              1              5              10

ggc acc ctc tcg ctg ggc ggn ttt gcg ccc caa ctg ctg ctg gcc caa 98
Gly Thr Leu Ser Leu Gly Gly Phe Ala Pro Gln Leu Leu Leu Ala Gln
          15              20              25

ggg atg aat cag cca atg cgc gcg ccc att cat gtg ggt aaa tcg gcc 146
Gly Met Asn Gln Pro Met Arg Ala Pro Ile His Val Gly Lys Ser Gly
          30              35              40

ctg cgc gcc cgc gac gcc gag gcg ctt gcc acc tgg tac caa agc cac 194
Leu Arg Ala Arg Asp Ala Glu Ala Leu Ala Thr Trp Tyr Gln Ser His
          45              50              55              60

gtc ggc ctg caa gaa att ggc cgc gac ggc gcg acg atc cac atg ggt 242
Val Gly Leu Gln Glu Ile Gly Arg Asp Gly Ala Thr Ile His Met Gly
          65              70              75

gcg ggc ggc acc gtg ctg ctg gaa atc acg cag tac gac ggt atc gtg 290
Ala Gly Gly Thr Val Leu Leu Glu Ile Thr Gln Tyr Asp Gly Ile Val
          80              85              90

ctg gcg ccc atg cgc gtc gcg ggc ctt tat cac aac gcg ttc ctg ctg 338
Leu Ala Pro Met Arg Val Ala Gly Leu Tyr His Asn Ala Phe Leu Leu
          95              100              105

ccc gcg cgc gcg gat ctg gcg cgg tgg gtg ctg gac gcc tcg gca cgg 386
Pro Ala Arg Ala Asp Leu Ala Arg Trp Val Leu Asp Ala Ser Ala Arg
          110              115              120

caa ctg cgg atc gac ggc tat gcc gac cac ctt gtc agc gag gcg atg 434
Gln Leu Arg Ile Asp Gly Tyr Ala Asp His Leu Val Ser Glu Ala Met
          125              130              135              140

tac ctg acc gac ccc gaa ggc aac ggc gtc gaa atc tac gcc gac cgc 482
Tyr Leu Thr Asp Pro Glu Gly Asn Gly Val Glu Ile Tyr Ala Asp Arg
          145              150              155

ccc gcc agc gac tgg gtc tgg cgc aat ggt cag gtc gag atg gac agc 530
Pro Ala Ser Asp Trp Val Trp Arg Asn Gly Gln Val Glu Met Asp Ser
          160              165              170

ctg caa atc gac ttc tac agc atg atc gcc acg ctt gac ggc 572
Leu Gln Ile Asp Phe Tyr Ser Met Ile Ala Thr Leu Asp Gly
          175              180              185

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<210> 388

<211> 186
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 388
 Met Lys Arg Arg Asp Phe Leu Ser Ala Leu Ser Ala Gly Thr Leu Ser
 1 5 10 15
 Leu Gly Gly Phe Ala Pro Gln Leu Leu Leu Ala Gln Gly Met Asn Gln
 20 25 30
 Pro Met Arg Ala Pro Ile His Val Gly Lys Ser Gly Leu Arg Ala Arg
 35 40 45
 Asp Ala Glu Ala Leu Ala Thr Trp Tyr Gln Ser His Val Gly Leu Gln
 50 55 60
 Glu Ile Gly Arg Asp Gly Ala Thr Ile His Met Gly Ala Gly Gly Thr
 65 70 75 80
 Val Leu Leu Glu Ile Thr Gln Tyr Asp Gly Ile Val Leu Ala Pro Met
 85 90 95
 Arg Val Ala Gly Leu Tyr His Asn Ala Phe Leu Leu Pro Ala Arg Ala
 100 105 110
 Asp Leu Ala Arg Trp Val Leu Asp Ala Ser Ala Arg Gln Leu Arg Ile
 115 120 125
 Asp Gly Tyr Ala Asp His Leu Val Ser Glu Ala Met Tyr Leu Thr Asp
 130 135 140
 Pro Glu Gly Asn Gly Val Glu Ile Tyr Ala Asp Arg Pro Ala Ser Asp
 145 150 155 160
 Trp Val Trp Arg Asn Gly Gln Val Glu Met Asp Ser Leu Gln Ile Asp
 165 170 175
 Phe Tyr Ser Met Ile Ala Thr Leu Asp Gly
 180 185

<210> 389
 <211> 762
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(739)
 <223> RXA02064

<400> 389
 ctagattaca tcctgtgcat cttctggcaa ttgtgaattc atttgactt aatgcgtgta 60
 ggtacttcac atctcgctg ctcgctctag actataacgc gtg agt aac gcc ttc 115
 Val Ser Asn Ala Phe
 1 5
 gag tat ctt cgc act tat gtc gag tcc act act gaa acc gac gct gct 163
 Glu Tyr Leu Arg Thr Tyr Val Glu Ser Thr Thr Glu Thr Asp Ala Ala

	10	15	20	
gta gcg cgc gct cgt gaa gac gcc gcc gag ttc ggt ctc ccc gcc ccg				211
Val Ala Arg Ala Arg Glu Asp Ala Ala Glu Phe Gly Leu Pro Ala Pro				
	25	30	35	
gat gaa atg act ggc cag ctg cta acc act ttg gct gcc acc acc aat				259
Asp Glu Met Thr Gly Gln Leu Leu Thr Thr Leu Ala Ala Thr Thr Asn				
	40	45	50	
ggc aac ggc tcc act ggt gcc atc gcg att acc ccg gct gcc ggg ttg				307
Gly Asn Gly Ser Thr Gly Ala Ile Ala Ile Thr Pro Ala Ala Gly Leu				
	55	60	65	
gtg ggt ctg tat atc ctg aac gga ctg gcc gat aac acc aca ctg acc				355
Val Gly Leu Tyr Ile Leu Asn Gly Leu Ala Asp Asn Thr Thr Leu Thr				
	70	75	80	85
tgc att gat cct gaa tca gag cat cag cgc cag gcc aaa gca ctc ttc				403
Cys Ile Asp Pro Glu Ser Glu His Gln Arg Gln Ala Lys Ala Leu Phe				
	90	95	100	
cgc gag gcc ggc tat tcc ccc agc cgc gta cgc ttc ttg ctc tcg cgc				451
Arg Glu Ala Gly Tyr Ser Pro Ser Arg Val Arg Phe Leu Leu Ser Arg				
	105	110	115	
ccg ctc gac gtg atg agt cgc ctt gcc aac gac agc tat cag ctt gtc				499
Pro Leu Asp Val Met Ser Arg Leu Ala Asn Asp Ser Tyr Gln Leu Val				
	120	125	130	
ttc ggc caa gtc tcc ccc atg gat tta aag gcg ctt gtc gac gcc gcc				547
Phe Gly Gln Val Ser Pro Met Asp Leu Lys Ala Leu Val Asp Ala Ala				
	135	140	145	
tgg ccg ctt ctt cga cga ggc ggt gcg ctg gtg ctc gcc gat gcg ctc				595
Trp Pro Leu Leu Arg Arg Gly Gly Ala Leu Val Leu Ala Asp Ala Leu				
	150	155	160	165
ctt gac ggc acc att gcg gat caa acc cgc aag gat cgt gac acc caa				643
Leu Asp Gly Thr Ile Ala Asp Gln Thr Arg Lys Asp Arg Asp Thr Gln				
	170	175	180	
gca gca cgt gac gcc gat gaa tat att cgt tcc att gaa ggc gca cac				691
Ala Ala Arg Asp Ala Asp Glu Tyr Ile Arg Ser Ile Glu Gly Ala His				
	185	190	195	
gtt gct cgc ctg ccc ctt ggt gca ggc tta acc gtg gtg act aaa gcc				739
Val Ala Arg Leu Pro Leu Gly Ala Gly Leu Thr Val Val Thr Lys Ala				
	200	205	210	
tagaggggga cgtcgagaag cga				762

<210> 390

<211> 213

<212> PRT

<213> Corynebacterium glutamicum

<400> 390

Val	Ser	Asn	Ala	Phe	Glu	Tyr	Leu	Arg	Thr	Tyr	Val	Glu	Ser	Thr	Thr
1					5				10					15	


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<210> 391
<211> 978
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(955)
<223> RXN00639
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<400> 391
agtgttgтта  tсgagttcag  ccgatcacaа  agattttttcc  gctaggcagt  gatccgactc  60
gcaccccccta  cttcaccccc  aaagtctcta  ggagtatgac  atg  act  tca  gct  gaa      115
                                     Met Thr Ser Ala Glu
                                     1                               5

cag  atc  gtt  gat  cca  аca  gcc  cac  gat  tсg  ggc  аac  аag  gca  act  gac      163
Gln Ile Val Asp Pro Thr Ala His Asp Ser Gly Asn Lys Ala Thr Asp
          10                      15                      20

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aag ttc aag gca aac cgc gtt tcc tcc gat acc tcc aag gaa cgc gca	211
Lys Phe Lys Ala Asn Arg Val Ser Ser Asp Thr Ser Lys Glu Arg Ala	
25 30 35	
aac gcg atc tac gta gat ctg ctc gcg gcg atc gcc cag gtt gct cac	259
Asn Ala Ile Tyr Val Asp Leu Leu Ala Ala Ile Ala Gln Val Ala His	
40 45 50	
aag cac gaa gtc acc tac gaa gag tac gca gtg ctc aag cag tgg atg	307
Lys His Glu Val Thr Tyr Glu Glu Tyr Ala Val Leu Lys Gln Trp Met	
55 60 65	
atc gac gtt gga gaa tac ggc gag tgg cca ctg tgg ttg gac gtt ttc	355
Ile Asp Val Gly Glu Tyr Gly Glu Trp Pro Leu Trp Leu Asp Val Phe	
70 75 80 85	
gtt gag cat gag atc gaa gag atc aac tac aac cgc cac gac tac acc	403
Val Glu His Glu Ile Glu Glu Ile Asn Tyr Asn Arg His Asp Tyr Thr	
90 95 100	
gga acc aag ggt tcc atc gaa ggc cct tat tac gta gag aac tct ccg	451
Gly Thr Lys Gly Ser Ile Glu Gly Pro Tyr Tyr Val Glu Asn Ser Pro	
105 110 115	
aag ctc cct tgg gat gct gaa atg cca atg cgt gac aag gac cgc gca	499
Lys Leu Pro Trp Asp Ala Glu Met Pro Met Arg Asp Lys Asp Arg Ala	
120 125 130	
tgc acc cca ctg atc ttc gag ggg cag gtt act gac ctc gac ggc aac	547
Cys Thr Pro Leu Ile Phe Glu Gly Gln Val Thr Asp Leu Asp Gly Asn	
135 140 145	
ggt ctt gat gga gca gaa gtt gag ctc tgg cac gca gat gag gac gga	595
Gly Leu Asp Gly Ala Glu Val Glu Leu Trp His Ala Asp Glu Asp Gly	
150 155 160 165	
tac tac tcc cag ttc gcg cct gga atc cca gag tgg aac ctg cgt ggc	643
Tyr Tyr Ser Gln Phe Ala Pro Gly Ile Pro Glu Trp Asn Leu Arg Gly	
170 175 180	
acc atc gtt acc gat gag gaa ggc cgc tac aag atc aag acc ctg cag	691
Thr Ile Val Thr Asp Glu Glu Gly Arg Tyr Lys Ile Lys Thr Leu Gln	
185 190 195	
cct gcg cct tac cag atc cct cat gat ggc cca acc ggt tgg ttc att	739
Pro Ala Pro Tyr Gln Ile Pro His Asp Gly Pro Thr Gly Trp Phe Ile	
200 205 210	
gag tct tac ggt ggg cac cca tgg cgc cca gcc cac ctc cac ttg cgc	787
Glu Ser Tyr Gly Gly His Pro Trp Arg Pro Ala His Leu His Leu Arg	
215 220 225	
gtt tcc cac ccg ggc tac cgc acc atc acc acc cag ctt tac ttc gag	835
Val Ser His Pro Gly Tyr Arg Thr Ile Thr Thr Gln Leu Tyr Phe Glu	
230 235 240 245	
ggt ggc gag tgg gtc gaa aac gac gtt gca acc gct gtg aag cca gaa	883
Gly Gly Glu Trp Val Glu Asn Asp Val Ala Thr Ala Val Lys Pro Glu	
250 255 260	

ctg gtc ctg cac cct gag act ggc gag gat ggt aac cac gtt cac tac 931
 Leu Val Leu His Pro Glu Thr Gly Glu Asp Gly Asn His Val His Tyr
 265 270 275

cca ttc gtc ctg gat aag gaa gac tagtttttct acctagctag cat 978
 Pro Phe Val Leu Asp Lys Glu Asp
 280 285

<210> 392

<211> 285

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 392

Met Thr Ser Ala Glu Gln Ile Val Asp Pro Thr Ala His Asp Ser Gly
 1 5 10 15

Asn Lys Ala Thr Asp Lys Phe Lys Ala Asn Arg Val Ser Ser Asp Thr
 20 25 30

Ser Lys Glu Arg Ala Asn Ala Ile Tyr Val Asp Leu Leu Ala Ala Ile
 35 40 45

Ala Gln Val Ala His Lys His Glu Val Thr Tyr Glu Glu Tyr Ala Val
 50 55 60

Leu Lys Gln Trp Met Ile Asp Val Gly Glu Tyr Gly Glu Trp Pro Leu
 65 70 75 80

Trp Leu Asp Val Phe Val Glu His Glu Ile Glu Glu Ile Asn Tyr Asn
 85 90 95

Arg His Asp Tyr Thr Gly Thr Lys Gly Ser Ile Glu Gly Pro Tyr Tyr
 100 105 110

Val Glu Asn Ser Pro Lys Leu Pro Trp Asp Ala Glu Met Pro Met Arg
 115 120 125

Asp Lys Asp Arg Ala Cys Thr Pro Leu Ile Phe Glu Gly Gln Val Thr
 130 135 140

Asp Leu Asp Gly Asn Gly Leu Asp Gly Ala Glu Val Glu Leu Trp His
 145 150 155 160

Ala Asp Glu Asp Gly Tyr Tyr Ser Gln Phe Ala Pro Gly Ile Pro Glu
 165 170 175

Trp Asn Leu Arg Gly Thr Ile Val Thr Asp Glu Glu Gly Arg Tyr Lys
 180 185 190

Ile Lys Thr Leu Gln Pro Ala Pro Tyr Gln Ile Pro His Asp Gly Pro
 195 200 205

Thr Gly Trp Phe Ile Glu Ser Tyr Gly Gly His Pro Trp Arg Pro Ala
 210 215 220

His Leu His Leu Arg Val Ser His Pro Gly Tyr Arg Thr Ile Thr Thr
 225 230 235 240

Gln Leu Tyr Phe Glu Gly Gly Glu Trp Val Glu Asn Asp Val Ala Thr

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                245                250                255
Ala Val Lys Pro Glu Leu Val Leu His Pro Glu Thr Gly Glu Asp Gly
                260                265                270

Asn His Val His Tyr Pro Phe Val Leu Asp Lys Glu Asp
                275                280                285

<210> 393
<211> 760
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(760)
<223> FRXA00639

<400> 393
agtgttgta tcgagttcag ccgatcacia agatTTTTcc gctaggcagt gatccgactc 60

gcaccccccta cttcaccccc aaagtctcta ggagtatgac atg act tca gct gaa 115
                                         Met Thr Ser Ala Glu
                                         1                    5

cag atc gtt gat cca aca gcc cac gat tcg ggc aac aag gca act gac 163
Gln Ile Val Asp Pro Thr Ala His Asp Ser Gly Asn Lys Ala Thr Asp
                10                15                20

aag ttc aag gca aac cgc gtt tcc tcc gat acc tcc aag gaa cgc gca 211
Lys Phe Lys Ala Asn Arg Val Ser Ser Asp Thr Ser Lys Glu Arg Ala
                25                30                35

aac gcg atc tac gta gat ctg ctc gcg gcg atc gcc cag gtt gct cac 259
Asn Ala Ile Tyr Val Asp Leu Leu Ala Ala Ile Ala Gln Val Ala His
                40                45                50

aag cac gaa gtc acc tac gaa gag tac gca gtg ctc aag cag tgg atg 307
Lys His Glu Val Thr Tyr Glu Glu Tyr Ala Val Leu Lys Gln Trp Met
                55                60                65

atc gac gtt gga gaa tac gcc gag tgg cca ctg tgg ttg gac gtt ttc 355
Ile Asp Val Gly Glu Tyr Gly Glu Trp Pro Leu Trp Leu Asp Val Phe
                70                75                80                85

gtt gag cat gag atc gaa gag atc aac tac aac cgc cac gac tac acc 403
Val Glu His Glu Ile Glu Glu Ile Asn Tyr Asn Arg His Asp Tyr Thr
                90                95                100

gga acc aag ggt tcc atc gaa gcc cct tat tac gta gag aac tct ccg 451
Gly Thr Lys Gly Ser Ile Glu Gly Pro Tyr Tyr Val Glu Asn Ser Pro
                105                110                115

aag ctc cct tgg gat gct gaa atg cca atg cgt gac aag gac cgc gca 499
Lys Leu Pro Trp Asp Ala Glu Met Pro Met Arg Asp Lys Asp Arg Ala
                120                125                130

tgc acc cca ctg atc ttc gag ggg cag gtt act gac ctc gac ggc aac 547
Cys Thr Pro Leu Ile Phe Glu Gly Gln Val Thr Asp Leu Asp Gly Asn
                135                140                145

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ggt ctt gat gga gca gaa gtt gag ctc tgg cac gca gat gag gac gga 595
 Gly Leu Asp Gly Ala Glu Val Glu Leu Trp His Ala Asp Glu Asp Gly
 150 155 160 165

tac tac tcc cag ttc gcg cct gga atc cca gag tgg aac ctg cgt ggc 643
 Tyr Tyr Ser Gln Phe Ala Pro Gly Ile Pro Glu Trp Asn Leu Arg Gly
 170 175 180

acc atc gtt acc gat gag gaa ggc cgc tac aag atc aag acc ctg cag 691
 Thr Ile Val Thr Asp Glu Glu Gly Tyr Lys Ile Lys Thr Leu Gln
 185 190 195

cct gcg cct tac cag atc cct cat gat ggc cca acc ggt tgg ttc att 739
 Pro Ala Pro Tyr Gln Ile Pro His Asp Gly Pro Thr Gly Trp Phe Ile
 200 205 210

gag tct tac ggt ggg cac cca 760
 Glu Ser Tyr Gly Gly His Pro
 215 220

<210> 394

<211> 220

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 394

Met Thr Ser Ala Glu Gln Ile Val Asp Pro Thr Ala His Asp Ser Gly
 1 5 10 15

Asn Lys Ala Thr Asp Lys Phe Lys Ala Asn Arg Val Ser Ser Asp Thr
 20 25 30

Ser Lys Glu Arg Ala Asn Ala Ile Tyr Val Asp Leu Leu Ala Ala Ile
 35 40 45

Ala Gln Val Ala His Lys His Glu Val Thr Tyr Glu Glu Tyr Ala Val
 50 55 60

Leu Lys Gln Trp Met Ile Asp Val Gly Glu Tyr Gly Glu Trp Pro Leu
 65 70 75 80

Trp Leu Asp Val Phe Val Glu His Glu Ile Glu Glu Ile Asn Tyr Asn
 85 90 95

Arg His Asp Tyr Thr Gly Thr Lys Gly Ser Ile Glu Gly Pro Tyr Tyr
 100 105 110

Val Glu Asn Ser Pro Lys Leu Pro Trp Asp Ala Glu Met Pro Met Arg
 115 120 125

Asp Lys Asp Arg Ala Cys Thr Pro Leu Ile Phe Glu Gly Gln Val Thr
 130 135 140

Asp Leu Asp Gly Asn Gly Leu Asp Gly Ala Glu Val Glu Leu Trp His
 145 150 155 160

Ala Asp Glu Asp Gly Tyr Tyr Ser Gln Phe Ala Pro Gly Ile Pro Glu
 165 170 175

Trp Asn Leu Arg Gly Thr Ile Val Thr Asp Glu Glu Gly Arg Tyr Lys
 180 185 190

Ile Lys Thr Leu Gln Pro Ala Pro Tyr Gln Ile Pro His Asp Gly Pro
 195 200 205

Thr Gly Trp Phe Ile Glu Ser Tyr Gly Gly His Pro
 210 215 220

<210> 395

<211> 1584

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1561)

<223> RXN01653

<400> 395

ttcattcagg gtgaatgctc tccttggttc agatgttcaa cgctccataa agtagaccgc 60

aatctagaca aagatgtcta ttttaattaa ggagcagaac atg gcc acg gcc gag 115
 Met Ala Thr Ala Glu
 1 5

aac aca aca cag gag aat cgg aaa atc ctg ttc aac gca ttt gat atg 163
 Asn Thr Thr Gln Glu Asn Arg Lys Ile Leu Phe Asn Ala Phe Asp Met
 10 15 20

aac tgc gtt gcg cat cag tcc cca gga ctg tgg aca cac ccg aag gat 211
 Asn Cys Val Ala His Gln Ser Pro Gly Leu Trp Thr His Pro Lys Asp
 25 30 35

aag gcg cga gac tac aac act ctt gat tac tgg gtg cac ctt gcc aag 259
 Lys Ala Arg Asp Tyr Asn Thr Leu Asp Tyr Trp Val His Leu Ala Lys
 40 45 50

act ttg gag aag ggc ctt ttc gac ggc ctt ttc atc gca gat gtg ctt 307
 Thr Leu Glu Lys Gly Leu Phe Asp Gly Leu Phe Ile Ala Asp Val Leu
 55 60 65

gga act tac gat gtt tat ggt tct agt aat gaa gcg gcg ttg agc agt 355
 Gly Thr Tyr Asp Val Tyr Gly Ser Ser Asn Glu Ala Ala Leu Ser Ser
 70 75 80 85

ggt gcg cag gtg cct gtc aat gat ccg atc ctt ctt gtt tct gcg atg 403
 Gly Ala Gln Val Pro Val Asn Asp Pro Ile Leu Leu Val Ser Ala Met
 90 95 100

gcc tat gcc aca aag aac ctc ggg ttt ggc att act gca ggt act gcc 451
 Ala Tyr Ala Thr Lys Asn Leu Gly Phe Gly Ile Thr Ala Gly Thr Ala
 105 110 115

tat gag cac ccg tat cct ttt gcg cgg cgt ctg gcc aca ctt gat cac 499
 Tyr Glu His Pro Tyr Pro Phe Ala Arg Arg Leu Ala Thr Leu Asp His
 120 125 130

ctg act aat ggg cgt gtg ggg tgg aat gtg gtt act ggc tat ctt ccc 547
 Leu Thr Asn Gly Arg Val Gly Trp Asn Val Val Thr Gly Tyr Leu Pro

135	140	145	
tct gct gct caa aac atg ggt gac acc gat cag ctg cca cat gat gag Ser Ala Ala Gln Asn Met Gly Asp Thr Asp Gln Leu Pro His Asp Glu 150 155 160 165			595
cgc tat gac aaa gca gat gaa tac ctg gaa gtg atc tac aag ctt ctc Arg Tyr Asp Lys Ala Asp Glu Tyr Leu Glu Val Ile Tyr Lys Leu Leu 170 175 180			643
gag ggc tcc tgg gaa gac gat gct gtt caa aac aat acg gag acg agt Glu Gly Ser Trp Glu Asp Asp Ala Val Gln Asn Asn Thr Glu Thr Ser 185 190 195			691
gtc ttt acg gac tcc tcc aaa gtg cac gcc att aat cat cat ggc aag Val Phe Thr Asp Ser Ser Lys Val His Ala Ile Asn His His Gly Lys 200 205 210			739
tac ttt gat gtg ccg ggc att gcc atc act gag ccg agt gtg cag cgt Tyr Phe Asp Val Pro Gly Ile Ala Ile Thr Glu Pro Ser Val Gln Arg 215 220 225			787
acg ccg gtg atc tac cag gcg ggt gca tcg ccg cgc gga ttg aaa ttc Thr Pro Val Ile Tyr Gln Ala Gly Ala Ser Pro Arg Gly Leu Lys Phe 230 235 240 245			835
gct ggt gag aat gca gaa gca gtg ttt atc aat tcc agc acc gtg gag Ala Gly Glu Asn Ala Glu Ala Val Phe Ile Asn Ser Ser Thr Val Glu 250 255 260			883
gca atc acc aag act gtc gca aaa att cgc gct gct gcg gtc gct gcg Ala Ile Thr Lys Thr Val Ala Lys Ile Arg Ala Ala Val Ala Ala 265 270 275			931
gga cgt gat cca cat gcg gtg aag atc ttt gcg atg caa acc atc atc Gly Arg Asp Pro His Ala Val Lys Ile Phe Ala Met Gln Thr Ile Ile 280 285 290			979
act ggt gaa aca gaa gca gat gcg cag gca aag ctg gag gaa tac agt Thr Gly Glu Thr Glu Ala Asp Ala Gln Ala Lys Leu Glu Glu Tyr Ser 295 300 305			1027
cgc tat atc gat cct gtc ggt ggt ctg acc ttg atg tct gga tgg acc Arg Tyr Ile Asp Pro Val Gly Gly Leu Thr Leu Met Ser Gly Trp Thr 310 315 320 325			1075
ggc gcg gat ctg tcg cag tat gac ctg gat gaa ccg atc acc aat att Gly Ala Asp Leu Ser Gln Tyr Asp Leu Asp Glu Pro Ile Thr Asn Ile 330 335 340			1123
gag tca aac gct att cag tcc act gca gcc acc att agc aac ggc acc Glu Ser Asn Ala Ile Gln Ser Thr Ala Ala Thr Ile Ser Asn Gly Thr 345 350 355			1171
ggt gaa ggt gcg tgg acg gta cgc aaa ctg ggt gag gca acc ggc atc Gly Glu Gly Ala Trp Thr Val Arg Lys Leu Gly Glu Ala Thr Gly Ile 360 365 370			1219
ggc ggc ttc gga cca gtg ctt gtg gga tct ggc gct aac gtt gcc gcg Gly Gly Phe Gly Pro Val Leu Val Gly Ser Gly Ala Asn Val Ala Ala 375 380 385			1267

gaa ctt gca cgc atc cag gat ctc agc gat gtt gat ggt ttc aac ctt 1315
 Glu Leu Ala Arg Ile Gln Asp Leu Ser Asp Val Asp Gly Phe Asn Leu
 390 395 400 405
 gct tat gcc atc acc cca gga act ttt gaa gat gtc gtg gac ttt gtg 1363
 Ala Tyr Ala Ile Thr Pro Gly Thr Phe Glu Asp Val Val Asp Phe Val
 410 415 420
 gtg cct gag ctg caa aaa ctt agc cgc tac aag acg gaa tac gcg ccg 1411
 Val Pro Glu Leu Gln Lys Leu Ser Arg Tyr Lys Thr Glu Tyr Ala Pro
 425 430 435
 ggt tcc ttg cgc aac aaa ttg ctc ggt aaa ggt gat cgc ctg gac gat 1459
 Gly Ser Leu Arg Asn Lys Leu Leu Gly Lys Gly Asp Arg Leu Asp Asp
 440 445 450
 acc cac cgc ggc gca agc tac cgc cta ggc gct cgg aac tcc acc gcc 1507
 Thr His Arg Gly Ala Ser Tyr Arg Leu Gly Ala Arg Asn Ser Thr Ala
 455 460 465
 act att gat ctc agt tcc ata tcc gcc caa cta gtt tcc cag gga gcc 1555
 Thr Ile Asp Leu Ser Ser Ile Ser Ala Gln Leu Val Ser Gln Gly Ala
 470 475 480 485
 cac tca tgatctcacc gcaaacaatc atc 1584
 His Ser

<210> 396

<211> 487

<212> PRT

<213> Corynebacterium glutamicum

<400> 396

Met Ala Thr Ala Glu Asn Thr Thr Gln Glu Asn Arg Lys Ile Leu Phe
 1 5 10 15
 Asn Ala Phe Asp Met Asn Cys Val Ala His Gln Ser Pro Gly Leu Trp
 20 25 30
 Thr His Pro Lys Asp Lys Ala Arg Asp Tyr Asn Thr Leu Asp Tyr Trp
 35 40 45
 Val His Leu Ala Lys Thr Leu Glu Lys Gly Leu Phe Asp Gly Leu Phe
 50 55 60
 Ile Ala Asp Val Leu Gly Thr Tyr Asp Val Tyr Gly Ser Ser Asn Glu
 65 70 75 80
 Ala Ala Leu Ser Ser Gly Ala Gln Val Pro Val Asn Asp Pro Ile Leu
 85 90 95
 Leu Val Ser Ala Met Ala Tyr Ala Thr Lys Asn Leu Gly Phe Gly Ile
 100 105 110
 Thr Ala Gly Thr Ala Tyr Glu His Pro Tyr Pro Phe Ala Arg Arg Leu
 115 120 125
 Ala Thr Leu Asp His Leu Thr Asn Gly Arg Val Gly Trp Asn Val Val

130	135	140
Thr Gly Tyr Leu Pro Ser Ala Ala Gln Asn Met Gly Asp Thr Asp Gln 145 150 155 160		
Leu Pro His Asp Glu Arg Tyr Asp Lys Ala Asp Glu Tyr Leu Glu Val 165 170 175		
Ile Tyr Lys Leu Leu Glu Gly Ser Trp Glu Asp Asp Ala Val Gln Asn 180 185 190		
Asn Thr Glu Thr Ser Val Phe Thr Asp Ser Ser Lys Val His Ala Ile 195 200 205		
Asn His His Gly Lys Tyr Phe Asp Val Pro Gly Ile Ala Ile Thr Glu 210 215 220		
Pro Ser Val Gln Arg Thr Pro Val Ile Tyr Gln Ala Gly Ala Ser Pro 225 230 235 240		
Arg Gly Leu Lys Phe Ala Gly Glu Asn Ala Glu Ala Val Phe Ile Asn 245 250 255		
Ser Ser Thr Val Glu Ala Ile Thr Lys Thr Val Ala Lys Ile Arg Ala 260 265 270		
Ala Ala Val Ala Ala Gly Arg Asp Pro His Ala Val Lys Ile Phe Ala 275 280 285		
Met Gln Thr Ile Ile Thr Gly Glu Thr Glu Ala Asp Ala Gln Ala Lys 290 295 300		
Leu Glu Glu Tyr Ser Arg Tyr Ile Asp Pro Val Gly Gly Leu Thr Leu 305 310 315 320		
Met Ser Gly Trp Thr Gly Ala Asp Leu Ser Gln Tyr Asp Leu Asp Glu 325 330 335		
Pro Ile Thr Asn Ile Glu Ser Asn Ala Ile Gln Ser Thr Ala Ala Thr 340 345 350		
Ile Ser Asn Gly Thr Gly Glu Gly Ala Trp Thr Val Arg Lys Leu Gly 355 360 365		
Glu Ala Thr Gly Ile Gly Gly Phe Gly Pro Val Leu Val Gly Ser Gly 370 375 380		
Ala Asn Val Ala Ala Glu Leu Ala Arg Ile Gln Asp Leu Ser Asp Val 385 390 395 400		
Asp Gly Phe Asn Leu Ala Tyr Ala Ile Thr Pro Gly Thr Phe Glu Asp 405 410 415		
Val Val Asp Phe Val Val Pro Glu Leu Gln Lys Leu Ser Arg Tyr Lys 420 425 430		
Thr Glu Tyr Ala Pro Gly Ser Leu Arg Asn Lys Leu Leu Gly Lys Gly 435 440 445		
Asp Arg Leu Asp Asp Thr His Arg Gly Ala Ser Tyr Arg Leu Gly Ala 450 455 460		

Arg Asn Ser Thr Ala Thr Ile Asp Leu Ser Ser Ile Ser Ala Gln Leu
 465 470 475 480

Val Ser Gln Gly Ala His Ser
 485

<210> 397

<211> 460

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(460)

<223> FRXA00797

<400> 397

ttcattcagg gtgaatgctc tccttgtttc agatgttcaa cgctccataa agtagaccgc 60

aatctagaca aagatgtcta ttttaattaa ggagcagaac atg gcc acg gcc gag 115
 Met Ala Thr Ala Glu
 1 5

aac aca aca cag gag aat cgg aaa atc ctg ttc aac gca ttt gat atg 163
 Asn Thr Thr Gln Glu Asn Arg Lys Ile Leu Phe Asn Ala Phe Asp Met
 10 15 20

aac tgc gtt gcg cat cag tcc cca gga ctg tgg aca cac ccg aag gat 211
 Asn Cys Val Ala His Gln Ser Pro Gly Leu Trp Thr His Pro Lys Asp
 25 30 35

aag gcg cga gac tac aac act ctt gat tac tgg gtg cac ctt gcc aag 259
 Lys Ala Arg Asp Tyr Asn Thr Leu Asp Tyr Trp Val His Leu Ala Lys
 40 45 50

act ttg gag aag ggc ctt ttc gac ggc ctt ttc atc gca gat gtg ctt 307
 Thr Leu Glu Lys Gly Leu Phe Asp Gly Leu Phe Ile Ala Asp Val Leu
 55 60 65

gga act tac gat gtt tat ggt tct agt aat gaa gcg gcg ttg agc agt 355
 Gly Thr Tyr Asp Val Tyr Gly Ser Ser Asn Glu Ala Ala Leu Ser Ser
 70 75 80 85

ggt gcg cag gtg cct gtc aat gat ccg atc ctt ctt gtt tct gcg atg 403
 Gly Ala Gln Val Pro Val Asn Asp Pro Ile Leu Leu Val Ser Ala Met
 90 95 100

gcc tat gcc aca aag aac ctc ggg ttt ggc att act gca ggt act gcc 451
 Ala Tyr Ala Thr Lys Asn Leu Gly Phe Gly Ile Thr Ala Gly Thr Ala
 105 110 115

tat gag cac 460
 Tyr Glu His
 120

<210> 398

<211> 120

<212> PRT

<213> Corynebacterium glutamicum

<400> 398

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Met Ala Thr Ala Glu Asn Thr Thr Gln Glu Asn Arg Lys Ile Leu Phe
 1             5             10             15

Asn Ala Phe Asp Met Asn Cys Val Ala His Gln Ser Pro Gly Leu Trp
          20             25             30

Thr His Pro Lys Asp Lys Ala Arg Asp Tyr Asn Thr Leu Asp Tyr Trp
          35             40             45

Val His Leu Ala Lys Thr Leu Glu Lys Gly Leu Phe Asp Gly Leu Phe
 50             55             60

Ile Ala Asp Val Leu Gly Thr Tyr Asp Val Tyr Gly Ser Ser Asn Glu
 65             70             75             80

Ala Ala Leu Ser Ser Gly Ala Gln Val Pro Val Asn Asp Pro Ile Leu
          85             90             95

Leu Val Ser Ala Met Ala Tyr Ala Thr Lys Asn Leu Gly Phe Gly Ile
          100             105             110

Thr Ala Gly Thr Ala Tyr Glu His
      115             120

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<210> 399

<211> 962

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(939)

<223> FRXA01653

<400> 399

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gga agt gat cta caa gct tct cga ggg ctc ctg gaa gac gat gct gtt      48
Gly Ser Asp Leu Gln Ala Ser Arg Gly Leu Leu Glu Asp Asp Ala Val
 1             5             10             15

caa aac aat acg gag acg agt gtc ttt acg gac tcc tcc aaa gtg cac      96
Gln Asn Asn Thr Glu Thr Ser Val Phe Thr Asp Ser Ser Lys Val His
          20             25             30

gcc att aat cat cat ggc aag tac ttt gat gtg ccg ggc att gcc atc     144
Ala Ile Asn His His Gly Lys Tyr Phe Asp Val Pro Gly Ile Ala Ile
          35             40             45

act gag ccg agt gtg cag cgt acg ccg gtg atc tac cag gcg ggt gca     192
Thr Glu Pro Ser Val Gln Arg Thr Pro Val Ile Tyr Gln Ala Gly Ala
          50             55             60

tcg ccg cgc gga ttg aaa ttc gct ggt gag aat gca gaa gca gtg ttt     240
Ser Pro Arg Gly Leu Lys Phe Ala Gly Glu Asn Ala Glu Ala Val Phe
          65             70             75             80

atc aat tcc agc acc gtg gag gca atc acc aag act gtc gca aaa att     288
Ile Asn Ser Ser Thr Val Glu Ala Ile Thr Lys Thr Val Ala Lys Ile

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85										90					95					
cgc	gct	gct	gcg	gtc	gct	gcg	gga	cgt	gat	cca	cat	gcg	gtg	aag	atc	336				
Arg	Ala	Ala	Ala	Val	Ala	Ala	Gly	Arg	Asp	Pro	His	Ala	Val	Lys	Ile					
			100					105					110							
ttt	gcg	atg	caa	acc	atc	atc	act	ggg	gaa	aca	gaa	gca	gat	gcg	cag	384				
Phe	Ala	Met	Gln	Thr	Ile	Ile	Thr	Gly	Glu	Thr	Glu	Ala	Asp	Ala	Gln					
		115					120					125								
gca	aag	ctg	gag	gaa	tac	agt	cgc	tat	atc	gat	cct	gtc	ggg	ggg	ctg	432				
Ala	Lys	Leu	Glu	Glu	Tyr	Ser	Arg	Tyr	Ile	Asp	Pro	Val	Gly	Gly	Leu					
		130				135					140									
acc	ttg	atg	tct	gga	tgg	acc	ggc	gcg	gat	ctg	tcg	cag	tat	gac	ctg	480				
Thr	Leu	Met	Ser	Gly	Trp	Thr	Gly	Ala	Asp	Leu	Ser	Gln	Tyr	Asp	Leu					
		145			150					155					160					
gat	gaa	ccg	atc	acc	aat	att	gag	tca	aac	gct	att	cag	tcc	act	gca	528				
Asp	Glu	Pro	Ile	Thr	Asn	Ile	Glu	Ser	Asn	Ala	Ile	Gln	Ser	Thr	Ala					
				165					170					175						
gcc	acc	att	agc	aac	ggc	acc	ggg	gaa	ggg	gcg	tgg	acg	gta	cgc	aaa	576				
Ala	Thr	Ile	Ser	Asn	Gly	Thr	Gly	Glu	Gly	Ala	Trp	Thr	Val	Arg	Lys					
			180					185					190							
ctg	ggg	gag	gca	acc	ggc	atc	ggc	ggc	ttc	gga	cca	gtg	ctt	gtg	gga	624				
Leu	Gly	Glu	Ala	Thr	Gly	Ile	Gly	Gly	Phe	Gly	Pro	Val	Leu	Val	Gly					
		195				200						205								
tct	ggc	gct	aac	gtt	gcc	gcg	gaa	ctt	gca	cgc	atc	cag	gat	ctc	agc	672				
Ser	Gly	Ala	Asn	Val	Ala	Ala	Glu	Leu	Ala	Arg	Ile	Gln	Asp	Leu	Ser					
		210				215					220									
gat	gtt	gat	ggg	ttc	aac	ctt	gct	tat	gcc	atc	acc	cca	gga	act	ttt	720				
Asp	Val	Asp	Gly	Phe	Asn	Leu	Ala	Tyr	Ala	Ile	Thr	Pro	Gly	Thr	Phe					
		225			230					235					240					
gaa	gat	gtc	gtg	gac	ttt	gtg	gtg	cct	gag	ctg	caa	aaa	ctt	agc	cgc	768				
Glu	Asp	Val	Val	Asp	Phe	Val	Val	Pro	Glu	Leu	Gln	Lys	Leu	Ser	Arg					
				245					250					255						
tac	aag	acg	gaa	tac	gcg	ccg	ggg	tcc	ttg	cgc	aac	aaa	ttg	ctc	ggg	816				
Tyr	Lys	Thr	Glu	Tyr	Ala	Pro	Gly	Ser	Leu	Arg	Asn	Lys	Leu	Leu	Gly					
			260					265					270							
aaa	ggg	gat	cgc	ctg	gac	gat	acc	cac	cgc	ggc	gca	agc	tac	cgc	cta	864				
Lys	Gly	Asp	Arg	Leu	Asp	Asp	Thr	His	Arg	Gly	Ala	Ser	Tyr	Arg	Leu					
		275					280					285								
ggc	gct	cgg	aac	tcc	acc	gcc	act	att	gat	ctc	agt	tcc	ata	tcc	gcc	912				
Gly	Ala	Arg	Asn	Ser	Thr	Ala	Thr	Ile	Asp	Leu	Ser	Ser	Ile	Ser	Ala					
		290				295					300									
caa	cta	gtt	tcc	cag	gga	gcc	cac	tca	tgatctcacc	gcaaacaatc	atc					962				
Gln	Leu	Val	Ser	Gln	Gly	Ala	His	Ser												
		305			310															

<210> 400

<211> 313

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 400

Gly	Ser	Asp	Leu	Gln	Ala	Ser	Arg	Gly	Leu	Leu	Glu	Asp	Asp	Ala	Val	1	5	10	15
Gln	Asn	Asn	Thr	Glu	Thr	Ser	Val	Phe	Thr	Asp	Ser	Ser	Lys	Val	His	20	25	30	
Ala	Ile	Asn	His	His	Gly	Lys	Tyr	Phe	Asp	Val	Pro	Gly	Ile	Ala	Ile	35	40	45	
Thr	Glu	Pro	Ser	Val	Gln	Arg	Thr	Pro	Val	Ile	Tyr	Gln	Ala	Gly	Ala	50	55	60	
Ser	Pro	Arg	Gly	Leu	Lys	Phe	Ala	Gly	Glu	Asn	Ala	Glu	Ala	Val	Phe	65	70	75	80
Ile	Asn	Ser	Ser	Thr	Val	Glu	Ala	Ile	Thr	Lys	Thr	Val	Ala	Lys	Ile	85	90	95	
Arg	Ala	Ala	Ala	Val	Ala	Ala	Gly	Arg	Asp	Pro	His	Ala	Val	Lys	Ile	100	105	110	
Phe	Ala	Met	Gln	Thr	Ile	Ile	Thr	Gly	Glu	Thr	Glu	Ala	Asp	Ala	Gln	115	120	125	
Ala	Lys	Leu	Glu	Glu	Tyr	Ser	Arg	Tyr	Ile	Asp	Pro	Val	Gly	Gly	Leu	130	135	140	
Thr	Leu	Met	Ser	Gly	Trp	Thr	Gly	Ala	Asp	Leu	Ser	Gln	Tyr	Asp	Leu	145	150	155	160
Asp	Glu	Pro	Ile	Thr	Asn	Ile	Glu	Ser	Asn	Ala	Ile	Gln	Ser	Thr	Ala	165	170	175	
Ala	Thr	Ile	Ser	Asn	Gly	Thr	Gly	Glu	Gly	Ala	Trp	Thr	Val	Arg	Lys	180	185	190	
Leu	Gly	Glu	Ala	Thr	Gly	Ile	Gly	Gly	Phe	Gly	Pro	Val	Leu	Val	Gly	195	200	205	
Ser	Gly	Ala	Asn	Val	Ala	Ala	Glu	Leu	Ala	Arg	Ile	Gln	Asp	Leu	Ser	210	215	220	
Asp	Val	Asp	Gly	Phe	Asn	Leu	Ala	Tyr	Ala	Ile	Thr	Pro	Gly	Thr	Phe	225	230	235	240
Glu	Asp	Val	Val	Asp	Phe	Val	Val	Pro	Glu	Leu	Gln	Lys	Leu	Ser	Arg	245	250	255	
Tyr	Lys	Thr	Glu	Tyr	Ala	Pro	Gly	Ser	Leu	Arg	Asn	Lys	Leu	Leu	Gly	260	265	270	
Lys	Gly	Asp	Arg	Leu	Asp	Asp	Thr	His	Arg	Gly	Ala	Ser	Tyr	Arg	Leu	275	280	285	
Gly	Ala	Arg	Asn	Ser	Thr	Ala	Thr	Ile	Asp	Leu	Ser	Ser	Ile	Ser	Ala	290	295	300	

Gln Leu Val Ser Gln Gly Ala His Ser
305 310

<210> 401

<211> 780

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(757)

<223> RXN02530

<400> 401

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accccttcca aaccttgagt cccgtgatac aattgttgat atg tca aca aat tat 115
Met Ser Thr Asn Tyr
1 5

gaa gca atc atc att gga gca ggt cag gct gga ctc gcg gcg gcg cat 163
Glu Ala Ile Ile Ile Gly Ala Gly Gln Ala Gly Leu Ala Ala Ala His
10 15 20

gaa ctt tcc cgc cgc ggt ttc act ccc gga aaa gat ttt ctc gtc ctc 211
Glu Leu Ser Arg Arg Gly Phe Thr Pro Gly Lys Asp Phe Leu Val Leu
25 30 35

gat tcc aac gac ggg ccc ggt ggc gcc tgg cgg cat agg tgg gat tca 259
Asp Ser Asn Asp Gly Pro Gly Gly Ala Trp Arg His Arg Trp Asp Ser
40 45 50

ctc aca tta ggt aaa gcc cac gga atc gcc gat ctc cca ggg ctt ccc 307
Leu Thr Leu Gly Lys Ala His Gly Ile Ala Asp Leu Pro Gly Leu Pro
55 60 65

atg aat cgc ccc gat ccg aaa act ccg gct tcc aca ttg gtt gct ggt 355
Met Asn Arg Pro Asp Pro Lys Thr Pro Ala Ser Thr Leu Val Ala Gly
70 75 80 85

tat tac ggc gct tac gag aac gag ttc tcc ttc gca gtt gtg cgc cca 403
Tyr Tyr Gly Ala Tyr Glu Asn Glu Phe Ser Phe Ala Val Val Arg Pro
90 95 100

gtc aaa gtc tca cga gtt gag ccc act tcc gag gat cct tcg agc cca 451
Val Lys Val Ser Arg Val Glu Pro Thr Ser Glu Asp Pro Ser Ser Pro
105 110 115

ttg cgc gtg agc agc gac gat ggt cga gag tgg att acc cgc atg gtt 499
Leu Arg Val Ser Ser Asp Asp Gly Arg Glu Trp Ile Thr Arg Met Val
120 125 130

ctt aat gca aca ggt acg tgg aca aac cct tat gtt ccg tac att cct 547
Leu Asn Ala Thr Gly Thr Trp Thr Asn Pro Tyr Val Pro Tyr Ile Pro
135 140 145

ggc atc gat aaa ttc cag ggc aag cag ctc cac acc gtt aat tac cgc 595
Gly Ile Asp Lys Phe Gln Gly Lys Gln Leu His Thr Val Asn Tyr Arg
150 155 160 165

aag gcc gag gat ttc aaa ggt aag aaa gtc ctg gtc gtc ggc ggt ggt 643
 Lys Ala Glu Asp Phe Lys Gly Lys Lys Val Leu Val Val Gly Gly Gly
 170 175 180
 ttg agt gct gtg caa ttt ctg ctg gag ttg gaa ggc ttg gcg gaa acc 691
 Leu Ser Ala Val Gln Phe Leu Leu Glu Leu Glu Gly Leu Ala Glu Thr
 185 190 195
 acc tgg gcg acg cgt cgt ccg cga act tac gca gcg cga gtt cga cgc 739
 Thr Trp Ala Thr Arg Arg Pro Arg Thr Tyr Ala Ala Arg Val Arg Arg
 200 205 210
 cgg ctg ggg cat tgc ggt tgagcgcgcc gtccgcgaac gca 780
 Arg Leu Gly His Cys Gly
 215

<210> 402

<211> 219

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 402

Met Ser Thr Asn Tyr Glu Ala Ile Ile Ile Gly Ala Gly Gln Ala Gly
 1 5 10 15
 Leu Ala Ala Ala His Glu Leu Ser Arg Arg Gly Phe Thr Pro Gly Lys
 20 25 30
 Asp Phe Leu Val Leu Asp Ser Asn Asp Gly Pro Gly Gly Ala Trp Arg
 35 40 45
 His Arg Trp Asp Ser Leu Thr Leu Gly Lys Ala His Gly Ile Ala Asp
 50 55 60
 Leu Pro Gly Leu Pro Met Asn Arg Pro Asp Pro Lys Thr Pro Ala Ser
 65 70 75 80
 Thr Leu Val Ala Gly Tyr Tyr Gly Ala Tyr Glu Asn Glu Phe Ser Phe
 85 90 95
 Ala Val Val Arg Pro Val Lys Val Ser Arg Val Glu Pro Thr Ser Glu
 100 105 110
 Asp Pro Ser Ser Pro Leu Arg Val Ser Ser Asp Asp Gly Arg Glu Trp
 115 120 125
 Ile Thr Arg Met Val Leu Asn Ala Thr Gly Thr Trp Thr Asn Pro Tyr
 130 135 140
 Val Pro Tyr Ile Pro Gly Ile Asp Lys Phe Gln Gly Lys Gln Leu His
 145 150 155 160
 Thr Val Asn Tyr Arg Lys Ala Glu Asp Phe Lys Gly Lys Lys Val Leu
 165 170 175
 Val Val Gly Gly Gly Leu Ser Ala Val Gln Phe Leu Leu Glu Leu Glu
 180 185 190
 Gly Leu Ala Glu Thr Thr Trp Ala Thr Arg Arg Pro Arg Thr Tyr Ala
 195 200 205

Ala Arg Val Arg Arg Arg Leu Gly His Cys Gly
210 215

<210> 403

<211> 492

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (20)..(469)

<223> FRXA02530

<400> 403

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          Met Asn Arg Pro Asp Pro Lys Thr Pro Ala Gly
              1              5              10

aca ttg gtt gct ggt tat tac ggc gct tac gag aac gag ttc tcc ttc 100
Thr Leu Val Ala Gly Tyr Tyr Gly Ala Tyr Glu Asn Glu Phe Ser Phe
          15              20              25

gca gtt gtg cgc cca gtc aaa gtc tca cga gtt gag ccc act tcc gag 148
Ala Val Val Arg Pro Val Lys Val Ser Arg Val Glu Pro Thr Ser Glu
          30              35              40

gat cct tcg agc cca ttg cgc gtg agc agc gac gat ggt cga gag tgg 196
Asp Pro Ser Ser Pro Leu Arg Val Ser Ser Asp Asp Gly Arg Glu Trp
          45              50              55

att acc cgc atg gtt ctt aat gca aca ggt acg tgg aca aac cct tat 244
Ile Thr Arg Met Val Leu Asn Ala Thr Gly Thr Trp Thr Asn Pro Tyr
          60              65              70              75

gtt ccg tac att cct ggc atc gat aaa ttc cag ggc aag cag ctg cac 292
Val Pro Tyr Ile Pro Gly Ile Asp Lys Phe Gln Gly Lys Gln Leu His
          80              85              90

acc gtt aat tac cgc aag gcc gag gat ttc aaa ggt aag aaa gtc ctg 340
Thr Val Asn Tyr Arg Lys Ala Glu Asp Phe Lys Gly Lys Lys Val Leu
          95              100              105

gtc gtc ggc ggt ggt ttg agt gct gtg caa ttt ctg ctg gag ttg gaa 388
Val Val Gly Gly Gly Leu Ser Ala Val Gln Phe Leu Leu Glu Leu Glu
          110              115              120

ggc ttg gcg gaa acc acc tgg gcg acg cgt cgt ccg cga act tac gca 436
Gly Leu Ala Glu Thr Thr Trp Ala Thr Arg Arg Pro Arg Thr Tyr Ala
          125              130              135

gcg cga gtt cga cgc cgg ctg ggg cat tgc ggt tgagcgcgcc gtccgcgaac 489
Ala Arg Val Arg Arg Arg Leu Gly His Cys Gly
          140              145              150

gca 492

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<210> 404

<211> 150

<212> PRT

<213> Corynebacterium glutamicum

<400> 404

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Met Asn Arg Pro Asp Pro Lys Thr Pro Ala Gly Thr Leu Val Ala Gly
 1             5             10             15

Tyr Tyr Gly Ala Tyr Glu Asn Glu Phe Ser Phe Ala Val Val Arg Pro
          20             25             30

Val Lys Val Ser Arg Val Glu Pro Thr Ser Glu Asp Pro Ser Ser Pro
          35             40             45

Leu Arg Val Ser Ser Asp Asp Gly Arg Glu Trp Ile Thr Arg Met Val
 50             55             60

Leu Asn Ala Thr Gly Thr Trp Thr Asn Pro Tyr Val Pro Tyr Ile Pro
 65             70             75             80

Gly Ile Asp Lys Phe Gln Gly Lys Gln Leu His Thr Val Asn Tyr Arg
          85             90             95

Lys Ala Glu Asp Phe Lys Gly Lys Lys Val Leu Val Val Gly Gly Gly
          100             105             110

Leu Ser Ala Val Gln Phe Leu Leu Glu Leu Glu Gly Leu Ala Glu Thr
          115             120             125

Thr Trp Ala Thr Arg Arg Pro Arg Thr Tyr Ala Ala Arg Val Arg Arg
          130             135             140

Arg Leu Gly His Cys Gly
145             150

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<210> 405

<211> 1533

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1510)

<223> RXA02083

<400> 405

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gtgaaggccg ccttttgcgg aatgggtata ggaggcattc atg gag atg gtt atg 115
                               Met Glu Met Val Met
                               1             5

aag aat aag cgc gtt gcg att att ggt gca ggt ccg agt ggt atc gct 163
Lys Asn Lys Arg Val Ala Ile Ile Gly Ala Gly Pro Ser Gly Ile Ala
          10             15             20

cag ttg agg gcg ttt gag tct gct gaa aag cag ggg cat gag atc cct 211
Gln Leu Arg Ala Phe Glu Ser Ala Glu Lys Gln Gly His Glu Ile Pro
          25             30             35

gag ctg gtg tgt ttt gaa aag cag gat acc tgg ggt ggg cag tgg aat 259

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Glu	Leu	Val	Cys	Phe	Glu	Lys	Gln	Asp	Thr	Trp	Gly	Gly	Gln	Trp	Asn		
		40					45					50					
tac	tct	tgg	cgc	acg	gga	aca	gac	tct	tat	ggt	gag	cct	gtg	cac	tca	307	
Tyr	Ser	Trp	Arg	Thr	Gly	Thr	Asp	Ser	Tyr	Gly	Glu	Pro	Val	His	Ser		
	55					60					65						
agt	atg	tac	cga	aac	ctg	tgg	tca	aac	ggt	ccg	aag	gaa	gtt	ctc	gaa	355	
Ser	Met	Tyr	Arg	Asn	Leu	Trp	Ser	Asn	Gly	Pro	Lys	Glu	Val	Leu	Glu		
	70				75					80					85		
ttt	gct	gag	tac	agc	ttc	gat	gag	cac	ttc	gga	aag	cca	att	tct	tct	403	
Phe	Ala	Glu	Tyr	Ser	Phe	Asp	Glu	His	Phe	Gly	Lys	Pro	Ile	Ser	Ser		
				90					95					100			
tac	cct	cca	cgt	gaa	gtg	ttg	tgg	gat	tac	att	gca	ggt	cgt	gca	aag	451	
Tyr	Pro	Pro	Arg	Glu	Val	Leu	Trp	Asp	Tyr	Ile	Ala	Gly	Arg	Ala	Lys		
			105					110					115				
aag	tcg	aac	gtt	gag	aag	tac	atc	aag	ttc	gcg	cat	gtt	gtt	cgc	tgg	499	
Lys	Ser	Asn	Val	Glu	Lys	Tyr	Ile	Lys	Phe	Ala	His	Val	Val	Arg	Trp		
		120					125					130					
gtg	agt	ttt	gat	gag	gcc	acc	aag	ctg	ttc	acc	gtg	acg	gtg	gag	aac	547	
Val	Ser	Phe	Asp	Glu	Ala	Thr	Lys	Leu	Phe	Thr	Val	Thr	Val	Glu	Asn		
	135					140					145						
ctc	cgc	acc	ggt	gag	acc	agc	agt	gat	act	tat	gac	aac	gtg	att	gtt	595	
Leu	Arg	Thr	Gly	Glu	Thr	Ser	Ser	Asp	Thr	Tyr	Asp	Asn	Val	Ile	Val		
	150				155					160				165			
ggc	gct	gga	cac	ttc	agc	ttc	ccg	aac	gtc	cct	cac	ttt	gat	ggt	gtg	643	
Gly	Ala	Gly	His	Phe	Ser	Phe	Pro	Asn	Val	Pro	His	Phe	Asp	Gly	Val		
			170						175					180			
gag	act	ttc	cca	ggt	cag	atc	atg	cat	gct	cac	gag	ttc	cgt	ggt	gca	691	
Glu	Thr	Phe	Pro	Gly	Gln	Ile	Met	His	Ala	His	Glu	Phe	Arg	Gly	Ala		
			185					190					195				
gag	gct	gtt	gct	gac	aag	gat	att	ttg	ctg	att	ggt	gca	agt	tat	tct	739	
Glu	Ala	Val	Ala	Asp	Lys	Asp	Ile	Leu	Leu	Ile	Gly	Ala	Ser	Tyr	Ser		
		200					205					210					
gcg	gaa	gat	atc	ggt	acc	cag	gcg	tac	aag	atg	ggt	gct	cgt	tcg	gtg	787	
Ala	Glu	Asp	Ile	Gly	Thr	Gln	Ala	Tyr	Lys	Met	Gly	Ala	Arg	Ser	Val		
	215					220					225						
act	ttc	tct	tac	cgc	tca	aac	cca	atg	ggg	tat	gag	tgg	cct	gaa	gag	835	
Thr	Phe	Ser	Tyr	Arg	Ser	Asn	Pro	Met	Gly	Tyr	Glu	Trp	Pro	Glu	Glu		
	230				235					240					245		
atg	act	gag	ctt	cct	ttg	gtt	gag	cgt	ttc	gac	ggc	tcc	gag	gtt	cac	883	
Met	Thr	Glu	Leu	Pro	Leu	Val	Glu	Arg	Phe	Asp	Gly	Ser	Glu	Val	His		
				250					255					260			
ttt	gtc	aat	ggt	gaa	aag	cgc	aag	gtc	gac	atc	gtg	gtg	ttc	tgt	act	931	
Phe	Val	Asn	Gly	Glu	Lys	Arg	Lys	Val	Asp	Ile	Val	Val	Phe	Cys	Thr		
			265					270					275				
ggt	tac	tta	cac	cat	tac	cca	ttt	atg	ccg	tct	gag	ctg	act	tta	agc	979	
Gly	Tyr	Leu	His	His	Tyr	Pro	Phe	Met	Pro	Ser	Glu	Leu	Thr	Leu	Ser		

280	285	290	
tca cca aac aac ctg tac ccg gat acg ctt tat cgt ggc gtg gtg tcc			1027
Ser Pro Asn Asn Leu Tyr Pro Asp Thr Leu Tyr Arg Gly Val Val Ser			
295	300	305	
gag gct aat aac cag ctg ttc tgg ttg ggt gct cag gat cag tgg ctg			1075
Glu Ala Asn Asn Gln Leu Phe Trp Leu Gly Ala Gln Asp Gln Trp Leu			
310	315	320	325
acg ttc aac atg ttt gat gct cag gct tgg tat gtt cgc gat gtc att			1123
Thr Phe Asn Met Phe Asp Ala Gln Ala Trp Tyr Val Arg Asp Val Ile			
	330	335	340
ttg ggc cgc gtg gct ctt cct tcc aag gaa gcg cag cgc aat cat atg			1171
Leu Gly Arg Val Ala Leu Pro Ser Lys Glu Ala Gln Arg Asn His Met			
	345	350	355
gat aag tgg ctg tca cgt ttc gaa ggc ttg aag tct gag aat gat cag			1219
Asp Lys Trp Leu Ser Arg Phe Glu Gly Leu Lys Ser Glu Asn Asp Gln			
	360	365	370
att gat ttc cag tgc gat tac gtc gag gat ctt atc gat cag acc gat			1267
Ile Asp Phe Gln Cys Asp Tyr Val Glu Asp Leu Ile Asp Gln Thr Asp			
	375	380	385
tat cct tcg ttt gat ctg aag gaa gtc gcg aat atc ttg aag ggc tgg			1315
Tyr Pro Ser Phe Asp Leu Lys Glu Val Ala Asn Ile Leu Lys Gly Trp			
390	395	400	405
gtg aag tcg aag gag gag gat atc ctc aac tac cgt gat tac acc tat			1363
Val Lys Ser Lys Glu Glu Asp Ile Leu Asn Tyr Arg Asp Tyr Thr Tyr			
	410	415	420
act tcc gtg atg acg ggc acc acc tct gtt gaa cac cac act ccg tgg			1411
Thr Ser Val Met Thr Gly Thr Thr Ser Val Glu His His Thr Pro Trp			
	425	430	435
atg att gag ttg gat gat tct ttg gag cgt tac ctc agt gag cca cag			1459
Met Ile Glu Leu Asp Asp Ser Leu Glu Arg Tyr Leu Ser Glu Pro Gln			
	440	445	450
gaa gat gaa gct cgt cag gtt tac cgt ggc aag aaa gtc cgc gat aaa			1507
Glu Asp Glu Ala Arg Gln Val Tyr Arg Gly Lys Lys Val Arg Asp Lys			
	455	460	465
gcc taaggaaaag gcctaagcag ccc			1533
Ala			
470			

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<212> PRT

<213> Corynebacterium glutamicum

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Pro Ser Gly Ile Ala Gln Leu Arg Ala Phe Glu Ser Ala Glu Lys Gln

20					25					30					
Gly	His	Glu	Ile	Pro	Glu	Leu	Val	Cys	Phe	Glu	Lys	Gln	Asp	Thr	Trp
		35					40					45			
Gly	Gly	Gln	Trp	Asn	Tyr	Ser	Trp	Arg	Thr	Gly	Thr	Asp	Ser	Tyr	Gly
	50					55					60				
Glu	Pro	Val	His	Ser	Ser	Met	Tyr	Arg	Asn	Leu	Trp	Ser	Asn	Gly	Pro
	65					70					75				80
Lys	Glu	Val	Leu	Glu	Phe	Ala	Glu	Tyr	Ser	Phe	Asp	Glu	His	Phe	Gly
				85					90					95	
Lys	Pro	Ile	Ser	Ser	Tyr	Pro	Pro	Arg	Glu	Val	Leu	Trp	Asp	Tyr	Ile
			100					105					110		
Ala	Gly	Arg	Ala	Lys	Lys	Ser	Asn	Val	Glu	Lys	Tyr	Ile	Lys	Phe	Ala
		115					120					125			
His	Val	Val	Arg	Trp	Val	Ser	Phe	Asp	Glu	Ala	Thr	Lys	Leu	Phe	Thr
	130					135					140				
Val	Thr	Val	Glu	Asn	Leu	Arg	Thr	Gly	Glu	Thr	Ser	Ser	Asp	Thr	Tyr
	145					150					155				160
Asp	Asn	Val	Ile	Val	Gly	Ala	Gly	His	Phe	Ser	Phe	Pro	Asn	Val	Pro
				165					170					175	
His	Phe	Asp	Gly	Val	Glu	Thr	Phe	Pro	Gly	Gln	Ile	Met	His	Ala	His
			180					185					190		
Glu	Phe	Arg	Gly	Ala	Glu	Ala	Val	Ala	Asp	Lys	Asp	Ile	Leu	Leu	Ile
		195					200					205			
Gly	Ala	Ser	Tyr	Ser	Ala	Glu	Asp	Ile	Gly	Thr	Gln	Ala	Tyr	Lys	Met
	210					215					220				
Gly	Ala	Arg	Ser	Val	Thr	Phe	Ser	Tyr	Arg	Ser	Asn	Pro	Met	Gly	Tyr
	225					230					235				240
Glu	Trp	Pro	Glu	Glu	Met	Thr	Glu	Leu	Pro	Leu	Val	Glu	Arg	Phe	Asp
				245					250					255	
Gly	Ser	Glu	Val	His	Phe	Val	Asn	Gly	Glu	Lys	Arg	Lys	Val	Asp	Ile
			260					265					270		
Val	Val	Phe	Cys	Thr	Gly	Tyr	Leu	His	His	Tyr	Pro	Phe	Met	Pro	Ser
		275					280					285			
Glu	Leu	Thr	Leu	Ser	Ser	Pro	Asn	Asn	Leu	Tyr	Pro	Asp	Thr	Leu	Tyr
	290					295					300				
Arg	Gly	Val	Val	Ser	Glu	Ala	Asn	Asn	Gln	Leu	Phe	Trp	Leu	Gly	Ala
	305					310					315				320
Gln	Asp	Gln	Trp	Leu	Thr	Phe	Asn	Met	Phe	Asp	Ala	Gln	Ala	Trp	Tyr
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Val	Arg	Asp	Val	Ile	Leu	Gly	Arg	Val	Ala	Leu	Pro	Ser	Lys	Glu	Ala
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Gln Arg Asn His Met Asp Lys Trp Leu Ser Arg Phe Glu Gly Leu Lys
 355 360 365

Ser Glu Asn Asp Gln Ile Asp Phe Gln Cys Asp Tyr Val Glu Asp Leu
 370 375 380

Ile Asp Gln Thr Asp Tyr Pro Ser Phe Asp Leu Lys Glu Val Ala Asn
 385 390 395 400

Ile Leu Lys Gly Trp Val Lys Ser Lys Glu Glu Asp Ile Leu Asn Tyr
 405 410 415

Arg Asp Tyr Thr Tyr Thr Ser Val Met Thr Gly Thr Thr Ser Val Glu
 420 425 430

His His Thr Pro Trp Met Ile Glu Leu Asp Asp Ser Leu Glu Arg Tyr
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Leu Ser Glu Pro Gln Glu Asp Glu Ala Arg Gln Val Tyr Arg Gly Lys
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Lys Val Arg Asp Lys Ala
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 Met Ser Ala Thr Ser
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tcc gtc acc gtt gaa tgc ccg gcg gga acc atc acc ggc gag ccc cat 163
 Ser Val Thr Val Glu Cys Pro Ala Gly Thr Ile Thr Gly Glu Pro His
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tat ttc cgc tcg att ccc tac gca aag gcg cgc ccg ttt gct gat gcc 211
 Tyr Phe Arg Ser Ile Pro Tyr Ala Lys Ala Arg Pro Phe Ala Asp Ala
 25 30 35

gaa aag cta gaa ccc ctg cgc att gat gcg acc ggc aag cac gag ggt 259
 Glu Lys Leu Glu Pro Leu Arg Ile Asp Ala Thr Gly Lys His Glu Gly
 40 45 50

ctc tat tta acg ttg gca acc ccg gag gca cgg ttc ggc gcg gat gcc 307
 Leu Tyr Leu Thr Leu Ala Thr Pro Glu Ala Arg Phe Gly Ala Asp Ala
 55 60 65

ccg gtg atc gtt tat atc cac ggc gga gga tat gac ggt ggc acg cgt 355
 Pro Val Ile Val Tyr Ile His Gly Gly Gly Tyr Asp Gly Gly Thr Arg

70	75	80	85	
ttc gat gcc cgc acc gag ccc act ttc ttc cgt gag cag ggc ttt gtg				403
Phe Asp Ala Arg Thr Glu Pro Thr Phe Phe Arg Glu Gln Gly Phe Val	90	95	100	
gtg gtc tcc atc gat tac cgc gtc ggc ctg gag ggc ttt gcg cgc ttc				451
Val Val Ser Ile Asp Tyr Arg Val Gly Leu Glu Gly Phe Ala Arg Phe	105	110	115	
cac gac gac gag gcc aat cgt tac cgc ggc atc gat gat tgc gtg ctc				499
His Asp Asp Glu Ala Asn Arg Tyr Arg Gly Ile Asp Asp Cys Val Leu	120	125	130	
gcg ctg gag tgg gtg cag aaa aac atc gag cat ttc ggc ggc gat ccc				547
Ala Leu Glu Trp Val Gln Lys Asn Ile Glu His Phe Gly Gly Asp Pro	135	140	145	
acc aac gtc acc ctc atc ggg cag tcc gcg ggc gcc ggc atc gcg ctc				595
Thr Asn Val Thr Leu Ile Gly Gln Ser Ala Gly Ala Gly Ile Ala Leu	150	155	160	165
tgg ctc acg cgc cta gac cac tat aaa ggt gct ttt cga cgc ctg gtt				643
Trp Leu Thr Arg Leu Asp His Tyr Lys Gly Ala Phe Arg Arg Leu Val	170	175	180	
gcg ctc tcc ccc agc ttc ccg cgc cag cca ttc gct gcc cga aaa ggt				691
Ala Leu Ser Pro Ser Phe Pro Arg Gln Pro Phe Ala Ala Arg Lys Gly	185	190	195	
gct tta cga cgc gcc ctg ggc aaa ccc gtc acc cgc gcc tcg ctg gcg				739
Ala Leu Arg Arg Ala Leu Gly Lys Pro Val Thr Arg Ala Ser Leu Ala	200	205	210	
ggc atc aag ccc gca cgc ttg gac aaa ggc tac cgt cgc ttt gct cgc				787
Gly Ile Lys Pro Ala Arg Leu Asp Lys Gly Tyr Arg Arg Phe Ala Arg	215	220	225	
cgc tac ttc acc gac ctg gca ctc ggc cct acc cca tac gac ccg aat				835
Arg Tyr Phe Thr Asp Leu Ala Leu Gly Pro Thr Pro Tyr Asp Pro Asn	230	235	240	245
gag ctg gcc gac atc gat ttg atc atc tcc tcc acc cgc gat gaa atg				883
Glu Leu Ala Asp Ile Asp Leu Ile Ile Ser Ser Thr Arg Asp Glu Met	250	255	260	
tac gga cac cgc gca ggc tta tgg ttc gac cag cgt ggc ttc ggc gca				931
Tyr Gly His Arg Ala Gly Leu Trp Phe Asp Gln Arg Gly Phe Gly Ala	265	270	275	
aaa ctg gcc gcg cga ctt ttt ggc ctg gag aat tcg gat acc aat att				979
Lys Leu Ala Ala Arg Leu Phe Gly Leu Glu Asn Ser Asp Thr Asn Ile	280	285	290	
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Pro Phe Ala Asp Ala Glu Lys Leu Glu Pro Leu Arg Ile Asp Ala Thr
      35           40           45

Gly Lys His Glu Gly Leu Tyr Leu Thr Leu Ala Thr Pro Glu Ala Arg
      50           55           60

Phe Gly Ala Asp Ala Pro Val Ile Val Tyr Ile His Gly Gly Gly Tyr
      65           70           75           80

Asp Gly Gly Thr Arg Phe Asp Ala Arg Thr Glu Pro Thr Phe Phe Arg
      85           90           95

Glu Gln Gly Phe Val Val Val Ser Ile Asp Tyr Arg Val Gly Leu Glu
      100          105          110

Gly Phe Ala Arg Phe His Asp Asp Glu Ala Asn Arg Tyr Arg Gly Ile
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Asp Asp Cys Val Leu Ala Leu Glu Trp Val Gln Lys Asn Ile Glu His
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Phe Gly Gly Asp Pro Thr Asn Val Thr Leu Ile Gly Gln Ser Ala Gly
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Ala Gly Ile Ala Leu Trp Leu Thr Arg Leu Asp His Tyr Lys Gly Ala
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Phe Arg Arg Leu Val Ala Leu Ser Pro Ser Phe Pro Arg Gln Pro Phe
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Ala Ala Arg Lys Gly Ala Leu Arg Arg Ala Leu Gly Lys Pro Val Thr
      195          200          205

Arg Ala Ser Leu Ala Gly Ile Lys Pro Ala Arg Leu Asp Lys Gly Tyr
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Arg Arg Phe Ala Arg Arg Tyr Phe Thr Asp Leu Ala Leu Gly Pro Thr
      225          230          235          240

Pro Tyr Asp Pro Asn Glu Leu Ala Asp Ile Asp Leu Ile Ile Ser Ser
      245          250          255

Thr Arg Asp Glu Met Tyr Gly His Arg Ala Gly Leu Trp Phe Asp Gln
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				1															
gcg	ggt	tcg	gtg	ttg	gcg	gat	gag	atg	gtg	gtt	ccc	acc	tca	aca	ggg	163			
Ala	Gly	Ser	Val	Leu	Ala	Asp	Glu	Met	Val	Val	Pro	Thr	Ser	Thr	Gly				
				10						15						20			
ttt	gtt	aaa	ggc	gtc	aaa	gga	cca	ggg	ctt	aaa	acc	tgg	agg	gga	att	211			
Phe	Val	Lys	Gly	Val	Lys	Gly	Pro	Gly	Leu	Lys	Thr	Trp	Arg	Gly	Ile				
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Pro	Tyr	Gly	Arg	Asn	Thr	Gly	Gly	Lys	Tyr	Arg	Phe	Arg	Ala	Pro	Arg				
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Pro	Ala	Lys	Lys	Trp	Asp	Gly	Val	Arg	Asp	Cys	Ser	Met	Phe	Gly	Glu				
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gta	gct	tct	cag	cca	acg	tac	tcc	tgg	aca	gat	aag	att	cgc	ggt	tca	355			
Val	Ala	Ser	Gln	Pro	Thr	Tyr	Ser	Trp	Thr	Asp	Lys	Ile	Arg	Gly	Ser				
70						75						80						85	
gaa	gac	tgc	ctt	aac	ctc	gat	gtc	gtg	cgg	cct	gat	tcc	gaa	gaa	aag	403			
Glu	Asp	Cys	Leu	Asn	Leu	Asp	Val	Val	Arg	Pro	Asp	Ser	Glu	Glu	Lys				
				90						95						100			
ctt	cct	gtt	gtg	gtg	tat	ctc	cac	ggc	ggt	tcc	ttc	atc	atg	ggc	tca	451			
Leu	Pro	Val	Val	Val	Tyr	Leu	His	Gly	Gly	Ser	Phe	Ile	Met	Gly	Ser				
			105						110						115				
tca	agc	gaa	aaa	gcg	ctg	cgc	gga	tat	aac	ctc	gtc	aca	aac	atg	aat	499			
Ser	Ser	Glu	Lys	Ala	Leu	Arg	Gly	Tyr	Asn	Leu	Val	Thr	Asn	Met	Asn				
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gtg	gtc	tac	gtg	tcc	gtt	aat	ttc	cgc	ctc	ggc	gct	ttg	ggc	tat	cta	547			
Val	Val	Tyr	Val	Ser	Val	Asn	Phe	Arg	Leu	Gly	Ala	Leu	Gly	Tyr	Leu				
	135						140						145						
gat	ctg	cgt	tcc	gtg	ggg	gag	gat	tgc	gta	gcc	aac	ccc	gcg	ctc	cac	595			
Asp	Leu	Arg	Ser	Val	Gly	Glu	Asp	Cys	Val	Ala	Asn	Pro	Ala	Leu	His				
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gat	cag	ctc	ctg	gcc	ctg	cag	tgg	gtc	agc	cgt	aat	atc	aaa	gca	ttc	643			
Asp	Gln	Leu	Leu	Ala	Leu	Gln	Trp	Val	Ser	Arg	Asn	Ile	Lys	Ala	Phe				
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Gly Gly Asp Pro Asp Asn Val Thr Leu Met Gly Glu Ser Ala Gly Ala	
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gca gca gtg gtt gca ctc atg tgt gtg ccc gct gca gga gga cta ttc	739
Ala Ala Val Val Ala Leu Met Cys Val Pro Ala Ala Gly Gly Leu Phe	
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cac cgc gcc atc gcc caa tcc gcg ccg gtc atc tct gtg cac tca tct	787
His Arg Ala Ile Ala Gln Ser Ala Pro Val Ile Ser Val His Ser Ser	
215 220 225	
acc caa gca aaa ttc tgg gca cgt gaa ctg atc tac cgc atg gca ttg	835
Thr Gln Ala Lys Phe Trp Ala Arg Glu Leu Ile Tyr Arg Met Ala Leu	
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ccc agg gaa acc acc ttg gat gaa ctg cgc caa gaa tcc gcc gat gat	883
Pro Arg Glu Thr Thr Leu Asp Glu Leu Arg Gln Glu Ser Ala Asp Asp	
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cta gtg cgc gcc ggg cag tcg atg atg tgg cgc tcc ggc gaa ctg ctc	931
Leu Val Arg Ala Gly Gln Ser Met Met Trp Arg Ser Gly Glu Leu Leu	
265 270 275	
caa ctc aac tct tgt tac ggg ccc acg gtg gat ggt tcc ttg cta cct	979
Gln Leu Asn Ser Cys Tyr Gly Pro Thr Val Asp Gly Ser Leu Leu Pro	
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Glu His Pro Leu Thr Met Phe Glu Gln Gly Arg Gln His Arg Ile Pro	
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Phe Met Ile Gly Thr Asn Asn Gly Glu Thr Ser Phe Ser Lys Ala Phe	
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Tyr Leu Arg Ser Ser Ala Arg Arg Arg Ser Ala Leu Arg Met Leu Ser	
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Val Tyr Asp Pro His Asn Ala Glu Arg Val Val Ser Ala Tyr Gly Gly	
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Gly Glu Ala Arg Thr Asp Phe Ser Glu Leu Leu Ala Asp Ala Leu Phe	
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Trp Ala Pro Ser Val Arg Leu Ala Gln Ser His Ala Ser Gln Asp Glu	
375 380 385	
gat acc tgg atg tac cgc ttc gat tac gcc cca caa tcc atg cgg aaa	1315
Asp Thr Trp Met Tyr Arg Phe Asp Tyr Ala Pro Gln Ser Met Arg Lys	
390 395 400 405	
ctt ggc ctc ggc gcg att cac tct ttc gaa ctc aac gct gtc ttt ggc	1363
Leu Gly Leu Gly Ala Ile His Ser Phe Glu Leu Asn Ala Val Phe Gly	
410 415 420	

gat cat gaa tct tct cgc tcc atg aac ctt gcg aaa att gcc ggc ggc 1411
Asp His Glu Ser Ser Arg Ser Met Asn Leu Ala Lys Ile Ala Gly Gly
425 430 435

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Met Asp His Leu Asp Lys Val Thr Glu Leu Val Gln Glu His Trp Lys
440 445 450

caa ttc atc tac ttc ggc agg ccc ggt gaa gag tgg aag gct tac cgc 1507
Gln Phe Ile Tyr Phe Gly Arg Pro Gly Glu Glu Trp Lys Ala Tyr Arg
455 460 465

ggc cgc agc gat acc gaa ccg ggc cgt gct aca ttt gtc atc gat atc 1555
Gly Arg Ser Asp Thr Glu Pro Gly Arg Ala Thr Phe Val Ile Asp Ile
470 475 480 485

aac tcc cga atc gcg tgg gat cca cgc cag gac aaa cgc acg gcg tgg 1603
Asn Ser Arg Ile Ala Trp Asp Pro Arg Gln Asp Lys Arg Thr Ala Trp
490 495 500

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Glu Asn Tyr Asp Met Leu Glu Trp Gly Thr Gly Arg Pro Asp Leu Ala
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Asn Glu Leu Asp Phe Ile Glu Pro Glu Glu Thr Glu Glu Glu Gln Gln
520 525 530

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Phe Arg Ala Pro Arg Pro Ala Lys Lys Trp Asp Gly Val Arg Asp Cys
50 55 60

Ser Met Phe Gly Glu Val Ala Ser Gln Pro Thr Tyr Ser Trp Thr Asp
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Lys Ile Arg Gly Ser Glu Asp Cys Leu Asn Leu Asp Val Val Arg Pro
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Asp Ser Glu Glu Lys Leu Pro Val Val Val Tyr Leu His Gly Gly Ser
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Phe Ile Met Gly Ser Ser Ser Glu Lys Ala Leu Arg Gly Tyr Asn Leu
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 Val Thr Asn Met Asn Val Val Tyr Val Ser Val Asn Phe Arg Leu Gly
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 145 150 155 160
 Asn Pro Ala Leu His Asp Gln Leu Leu Ala Leu Gln Trp Val Ser Arg
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 Asn Ile Lys Ala Phe Gly Gly Asp Pro Asp Asn Val Thr Leu Met Gly
 180 185 190
 Glu Ser Ala Gly Ala Ala Ala Val Val Ala Leu Met Cys Val Pro Ala
 195 200 205
 Ala Gly Gly Leu Phe His Arg Ala Ile Ala Gln Ser Ala Pro Val Ile
 210 215 220
 Ser Val His Ser Ser Thr Gln Ala Lys Phe Trp Ala Arg Glu Leu Ile
 225 230 235 240
 Tyr Arg Met Ala Leu Pro Arg Glu Thr Thr Leu Asp Glu Leu Arg Gln
 245 250 255
 Glu Ser Ala Asp Asp Leu Val Arg Ala Gly Gln Ser Met Met Trp Arg
 260 265 270
 Ser Gly Glu Leu Leu Gln Leu Asn Ser Cys Tyr Gly Pro Thr Val Asp
 275 280 285
 Gly Ser Leu Leu Pro Glu His Pro Leu Thr Met Phe Glu Gln Gly Arg
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 Gln His Arg Ile Pro Phe Met Ile Gly Thr Asn Asn Gly Glu Thr Ser
 305 310 315 320
 Phe Ser Lys Ala Phe Tyr Leu Arg Ser Ser Ala Arg Arg Arg Ser Ala
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 Ser Ala Tyr Gly Gly Gly Glu Ala Arg Thr Asp Phe Ser Glu Leu Leu
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 Ala Asp Ala Leu Phe Trp Ala Pro Ser Val Arg Leu Ala Gln Ser His
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 Ala Ser Gln Asp Glu Asp Thr Trp Met Tyr Arg Phe Asp Tyr Ala Pro
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 Gln Ser Met Arg Lys Leu Gly Leu Gly Ala Ile His Ser Phe Glu Leu
 405 410 415
 Asn Ala Val Phe Gly Asp His Glu Ser Ser Arg Ser Met Asn Leu Ala
 420 425 430

Lys Ile Ala Gly Gly Met Asp His Leu Asp Lys Val Thr Glu Leu Val
 435 440 445
 Gln Glu His Trp Lys Gln Phe Ile Tyr Phe Gly Arg Pro Gly Glu Glu
 450 455 460
 Trp Lys Ala Tyr Arg Gly Arg Ser Asp Thr Glu Pro Gly Arg Ala Thr
 465 470 475 480
 Phe Val Ile Asp Ile Asn Ser Arg Ile Ala Trp Asp Pro Arg Gln Asp
 485 490 495
 Lys Arg Thr Ala Trp Glu Asn Tyr Asp Met Leu Glu Trp Gly Thr Gly
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 Arg Pro Asp Leu Ala Asn Glu Leu Asp Phe Ile Glu Pro Glu Glu Thr
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<222> (101)..(793)

<223> RXN00658

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 Val Arg His Asp Glu
 1 5
 cac tac cca gct gcg gca aac ctc att gct ttc gat aag gga tgg tcc 163
 His Tyr Pro Ala Ala Ala Asn Leu Ile Ala Phe Asp Lys Gly Trp Ser
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 Thr Leu Ile Ala Pro Gln Leu Glu Asp Pro Glu Ala Glu Glu Phe Thr
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 gcc gga ttc ctc acc gaa tac cag gac aat ctg atc act gcg ggc atg 259
 Ala Gly Phe Leu Thr Glu Tyr Gln Asp Asn Leu Ile Thr Ala Gly Met
 40 45 50
 gag cac cag gcg ctc gcg agc ggc ttc ccg gtg ggg cgt cgc ttc aag 307
 Glu His Gln Ala Leu Ala Ser Gly Phe Pro Val Gly Arg Arg Phe Lys
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 Ser Asp Ile Ala Leu Arg Arg Cys Asp Ala Val Thr Thr His Ile Gly
 70 75 80 85

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 His Glu His Ser Ala Asp Gly His Trp Arg Ile Tyr Val Phe Ala Gly
 90 95 100

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 Gln Ala Thr Pro Gln Asp Ser Glu Ser Ala Leu Asn Lys Trp Ala Gln
 105 110 115

tgg atg gag gaa agc gaa gac tca cca ctc aac cgc ttc acc cca gaa 499
 Trp Met Glu Glu Ser Glu Asp Ser Pro Leu Asn Arg Phe Thr Pro Glu
 120 125 130

gcc ggc gac cgc aac gca gtc ttc gat atc aag gct acc tac cag cag 547
 Ala Gly Asp Arg Asn Ala Val Phe Asp Ile Lys Ala Thr Tyr Gln Gln
 135 140 145

cat tac cac tcc ttc gac ctg ttc gat gcg cca gag gtc ttc ttc cca 595
 His Tyr His Ser Phe Asp Leu Phe Asp Ala Pro Glu Val Phe Phe Pro
 150 155 160 165

cga gtt gga cca tac aag ctg caa aac ctc gaa aac gtt tgg acc gca 643
 Arg Val Gly Pro Tyr Lys Leu Gln Asn Leu Glu Asn Val Trp Thr Ala
 170 175 180

ctg gat tcc caa gac atc ttt gag tcc cgt ggc atc agt cgc gat ggc 691
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 185 190 195

gca att gtt gtc gtt cgc cca gac cag tac gtc gca gca gtc ctc cca 739
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 200 205 210

ctc gaa gac acc gca gca ctg gct gag ttc ttc aat ggc aat ctg ctt 787
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<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 412

Val Arg His Asp Glu His Tyr Pro Ala Ala Ala Asn Leu Ile Ala Phe
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Asp Lys Gly Trp Ser Thr Leu Ile Ala Pro Gln Leu Glu Asp Pro Glu
 20 25 30

Ala Glu Glu Phe Thr Ala Gly Phe Leu Thr Glu Tyr Gln Asp Asn Leu
 35 40 45

Ile Thr Ala Gly Met Glu His Gln Ala Leu Ala Ser Gly Phe Pro Val
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Gly Arg Arg Phe Lys Ser Asp Ile Ala Leu Arg Arg Cys Asp Ala Val

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<223> FRXA00658
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Val Arg His Asp Glu
1 5

cac tac cca gct gcg gca aac ctc att gct ttc gat aag gga tgg tcc 163
His Tyr Pro Ala Ala Ala Asn Leu Ile Ala Phe Asp Lys Gly Trp Ser
10 15 20

acc ctc atc gcc cct cag ctg gaa gat cca gag gcg gag gag ttc acc 211
Thr Leu Ile Ala Pro Gln Leu Glu Asp Pro Glu Ala Glu Glu Phe Thr
25 30 35

gcc gga ttc ctc acc gaa tac cag gac aat ctg atc act gcg ggc atg 259
Ala Gly Phe Leu Thr Glu Tyr Gln Asp Asn Leu Ile Thr Ala Gly Met
40 45 50

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gag cac cag gcg ctc gcg agc ggc ttc ccg gtg ggg cgt cgc ttc aag 307
 Glu His Gln Ala Leu Ala Ser Gly Phe Pro Val Gly Arg Arg Phe Lys
 55 60 65

tcc gat att gct tta cga cgc tgc gat gcg gtg acc acc cac atc ggc 355
 Ser Asp Ile Ala Leu Arg Arg Cys Asp Ala Val Thr Thr His Ile Gly
 70 75 80 85

cac gaa cac tcc gcc gat ggt cac tgg agg atc tac gta ttc gct ggc 403
 His Glu His Ser Ala Arg Gly His Trp Arg Ile Tyr Val Phe Ala Gly
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caa gcc acc cca caa 418
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<400> 414
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Ala Glu Glu Phe Thr Ala Gly Phe Leu Thr Glu Tyr Gln Asp Asn Leu
 35 40 45

Ile Thr Ala Gly Met Glu His Gln Ala Leu Ala Ser Gly Phe Pro Val
 50 55 60

Gly Arg Arg Phe Lys Ser Asp Ile Ala Leu Arg Arg Cys Asp Ala Val
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Thr Thr His Ile Gly His Glu His Ser Ala Asp Gly His Trp Arg Ile
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Tyr Val Phe Ala Gly Gln Ala Thr Pro Gln
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 Met Gln Phe His Tyr

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gaa	gga	tac	gca	acc	ggt	gac	cca	atg	gag	atg	cgc	gcg	gaa	ggt	agc	163		
Glu	Gly	Tyr	Ala	Thr	Gly	Asp	Pro	Met	Glu	Met	Arg	Ala	Glu	Gly	Ser			
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gga	atc	aac	cgc	ccg	gac	gat	ctc	ccc	gag	gtc	atg	gat	gtt	ctc	atc	211		
Gly	Ile	Asn	Arg	Pro	Asp	Asp	Leu	Pro	Glu	Val	Met	Asp	Val	Leu	Ile			
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gtt	ggt	gca	ggt	ccg	gct	ggc	acc	atc	gca	gcg	gct	cag	ctt	tcc	cga	259		
Val	Gly	Ala	Gly	Pro	Ala	Gly	Thr	Ile	Ala	Ala	Ala	Gln	Leu	Ser	Arg			
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Phe	Pro	Asn	Val	Thr	Thr	Arg	Leu	Val	Glu	Arg	Ser	Asp	Arg	Arg	Leu			
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Glu	Leu	Ala	Asn	Ala	Asp	Gly	Val	His	Ser	Arg	Thr	Ile	Glu	Thr	Phe			
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cag	gca	ttt	ggt	ttc	gcc	cac	gag	atc	ctc	gcc	gaa	gct	cat	gaa	atc	403		
Gln	Ala	Phe	Gly	Phe	Ala	His	Glu	Ile	Leu	Ala	Glu	Ala	His	Glu	Ile			
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acc	gac	atg	gcg	ttc	tgg	aag	ccg	gac	ccg	caa	aac	cct	cgt	gag	atc	451		
Thr	Asp	Met	Ala	Phe	Trp	Lys	Pro	Asp	Pro	Gln	Asn	Pro	Arg	Glu	Ile			
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att	cgc	gac	aac	agc	acc	cgc	gag	ctg	cca	cag	cac	atc	agt	gaa	ttt	499		
Ile	Arg	Asp	Asn	Ser	Thr	Arg	Glu	Leu	Pro	Gln	His	Ile	Ser	Glu	Phe			
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ccg	atg	gcg	ttg	ctc	acc	cag	acc	cgc	atc	atc	gac	cac	ttc	aac	cgg	547		
Pro	Met	Ala	Leu	Leu	Thr	Gln	Thr	Arg	Ile	Ile	Asp	His	Phe	Asn	Arg			
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ttc	atg	aag	aac	tcc	cca	acc	agg	atg	aag	cct	gac	tat	gga	tac	gag	595		
Phe	Met	Lys	Asn	Ser	Pro	Thr	Arg	Met	Lys	Pro	Asp	Tyr	Gly	Tyr	Glu			
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ttc	gtg	gac	ttt	gaa	gta	gaa	gaa	gac	gca	gaa	tat	ccg	gta	att	gtc	643		
Phe	Val	Asp	Phe	Glu	Val	Glu	Glu	Asp	Ala	Glu	Tyr	Pro	Val	Ile	Val			
				170					175					180				
acc	ctc	cgc	cgc	acc	agt	ggc	gag	caa	act	ggc	gaa	ttg	gtc	acc	gtc	691		
Thr	Leu	Arg	Arg	Thr	Ser	Gly	Glu	Gln	Thr	Gly	Glu	Leu	Val	Thr	Val			
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cga	acc	aag	tac	ctg	gtc	ggt	gcc	gat	ggt	gca	cga	agc	caa	gtg	cgc	739		
Arg	Thr	Lys	Tyr	Leu	Val	Gly	Ala	Asp	Gly	Ala	Arg	Ser	Gln	Val	Arg			
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aaa	tca	ctg	gga	tac	cga	ctc	caa	ggt	aag	cag	gct	aac	cac	gct	tgg	787		
Lys	Ser	Leu	Gly	Tyr	Arg	Leu	Gln	Gly										

aag tgc acc atc aaa tct gat tgc ggt cgc acc atc ttg ctc atc cca	883
Lys Cys Thr Ile Lys Ser Asp Ser Gly Arg Thr Ile Leu Leu Ile Pro	
250 255 260	
cgt gag ggt ggc ttc ctc ttc cgt ctc tac gtt gac ctg ggc gaa gta	931
Arg Glu Gly Gly Phe Leu Phe Arg Leu Tyr Val Asp Leu Gly Glu Val	
265 270 275	
cct gat gat ggc agc aag gct gtt cgt gat acc cca ctc cag gat gtc	979
Pro Asp Asp Gly Ser Lys Ala Val Arg Asp Thr Pro Leu Gln Asp Val	
280 285 290	
atc gac acc gcg aac cag atc atg gct cca ttc acc ctc gac gtg aaa	1027
Ile Asp Thr Ala Asn Gln Ile Met Ala Pro Phe Thr Leu Asp Val Lys	
295 300 305	
aac gtt gtg tgg aac tcc atc tac gag gta ggc cac cgc gtc gca gac	1075
Asn Val Val Trp Asn Ser Ile Tyr Glu Val Gly His Arg Val Ala Asp	
310 315 320 325	
cat ttc gat gac cgt gtt tca gaa aaa acc tgc agc gaa cac cca cgc	1123
His Phe Asp Asp Arg Val Ser Glu Lys Thr Ser Ser Glu His Pro Arg	
330 335 340	
att ttc att gct ggc gac gcc tgc cac acc cac agc gct aag gct ggc	1171
Ile Phe Ile Ala Gly Asp Ala Cys His Thr His Ser Ala Lys Ala Gly	
345 350 355	
cag ggc atg aac gtg tcc atg cag gac gga ttc aac ctt ggc tgg aag	1219
Gln Gly Met Asn Val Ser Met Gln Asp Gly Phe Asn Leu Gly Trp Lys	
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ctt gga cat gtg gcc agc gga aat agc cca cgc gaa cta ctt cag acc	1267
Leu Gly His Val Ala Ser Gly Asn Ser Pro Arg Glu Leu Leu Gln Thr	
375 380 385	
tac gct gaa gag cgc gaa gac att gcc tac aag ctc atc gag tac gac	1315
Tyr Ala Glu Glu Arg Glu Asp Ile Ala Tyr Lys Leu Ile Glu Tyr Asp	
390 395 400 405	
aag aac tgg tca aca ctc atg gca aag cca agc agc gaa atg ggc agt	1363
Lys Asn Trp Ser Thr Leu Met Ala Lys Pro Ser Ser Glu Met Gly Ser	
410 415 420	
gcc caa gac ctt gag gat ttc tac cgc gcg aac tct gag ttc aat gcc	1411
Ala Gln Asp Leu Glu Asp Phe Tyr Arg Ala Asn Ser Glu Phe Asn Ala	
425 430 435	
ggc tac atg acc cac tat cct cct tct tcc atc aca atg gat ggc agc	1459
Gly Tyr Met Thr His Tyr Pro Pro Ser Ser Ile Thr Met Asp Gly Ser	
440 445 450	
aac caa gat ctg gca aag ggc tac cca att ggc cga cgc ttc aag tca	1507
Asn Gln Asp Leu Ala Lys Gly Tyr Pro Ile Gly Arg Arg Phe Lys Ser	
455 460 465	
gcg atg gtt ggt cga gtc tgc gac ttc acc gaa aca cac ctc ggt cac	1555
Ala Met Val Gly Arg Val Cys Asp Phe Thr Glu Thr His Leu Gly His	
470 475 480 485	

caa gca aca gcc gac gga cgc atg cgc gca tac gtc ttc gca gga tcc 1603
 Gln Ala Thr Ala Asp Gly Arg Met Arg Ala Tyr Val Phe Ala Gly Ser
 490 495 500

gat gca ctt aac ggc gag ggt tct gag cta gac cgc tgg gca gaa tgg 1651
 Asp Ala Leu Asn Gly Glu Gly Ser Glu Leu Asp Arg Trp Ala Glu Trp
 505 510 515

gca gag gcg aac ctt gac ccc acg ctt gtc gac gcc aag gtg att tac 1699
 Ala Glu Ala Asn Leu Asp Pro Thr Leu Val Asp Ala Lys Val Ile Tyr
 520 525 530

caa agc cct tat acc gag ctc gac acc cgc cag gtt cca tcc gtg ttc 1747
 Gln Ser Pro Tyr Thr Glu Leu Asp Thr Arg Gln Val Pro Ser Val Phe
 535 540 545

aaa cct gca gtc ggg atc ttc gaa ctg acc aat gtg gaa aac tcc ttc 1795
 Lys Pro Ala Val Gly Ile Phe Glu Leu Thr Asn Val Glu Asn Ser Phe
 550 555 560 565

ggt atc acc acg gac tcc gac atc ttt gat agt cgc gag atc tcc cgc 1843
 Gly Ile Thr Thr Asp Ser Asp Ile Phe Asp Ser Arg Glu Ile Ser Arg
 570 575 580

gat ggt gtc gtg gtg gta gtc cga cca gac caa tac gtt tcc gga atc 1891
 Asp Gly Val Val Val Val Val Arg Pro Asp Gln Tyr Val Ser Gly Ile
 585 590 595

ttc cca ctc act gat acc caa ggg ctt ggc gaa ttc ctc acc gga tac 1939
 Phe Pro Leu Thr Asp Thr Gln Gly Leu Gly Glu Phe Leu Thr Gly Tyr
 600 605 610

ttc ccc aaa atg aaa ggc gca cat cag cta atc aac gcg aac 1981
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taaggcacag ctgttaaaac agt 2004

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<211> 627

<212> PRT

<213> Corynebacterium glutamicum

<400> 416

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Met Asp Val Leu Ile Val Gly Ala Gly Pro Ala Gly Thr Ile Ala Ala
 35 40 45

Ala Gln Leu Ser Arg Phe Pro Asn Val Thr Thr Arg Leu Val Glu Arg
 50 55 60

Ser Asp Arg Arg Leu Glu Leu Ala Asn Ala Asp Gly Val His Ser Arg
 65 70 75 80

Thr Ile Glu Thr Phe Gln Ala Phe Gly Phe Ala His Glu Ile Leu Ala

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Glu	Ala	His	Glu	Ile	Thr	Asp	Met	Ala	Phe	Trp	Lys	Pro	Asp	Pro	Gln		
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Asn	Pro	Arg	Glu	Ile	Ile	Arg	Asp	Asn	Ser	Thr	Arg	Glu	Leu	Pro	Gln		
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His	Ile	Ser	Glu	Phe	Pro	Met	Ala	Leu	Leu	Thr	Gln	Thr	Arg	Ile	Ile		
			130				135				140						
Asp	His	Phe	Asn	Arg	Phe	Met	Lys	Asn	Ser	Pro	Thr	Arg	Met	Lys	Pro		
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Asp	Tyr	Gly	Tyr	Glu	Phe	Val	Asp	Phe	Glu	Val	Glu	Glu	Asp	Ala	Glu		
			165				170						175				
Tyr	Pro	Val	Ile	Val	Thr	Leu	Arg	Arg	Thr	Ser	Gly	Glu	Gln	Thr	Gly		
			180				185						190				
Glu	Leu	Val	Thr	Val	Arg	Thr	Lys	Tyr	Leu	Val	Gly	Ala	Asp	Gly	Ala		
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Arg	Ser	Gln	Val	Arg	Lys	Ser	Leu	Gly	Tyr	Arg	Leu	Gln	Gly	Lys	Gln		
210						215				220							
Ala	Asn	His	Ala	Trp	Gly	Val	Met	Asp	Ile	His	Ala	Asn	Thr	Glu	Phe		
225						230				235			240				
Pro	Asp	Val	Arg	Lys	Lys	Cys	Thr	Ile	Lys	Ser	Asp	Ser	Gly	Arg	Thr		
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Ile	Leu	Leu	Ile	Pro	Arg	Glu	Gly	Gly	Phe	Leu	Phe	Arg	Leu	Tyr	Val		
			260				265						270				
Asp	Leu	Gly	Glu	Val	Pro	Asp	Asp	Gly	Ser	Lys	Ala	Val	Arg	Asp	Thr		
275						280						285					
Pro	Leu	Gln	Asp	Val	Ile	Asp	Thr	Ala	Asn	Gln	Ile	Met	Ala	Pro	Phe		
290						295						300					
Thr	Leu	Asp	Val	Lys	Asn	Val	Val	Trp	Asn	Ser	Ile	Tyr	Glu	Val	Gly		
305						310						315			320		
His	Arg	Val	Ala	Asp	His	Phe	Asp	Asp	Arg	Val	Ser	Glu	Lys	Thr	Ser		
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Ser	Glu	His	Pro	Arg	Ile	Phe	Ile	Ala	Gly	Asp	Ala	Cys	His	Thr	His		
			340				345						350				
Ser	Ala	Lys	Ala	Gly	Gln	Gly	Met	Asn	Val	Ser	Met	Gln	Asp	Gly	Phe		
355						360						365					
Asn	Leu	Gly	Trp	Lys	Leu	Gly	His	Val	Ala	Ser	Gly	Asn	Ser	Pro	Arg		
370						375						380					
Glu	Leu	Leu	Gln	Thr	Tyr	Ala	Glu	Glu	Arg	Glu	Asp	Ile	Ala	Tyr	Lys		
385						390						395			400		
Leu	Ile	Glu	Tyr	Asp	Lys	Asn	Trp	Ser	Thr	Leu	Met	Ala	Lys	Pro	Ser		
			405				410						415				

Ser Glu Met Gly Ser Ala Gln Asp Leu Glu Asp Phe Tyr Arg Ala Asn
 420 425 430

Ser Glu Phe Asn Ala Gly Tyr Met Thr His Tyr Pro Pro Ser Ser Ile
 435 440 445

Thr Met Asp Gly Ser Asn Gln Asp Leu Ala Lys Gly Tyr Pro Ile Gly
 450 455 460

Arg Arg Phe Lys Ser Ala Met Val Gly Arg Val Cys Asp Phe Thr Glu
 465 470 475 480

Thr His Leu Gly His Gln Ala Thr Ala Asp Gly Arg Met Arg Ala Tyr
 485 490 495

Val Phe Ala Gly Ser Asp Ala Leu Asn Gly Glu Gly Ser Glu Leu Asp
 500 505 510

Arg Trp Ala Glu Trp Ala Glu Ala Asn Leu Asp Pro Thr Leu Val Asp
 515 520 525

Ala Lys Val Ile Tyr Gln Ser Pro Tyr Thr Glu Leu Asp Thr Arg Gln
 530 535 540

Val Pro Ser Val Phe Lys Pro Ala Val Gly Ile Phe Glu Leu Thr Asn
 545 550 555 560

Val Glu Asn Ser Phe Gly Ile Thr Thr Asp Ser Asp Ile Phe Asp Ser
 565 570 575

Arg Glu Ile Ser Arg Asp Gly Val Val Val Val Val Arg Pro Asp Gln
 580 585 590

Tyr Val Ser Gly Ile Phe Pro Leu Thr Asp Thr Gln Gly Leu Gly Glu
 595 600 605

Phe Leu Thr Gly Tyr Phe Pro Lys Met Lys Gly Ala His Gln Leu Ile
 610 615 620

Asn Ala Asn
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<210> 417

<211> 735

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(712)

<223> RXN01461

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 Met Ile Asp Thr Gly
 1 5

aag aac ggc gag ttc cgc tac gag cag tcg aat atc atc gat cag aac 163
Lys Asn Gly Glu Phe Arg Tyr Glu Gln Ser Asn Ile Ile Asp Gln Asn
10 15 20
gaa gcc gag ttc ggc atc act cct tca cag acc gtg ggc cct tac gtc 211
Glu Ala Glu Phe Gly Ile Thr Pro Ser Gln Thr Val Gly Pro Tyr Val
25 30 35
cac atc ggt ttg acc ctt gaa ggt gcg gag cat ctc gtg gag cca ggt 259
His Ile Gly Leu Thr Leu Glu Gly Ala Glu His Leu Val Glu Pro Gly
40 45 50
tcg gaa ggc gcg gtg tcc ttt act gtt tcc gca act gat ggc aac ggc 307
Ser Glu Gly Ala Val Ser Phe Thr Val Ser Ala Thr Asp Gly Asn Gly
55 60 65
gac ccc atc gcg gat gcc atg ttt gaa ctg tgg cag gcc gat cca gag 355
Asp Pro Ile Ala Asp Ala Met Phe Glu Leu Trp Gln Ala Asp Pro Glu
70 75 80 85
ggc atc cac aac tct gat ttg gat cca aac cgc aca gca cca gca acc 403
Gly Ile His Asn Ser Asp Leu Asp Pro Asn Arg Thr Ala Pro Ala Thr
90 95 100
gca gat ggc ttc cgc ggg ctt ggt cgc gcg atg gca aac gcg cag ggt 451
Ala Asp Gly Phe Arg Gly Leu Gly Arg Ala Met Ala Asn Ala Gln Gly
105 110 115
gag gca acg ttc acc act ttg gtt ccg gga gca ttc gca gat gag gca 499
Glu Ala Thr Phe Thr Thr Leu Val Pro Gly Ala Phe Ala Asp Glu Ala
120 125 130
cca cac ttc aag gtt ggt gtg ttc gcc cgt ggc atg ctg gag cgt ctg 547
Pro His Phe Lys Val Gly Val Phe Ala Arg Gly Met Leu Glu Arg Leu
135 140 145
tac act cgc gca tac ctg cca gac gcc gat ttg agc acc gac cca gtt 595
Tyr Thr Arg Ala Tyr Leu Pro Asp Ala Asp Leu Ser Thr Asp Pro Val
150 155 160 165
ttg gct gtg gtc cca gct gat cga cgt gac ctc ctg gtg gct caa aag 643
Leu Ala Val Val Pro Ala Asp Arg Arg Asp Leu Leu Val Ala Gln Lys
170 175 180
acc gat gat gga ttc cgc ttc gac atc act gtc cag gct gaa gac aat 691
Thr Asp Asp Gly Phe Arg Phe Asp Ile Thr Val Gln Ala Glu Asp Asn
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Glu Thr Pro Phe Phe Gly Leu
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<210> 418

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 418

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                                         Met Ile Asp Thr Gly
                                         1                               5

aag aac ggc gag ttc cgc tac gag cag tcg aat atc atc gat cag aac      163
Lys Asn Gly Glu Phe Arg Tyr Glu Gln Ser Asn Ile Ile Asp Gln Asn
                        10                               15                               20

gaa gcc gag ttc ggc atc act cct tca cag acc gtg ggc cct tac gtc      211
Glu Ala Glu Phe Gly Ile Thr Pro Ser Gln Thr Val Gly Pro Tyr Val

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His	Ile	Gly	Leu	Thr	Leu	Glu	Gly	Ala	Glu	His	Leu	Val	Glu	Pro	Gly															
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Ser	Glu	Gly	Ala	Val	Ser	Phe	Thr	Val	Ser	Ala	Thr	Asp	Gly	Asn	Gly															
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gac	ccc	atc	gcg	gat	gcc	atg	ttt	gaa	ctg	tgg	cag	gcc	gat	cca	gag	355														
Asp	Pro	Ile	Ala	Asp	Ala	Met	Phe	Glu	Leu	Trp	Gln	Ala	Asp	Pro	Glu															
70					75					80					85															
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Gly	Ile	His	Asn	Ser	Asp	Leu	Asp	Pro	Asn	Arg	Thr	Ala	Pro	Ala	Thr															
90					95					100																				
gca	gat	ggc	ttc	cgc	ggg	ctt	ggt	cgc	gcg	atg	gca	aac	gcg	cag	ggg	451														
Ala	Asp	Gly	Phe	Arg	Gly	Leu	Gly	Arg	Ala	Met	Ala	Asn	Ala	Gln	Gly															
105					110					115																				
gag	gca	acg	ttc	acc	act	ttg	ggt	cgc	gga	gca	ttc	gca	gat	gag	gca	499														
Glu	Ala	Thr	Phe	Thr	Thr	Leu	Val	Pro	Gly	Ala	Phe	Ala	Asp	Glu	Ala															
120					125					130																				
cca	cac	ttc	aag	gtt	ggg	gtg	ttc	gcc	cgt	ggc	atg	ctg	gag	cgt	ctg	547														
Pro	His	Phe	Lys	Val	Gly	Val	Phe	Ala	Arg	Gly	Met	Leu	Glu	Arg	Leu															
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<211> 153

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

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Ile	Ile	Asp	Gln	Asn	Glu	Ala	Glu	Phe	Gly	Ile	Thr	Pro	Ser	Gln	Thr
			20					25					30		

Val	Gly	Pro	Tyr	Val	His	Ile	Gly	Leu	Thr	Leu	Glu	Gly	Ala	Glu	His
		35					40					45			

Leu	Val	Glu	Pro	Gly	Ser	Glu	Gly	Ala	Val	Ser	Phe	Thr	Val	Ser	Ala
		50					55				60				

Thr	Asp	Gly	Asn	Gly	Asp	Pro	Ile	Ala	Asp	Ala	Met	Phe	Glu	Leu	Trp
	65				70					75					80

Gln	Ala	Asp	Pro	Glu	Gly	Ile	His	Asn	Ser	Asp	Leu	Asp	Pro	Asn	Arg
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Thr	Ala	Pro	Ala	Thr	Ala	Asp	Gly	Phe	Arg	Gly	Leu	Gly	Arg	Ala	Met
			100					105					110		

Ala Asn Ala Gln Gly Glu Ala Thr Phe Thr Thr Leu Val Pro Gly Ala
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Phe Ala Asp Glu Ala Pro His Phe Lys Val Gly Val Phe Ala Arg Gly
 130 135 140

Met Leu Glu Arg Leu Tyr Thr Arg Ala
 145 150

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 <211> 813
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(790)
 <223> RXA01462

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 Met Asp Ile Pro His
 1 5

ttc gcc ccg acg gga ggc gaa tac tcc cca ctg cac ttc ccg gag tac 163
 Phe Ala Pro Thr Gly Gly Glu Tyr Ser Pro Leu His Phe Pro Glu Tyr
 10 15 20

cgg acc acc atc aag cgc aac cca agc aac gat ctc atc atg gtt cct 211
 Arg Thr Thr Ile Lys Arg Asn Pro Ser Asn Asp Leu Ile Met Val Pro
 25 30 35

agt cgc ctc ggc gag tcc acg gga cct gtc ttc ggc gac cgc gac ttg 259
 Ser Arg Leu Gly Glu Ser Thr Gly Pro Val Phe Gly Asp Arg Asp Leu
 40 45 50

gga gac atc gac aac gac atg acc aag gtg aac ggt ggc gag gct atc 307
 Gly Asp Ile Asp Asn Asp Met Thr Lys Val Asn Gly Gly Glu Ala Ile
 55 60 65

ggc cag cgc atc ttc gtt cac ggc cgt gtc ctc ggt ttc gat ggc aag 355
 Gly Gln Arg Ile Phe Val His Gly Arg Val Leu Gly Phe Asp Gly Lys
 70 75 80 85

cca gtt ccg cac acc ttg gtc gag gcg tgg cag gca aac gcc gca ggc 403
 Pro Val Pro His Thr Leu Val Glu Ala Trp Gln Ala Asn Ala Ala Gly
 90 95 100

cgt tac cgc cac aag aat gac tcc tgg cca gcg cca ctg gat cca cac 451
 Arg Tyr Arg His Lys Asn Asp Ser Trp Pro Ala Pro Leu Asp Pro His
 105 110 115

ttc aac ggt gtt gca cgt act ctc acc gac aag gac ggc cag tac cac 499
 Phe Asn Gly Val Ala Arg Thr Leu Thr Asp Lys Asp Gly Gln Tyr His
 120 125 130

ttc tgg acc gtt atg cca ggt aat tac cct tgg ggt aac cac cac aac 547

Phe Trp Thr Val Met Pro Gly Asn Tyr Pro Trp Gly Asn His His Asn
 135 140 145
 gca tgg cgc ccg gcg cac att cac ttc tcg ctc tat ggt cgt cag ttt 595
 Ala Trp Arg Pro Ala His Ile His Phe Ser Leu Tyr Gly Arg Gln Phe
 150 155 160 165
 acg gag cgt ctg gtc acc cag atg tac ttc ccg aac gat cca ttg ttc 643
 Thr Glu Arg Leu Val Thr Gln Met Tyr Phe Pro Asn Asp Pro Leu Phe
 170 175 180
 ttc cag gat ccg atc tac aac gcg gtg cca aag ggt gca cgt gag cgc 691
 Phe Gln Asp Pro Ile Tyr Asn Ala Val Pro Lys Gly Ala Arg Glu Arg
 185 190 195
 atg atc gca acg ttc gac tat gac gag acc cgt gaa aac ttc gcg ctt 739
 Met Ile Ala Thr Phe Asp Tyr Asp Glu Thr Arg Glu Asn Phe Ala Leu
 200 205 210
 ggt tac aag ttc gac atc gtc ctt cgt ggc cgc aac gcc acc cca ttt 787
 Gly Tyr Lys Phe Asp Ile Val Leu Arg Gly Arg Asn Ala Thr Pro Phe
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 gag taaaggggttt tgcaatgatt gat 813
 Glu
 230
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 <211> 230
 <212> PRT
 <213> Corynebacterium glutamicum
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 His Phe Pro Glu Tyr Arg Thr Thr Ile Lys Arg Asn Pro Ser Asn Asp
 20 25 30
 Leu Ile Met Val Pro Ser Arg Leu Gly Glu Ser Thr Gly Pro Val Phe
 35 40 45
 Gly Asp Arg Asp Leu Gly Asp Ile Asp Asn Asp Met Thr Lys Val Asn
 50 55 60
 Gly Gly Glu Ala Ile Gly Gln Arg Ile Phe Val His Gly Arg Val Leu
 65 70 75 80
 Gly Phe Asp Gly Lys Pro Val Pro His Thr Leu Val Glu Ala Trp Gln
 85 90 95
 Ala Asn Ala Ala Gly Arg Tyr Arg His Lys Asn Asp Ser Trp Pro Ala
 100 105 110
 Pro Leu Asp Pro His Phe Asn Gly Val Ala Arg Thr Leu Thr Asp Lys
 115 120 125
 Asp Gly Gln Tyr His Phe Trp Thr Val Met Pro Gly Asn Tyr Pro Trp
 130 135 140

Gly Asn His His Asn Ala Trp Arg Pro Ala His Ile His Phe Ser Leu
 145 150 155 160
 Tyr Gly Arg Gln Phe Thr Glu Arg Leu Val Thr Gln Met Tyr Phe Pro
 165 170 175
 Asn Asp Pro Leu Phe Phe Gln Asp Pro Ile Tyr Asn Ala Val Pro Lys
 180 185 190
 Gly Ala Arg Glu Arg Met Ile Ala Thr Phe Asp Tyr Asp Glu Thr Arg
 195 200 205
 Glu Asn Phe Ala Leu Gly Tyr Lys Phe Asp Ile Val Leu Arg Gly Arg
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 Asn Ala Thr Pro Phe Glu
 225 230

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 <223> RXN00641

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 Met Ser Thr Pro Val
 1 5
 tca aat ttg gca agc gtt cag aaa act ctg gac cat gcg ctt gag gac 163
 Ser Asn Leu Ala Ser Val Gln Lys Thr Leu Asp His Ala Leu Glu Asp
 10 15 20
 cgc cct gaa gag gga atc gtc cgc gtc aac cgc aac atc ttc act gac 211
 Arg Pro Glu Glu Gly Ile Val Arg Val Asn Arg Asn Ile Phe Thr Asp
 25 30 35
 cct gag atc ttc gag ctg gag atg cgc cac atc ttc gaa ggc atc tgg 259
 Pro Glu Ile Phe Glu Leu Glu Met Arg His Ile Phe Glu Gly Ile Trp
 40 45 50
 atg gac atg gct cac gag tcc cag atc cct aac ggt gga gac tac ttc 307
 Met Asp Met Ala His Glu Ser Gln Ile Pro Asn Gly Gly Asp Tyr Phe
 55 60 65
 acc acc tac att ggc tgc cag cgg atc atg atc acc cgt tcc aag gaa 355
 Thr Thr Tyr Ile Gly Cys Gln Arg Ile Met Ile Thr Arg Ser Lys Glu
 70 75 80 85
 ggc aca ctc aac ggc ctg atc aac gcg tgt tct cac cgt ggc gcc atg 403
 Gly Thr Leu Asn Gly Leu Ile Asn Ala Cys Ser His Arg Gly Ala Met
 90 95 100
 ctc tgc cgt ggc aag agt gac aac cgc acc tcc ttg acc tgc cca ttc 451

Leu	Cys	Arg	Gly	Lys	Ser	Asp	Asn	Arg	Thr	Ser	Leu	Thr	Cys	Pro	Phe	
			105					110					115			
cac	ggc	tgg	cca	ttc	tgc	aac	ggc	ggc	gca	ctg	ctc	aag	gtc	aag	ggc	499
His	Gly	Trp	Pro	Phe	Cys	Asn	Gly	Gly	Ala	Leu	Leu	Lys	Val	Lys	Gly	
		120					125					130				
gaa	aaa	gaa	ggc	gcc	tac	cca	gag	aat	ttc	cgc	acc	gac	ggc	tcc	cac	547
Glu	Lys	Glu	Gly	Ala	Tyr	Pro	Glu	Asn	Phe	Arg	Thr	Asp	Gly	Ser	His	
	135					140					145					
gat	gtg	cgt	cgc	gtt	cct	aag	tta	gag	tcc	tac	cgt	ggc	ttc	ctc	ttc	595
Asp	Val	Arg	Arg	Val	Pro	Lys	Leu	Glu	Ser	Tyr	Arg	Gly	Phe	Leu	Phe	
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ggc	tcc	ctc	aac	gat	gat	gtc	gtt	tct	ttg	gaa	gag	cac	ctc	ggc	gac	643
Gly	Ser	Leu	Asn	Asp	Asp	Val	Val	Ser	Leu	Glu	Glu	His	Leu	Gly	Asp	
			170					175					180			
acc	cgt	acc	gtc	att	gac	atg	ctg	gtt	gac	caa	tcc	cca	gaa	ggc	ctc	691
Thr	Arg	Thr	Val	Ile	Asp	Met	Leu	Val	Asp	Gln	Ser	Pro	Glu	Gly	Leu	
			185					190					195			
gaa	gta	ctg	cgc	gga	tcc	tcc	acc	tac	acc	tac	gac	ggc	aac	tgg	aag	739
Glu	Val	Leu	Arg	Gly	Ser	Ser	Thr	Tyr	Thr	Tyr	Asp	Gly	Asn	Trp	Lys	
		200					205					210				
ctc	cag	acc	gaa	aac	ggc	gca	gac	ggc	tac	cac	gtt	tcc	tcc	acc	cac	787
Leu	Gln	Thr	Glu	Asn	Gly	Ala	Asp	Gly	Tyr	His	Val	Ser	Ser	Thr	His	
	215					220					225					
tgg	aac	tac	gct	gca	acc	acc	tcc	cgc	cgt	ggc	act	ggc	gaa	tcc	gcg	835
Trp	Asn	Tyr	Ala	Ala	Thr	Thr	Ser	Arg	Arg	Gly	Thr	Gly	Glu	Ser	Ala	
230					235					240					245	
aac	gaa	acc	aag	gca	atg	gac	gct	ggc	acc	tgg	ggc	aag	cag	ggc	ggc	883
Asn	Glu	Thr	Lys	Ala	Met	Asp	Ala	Gly	Thr	Trp	Gly	Lys	Gln	Gly	Gly	
			250					255					260			
gga	tac	ttc	tcc	tac	cct	tac	ggc	cac	atg	ctg	ctg	tgg	atg	tgg	tgg	931
Gly	Tyr	Phe	Ser	Tyr	Pro	Tyr	Gly	His	Met	Leu	Leu	Trp	Met	Trp	Trp	
			265				270						275			
ggc	aac	cca	gaa	gac	cgc	cca	ctg	ttc	gag	cgc	cgc	gac	gag	ttc	aag	979
Gly	Asn	Pro	Glu	Asp	Arg	Pro	Leu	Phe	Glu	Arg	Arg	Asp	Glu	Phe	Lys	
		280					285					290				
aag	gaa	ttc	ggc	gaa	gaa	aag	ggc	gag	ttc	atg	gtt	ggc	gct	tcc	cgc	1027
Lys	Glu	Phe	Gly	Glu	Glu	Lys	Gly	Glu	Phe	Met	Val	Gly	Ala	Ser	Arg	
	295					300					305					
aat	ctg	tgc	ctc	tac	ccc	aat	gtt	tac	ctg	atg	gat	cag	ttc	tcc	tca	1075
Asn	Leu	Cys	Leu	Tyr	Pro	Asn	Val	Tyr	Leu	Met	Asp	Gln	Phe	Ser	Ser	
310					315				320						325	
cag	atc	cgc	cac	atc	cgc	cca	atc	tca	gtt	gat	cag	acc	gaa	gtc	acc	1123
Gln	Ile	Arg	His	Ile	Arg	Pro	Ile	Ser	Val	Asp	Gln	Thr	Glu	Val	Thr	
			330					335					340			
atc	tac	tgc	atc	gca	cct	aag	ggc	gag	tcc	gcg	gaa	gca	cgt	gca	aac	1171
Ile	Tyr	Cys	Ile	Ala	Pro	Lys	Gly	Glu	Ser	Ala	Glu	Ala	Arg	Ala	Asn	

345										350										355										
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Arg Ile Arg Gln Tyr Glu Asp Phe Phe Asn Ala Thr Gly Met Ala Thr																														
360 365 370																														
cca gat gac ctg gag gaa ttc cgc tcc tgc cag aag acc tac cag gca	1267																													
Pro Asp Asp Leu Glu Glu Phe Arg Ser Cys Gln Lys Thr Tyr Gln Ala																														
375 380 385																														
tct gcc ttc cca tgg aat gac atg acc cgc ggt ttg ggc cac cag gta	1315																													
Ser Ala Phe Pro Trp Asn Asp Met Thr Arg Gly Leu Gly His Gln Val																														
390 395 400 405																														
cag gga cca aac gag gtt gcc aag ggc cta ggc atg aac gaa gtt ctt	1363																													
Gln Gly Pro Asn Glu Val Ala Lys Gly Leu Gly Met Asn Glu Val Leu																														
410 415 420																														
tcc tcc gga gca cgc acc gaa gat gaa ggc ctc tac cca atc cag cac	1411																													
Ser Ser Gly Ala Arg Thr Glu Asp Glu Gly Leu Tyr Pro Ile Gln His																														
425 430 435																														
ggc ttc tgg cat gaa ctc atg cag gag gct gtg aat aag cag agc atc	1459																													
Gly Phe Trp His Glu Leu Met Gln Glu Ala Val Asn Lys Gln Ser Ile																														
440 445 450																														
aag gaa aag gaa ttg gct gac gat acc gct tct tcc ctt gcc acc gta	1507																													
Lys Glu Lys Glu Leu Ala Asp Asp Thr Ala Ser Ser Leu Ala Thr Val																														
455 460 465																														
gct gca gcc aaa atc cgt gag gaa gca aag gca gcc gcg aag tcc gac	1555																													
Ala Ala Ala Lys Ile Arg Glu Glu Ala Lys Ala Ala Ala Lys Ser Asp																														
470 475 480 485																														
gct gga gag cct cgc cgc cgt cgt cgc acc cgc ggt tagtcgtcga	1601																													
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<211> 497

<212> PRT

<213> Corynebacterium glutamicum

<400> 424

Met Ser Thr Pro Val Ser Asn Leu Ala Ser Val Gln Lys Thr Leu Asp
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His Ala Leu Glu Asp Arg Pro Glu Glu Gly Ile Val Arg Val Asn Arg
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Asn Ile Phe Thr Asp Pro Glu Ile Phe Glu Leu Glu Met Arg His Ile
35 40 45

Phe Glu Gly Ile Trp Met Asp Met Ala His Glu Ser Gln Ile Pro Asn
50 55 60

Gly Gly Asp Tyr Phe Thr Thr Tyr Ile Gly Cys Gln Arg Ile Met Ile
65 70 75 80

Thr Arg Ser Lys Glu Gly Thr Leu Asn Gly Leu Ile Asn Ala Cys Ser
 85 90 95
 His Arg Gly Ala Met Leu Cys Arg Gly Lys Ser Asp Asn Arg Thr Ser
 100 105 110
 Leu Thr Cys Pro Phe His Gly Trp Pro Phe Cys Asn Gly Gly Ala Leu
 115 120 125
 Leu Lys Val Lys Gly Glu Lys Glu Gly Ala Tyr Pro Glu Asn Phe Arg
 130 135 140
 Thr Asp Gly Ser His Asp Val Arg Arg Val Pro Lys Leu Glu Ser Tyr
 145 150 155 160
 Arg Gly Phe Leu Phe Gly Ser Leu Asn Asp Asp Val Val Ser Leu Glu
 165 170 175
 Glu His Leu Gly Asp Thr Arg Thr Val Ile Asp Met Leu Val Asp Gln
 180 185 190
 Ser Pro Glu Gly Leu Glu Val Leu Arg Gly Ser Ser Thr Tyr Thr Tyr
 195 200 205
 Asp Gly Asn Trp Lys Leu Gln Thr Glu Asn Gly Ala Asp Gly Tyr His
 210 215 220
 Val Ser Ser Thr His Trp Asn Tyr Ala Ala Thr Thr Ser Arg Arg Gly
 225 230 235 240
 Thr Gly Glu Ser Ala Asn Glu Thr Lys Ala Met Asp Ala Gly Thr Trp
 245 250 255
 Gly Lys Gln Gly Gly Gly Tyr Phe Ser Tyr Pro Tyr Gly His Met Leu
 260 265 270
 Leu Trp Met Trp Trp Gly Asn Pro Glu Asp Arg Pro Leu Phe Glu Arg
 275 280 285
 Arg Asp Glu Phe Lys Lys Glu Phe Gly Glu Glu Lys Gly Glu Phe Met
 290 295 300
 Val Gly Ala Ser Arg Asn Leu Cys Leu Tyr Pro Asn Val Tyr Leu Met
 305 310 315 320
 Asp Gln Phe Ser Ser Gln Ile Arg His Ile Arg Pro Ile Ser Val Asp
 325 330 335
 Gln Thr Glu Val Thr Ile Tyr Cys Ile Ala Pro Lys Gly Glu Ser Ala
 340 345 350
 Glu Ala Arg Ala Asn Arg Ile Arg Gln Tyr Glu Asp Phe Phe Asn Ala
 355 360 365
 Thr Gly Met Ala Thr Pro Asp Asp Leu Glu Glu Phe Arg Ser Cys Gln
 370 375 380
 Lys Thr Tyr Gln Ala Ser Ala Phe Pro Trp Asn Asp Met Thr Arg Gly
 385 390 395 400

Leu Gly His Gln Val Gln Gly Pro Asn Glu Val Ala Lys Gly Leu Gly
 405 410 415
 Met Asn Glu Val Leu Ser Ser Gly Ala Arg Thr Glu Asp Glu Gly Leu
 420 425 430
 Tyr Pro Ile Gln His Gly Phe Trp His Glu Leu Met Gln Glu Ala Val
 435 440 445
 Asn Lys Gln Ser Ile Lys Glu Lys Glu Leu Ala Asp Asp Thr Ala Ser
 450 455 460
 Ser Leu Ala Thr Val Ala Ala Ala Lys Ile Arg Glu Glu Ala Lys Ala
 465 470 475 480
 Ala Ala Lys Ser Asp Ala Gly Glu Pro Arg Arg Arg Arg Arg Thr Arg
 485 490 495

Gly

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 <213> Corynebacterium glutamicum

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 <222> (101)..(349)
 <223> FRXA00640

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 <222> (350)..(367)
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 Met Ser Thr Pro Val
 1 5
 tca aat ttg gca agc gtt cag aaa act ctg gac cat gcg ctt gag gac 163
 Ser Asn Leu Ala Ser Val Gln Lys Thr Leu Asp His Ala Leu Glu Asp
 10 15 20
 cgc cct gaa gag gga atc gtc cgc gtc aac cgc aac atc ttc act gac 211
 Arg Pro Glu Glu Gly Ile Val Arg Val Asn Arg Asn Ile Phe Thr Asp
 25 30 35
 cct gag atc ttc gag ctg gag atg cgc cac atc ttc gaa ggc atc tgg 259
 Pro Glu Ile Phe Glu Leu Glu Met Arg His Ile Phe Glu Gly Ile Trp
 40 45 50
 atg gac atg gct cac gag tcc cag atc cct aac ggt gga gac tac ttc 307
 Met Asp Met Ala His Glu Ser Gln Ile Pro Asn Gly Gly Asp Tyr Phe
 55 60 65
 acc acc tac att ggc tgc cag cgg atc atg atc acc cgt tcc 349
 Thr Thr Tyr Ile Gly Cys Gln Arg Ile Met Ile Thr Arg Ser

70

75

80

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372

<210> 426

<211> 83

<212> PRT

<213> Corynebacterium glutamicum

<400> 426

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			20					25						30	

Asn	Ile	Phe	Thr	Asp	Pro	Glu	Ile	Phe	Glu	Leu	Glu	Met	Arg	His	Ile
		35					40					45			

Phe	Glu	Gly	Ile	Trp	Met	Asp	Met	Ala	His	Glu	Ser	Gln	Ile	Pro	Asn
	50					55						60			

Gly	Gly	Asp	Tyr	Phe	Thr	Thr	Tyr	Ile	Gly	Cys	Gln	Arg	Ile	Met	Ile
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Thr Arg Ser

<210> 427

<211> 1164

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

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<223> FRXA00641

<220>

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<222> (11)..(97)

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				Val	Arg	Arg	Val	Pro		
				1				5		

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Lys	Leu	Glu	Ser	Tyr	Arg	Gly	Phe	Leu	Phe	Gly	Ser	Leu	Asn	Asp	Asp	
			10				15							20		

gtc	gtt	tct	ttg	gaa	gag	cac	ctc	ggc	gac	acc	cgt	acc	gtc	att	gac	211
Val	Val	Ser	Leu	Glu	Glu	His	Leu	Gly	Asp	Thr	Arg	Thr	Val	Ile	Asp	
			25				30						35			

atg	ctg	gtt	gac	caa	tcc	cca	gaa	ggc	ctc	gaa	gta	ctg	cgc	gga	tcc	259
Met	Leu	Val	Asp	Gln	Ser	Pro	Glu	Gly	Leu	Glu	Val	Leu	Arg	Gly	Ser	

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tcc	acc	tac	acc	tac	gac	ggc	aac	tgg	aag	ctc	cag	acc	gaa	aac	ggt	307
Ser	Thr	Tyr	Thr	Tyr	Asp	Gly	Asn	Trp	Lys	Leu	Gln	Thr	Glu	Asn	Gly	
55					60					65						
gca	gac	ggc	tac	cac	gtt	tcc	tcc	acc	cac	tgg	aac	tac	gct	gca	acc	355
Ala	Asp	Gly	Tyr	His	Val	Ser	Ser	Thr	His	Trp	Asn	Tyr	Ala	Ala	Thr	
70					75					80					85	
acc	tcc	cgc	cgt	ggc	act	ggt	gaa	tcc	gcg	aac	gaa	acc	aag	gca	atg	403
Thr	Ser	Arg	Arg	Gly	Thr	Gly	Glu	Ser	Ala	Asn	Glu	Thr	Lys	Ala	Met	
					90					95					100	
gac	gct	ggt	acc	tgg	ggc	aag	cag	ggt	ggc	gga	tac	ttc	tcc	tac	cct	451
Asp	Ala	Gly	Thr	Trp	Gly	Lys	Gln	Gly	Gly	Gly	Tyr	Phe	Ser	Tyr	Pro	
					105					110					115	
tac	ggc	cac	atg	ctg	ctg	tgg	atg	tgg	tgg	ggc	aac	cca	gaa	gac	cgc	499
Tyr	Gly	His	Met	Leu	Leu	Trp	Met	Trp	Trp	Gly	Asn	Pro	Glu	Asp	Arg	
					120					125					130	
cca	ctg	ttc	gag	cgc	cgc	gac	gag	ttc	aag	aag	gaa	ttc	ggc	gaa	gaa	547
Pro	Leu	Phe	Glu	Arg	Arg	Asp	Glu	Phe	Lys	Lys	Glu	Phe	Gly	Glu	Glu	
					135					140					145	
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Lys	Gly	Glu	Phe	Met	Val	Gly	Ala	Ser	Arg	Asn	Leu	Cys	Leu	Tyr	Pro	
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aat	gtt	tac	ctg	atg	gat	cag	ttc	tcc	tca	cag	atc	cgc	cac	atc	cgc	643
Asn	Val	Tyr	Leu	Met	Asp	Gln	Phe	Ser	Ser	Gln	Ile	Arg	His	Ile	Arg	
					170					175					180	
cca	atc	tca	gtt	gat	cag	acc	gaa	gtc	acc	atc	tac	tgc	atc	gca	cct	691
Pro	Ile	Ser	Val	Asp	Gln	Thr	Glu	Val	Thr	Ile	Tyr	Cys	Ile	Ala	Pro	
					185					190					195	
aag	ggc	gag	tcc	gcg	gaa	gca	cgt	gca	aac	cgc	atc	cgc	cag	tac	gaa	739
Lys	Gly	Glu	Ser	Ala	Glu	Ala	Arg	Ala	Asn	Arg	Ile	Arg	Gln	Tyr	Glu	
200					205					210						
gac	ttc	ttc	aac	gca	acg	ggc	atg	gca	acc	cca	gat	gac	ctg	gag	gaa	787
Asp	Phe	Phe	Asn	Ala	Thr	Gly	Met	Ala	Thr	Pro	Asp	Asp	Leu	Glu	Glu	
215					220					225						
ttc	cgc	tcc	tgc	cag	aag	acc	tac	cag	gca	tct	gcc	ttc	cca	tgg	aat	835
Phe	Arg	Ser	Cys	Gln	Lys	Thr	Tyr	Gln	Ala	Ser	Ala	Phe	Pro	Trp	Asn	
230					235					240					245	
gac	atg	acc	cgc	ggt	ttg	ggc	cac	cag	gta	cag	gga	cca	aac	gag	gtt	883
Asp	Met	Thr	Arg	Gly	Leu	Gly	His	Gln	Val	Gln	Gly	Pro	Asn	Glu	Val	
					250					255					260	
gcc	aag	ggc	cta	ggc	atg	aac	gaa	gtt	ctt	tcc	tcc	gga	gca	cgc	acc	931
Ala	Lys	Gly	Leu	Gly	Met	Asn	Glu	Val	Leu	Ser	Ser	Gly	Ala	Arg	Thr	
265					270					275						
gaa	gat	gaag	ggc	ctc	tac	cca	atc	cag	cac	ggc	ttc	tgg	cat	gaa	ctc	979
Glu	Asp	Glu	Gly	Leu	Tyr	Pro	Ile	Gln	His	Gly	Phe	Trp	His	Glu	Leu	
280					285					290						

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 Met Gln Glu Ala Val Asn Lys Gln Ser Ile Lys Glu Lys Glu Leu Ala
 295 300 305

gac gat acc gct tct tcc ctt gcc acc gta gct gca gcc aaa atc cgt 1075
 Asp Asp Thr Ala Ser Ser Leu Ala Thr Val Ala Ala Ala Lys Ile Arg
 310 315 320 325

gag gaa gca aag gca gcc gcg aag tcc gac gct gga gag cct cgc cgc 1123
 Glu Glu Ala Lys Ala Ala Ala Lys Ser Asp Ala Gly Glu Pro Arg Arg
 330 335 340

cgt cgt cgc acc cgc ggt tagtcgtcga aaagcaaaaa atc 1164
 Arg Arg Arg Thr Arg Gly
 345

<210> 428

<211> 347

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 428

Val Arg Arg Val Pro Lys Leu Glu Ser Tyr Arg Gly Phe Leu Phe Gly
 1 5 10 15

Ser Leu Asn Asp Asp Val Val Ser Leu Glu Glu His Leu Gly Asp Thr
 20 25 30

Arg Thr Val Ile Asp Met Leu Val Asp Gln Ser Pro Glu Gly Leu Glu
 35 40 45

Val Leu Arg Gly Ser Ser Thr Tyr Thr Tyr Asp Gly Asn Trp Lys Leu
 50 55 60

Gln Thr Glu Asn Gly Ala Asp Gly Tyr His Val Ser Ser Thr His Trp
 65 70 75 80

Asn Tyr Ala Ala Thr Thr Ser Arg Arg Gly Thr Gly Glu Ser Ala Asn
 85 90 95

Glu Thr Lys Ala Met Asp Ala Gly Thr Trp Gly Lys Gln Gly Gly Gly
 100 105 110

Tyr Phe Ser Tyr Pro Tyr Gly His Met Leu Leu Trp Met Trp Trp Gly
 115 120 125

Asn Pro Glu Asp Arg Pro Leu Phe Glu Arg Arg Asp Glu Phe Lys Lys
 130 135 140

Glu Phe Gly Glu Glu Lys Gly Glu Phe Met Val Gly Ala Ser Arg Asn
 145 150 155 160

Leu Cys Leu Tyr Pro Asn Val Tyr Leu Met Asp Gln Phe Ser Ser Gln
 165 170 175

Ile Arg His Ile Arg Pro Ile Ser Val Asp Gln Thr Glu Val Thr Ile
 180 185 190

Tyr Cys Ile Ala Pro Lys Gly Glu Ser Ala Glu Ala Arg Ala Asn Arg

195	200	205
Ile Arg Gln Tyr Glu Asp Phe Phe Asn Ala Thr Gly Met Ala Thr Pro 210 215 220		
Asp Asp Leu Glu Glu Phe Arg Ser Cys Gln Lys Thr Tyr Gln Ala Ser 225 230 235 240		
Ala Phe Pro Trp Asn Asp Met Thr Arg Gly Leu Gly His Gln Val Gln 245 250 255		
Gly Pro Asn Glu Val Ala Lys Gly Leu Gly Met Asn Glu Val Leu Ser 260 265 270		
Ser Gly Ala Arg Thr Glu Asp Glu Gly Leu Tyr Pro Ile Gln His Gly 275 280 285		
Phe Trp His Glu Leu Met Gln Glu Ala Val Asn Lys Gln Ser Ile Lys 290 295 300		
Glu Lys Glu Leu Ala Asp Asp Thr Ala Ser Ser Leu Ala Thr Val Ala 305 310 315 320		
Ala Ala Lys Ile Arg Glu Glu Ala Lys Ala Ala Ala Lys Ser Asp Ala 325 330 335		
Gly Glu Pro Arg Arg Arg Arg Thr Arg Gly 340 345		

<210> 429
 <211> 615
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(592)
 <223> RXA00642

<400> 429
 aaaggcagcc gcgaagtccg acgctggaga gcctcgccgc cgctcgtcgca cccgcggtta 60
 gtcgtcgaaa agcaaaaaat cttttaagga gaacacctaa atg tct gaa atc acc 115
 Met Ser Glu Ile Thr
 1 5
 cgc tct gag atc gaa gct ttc ctc tac tac gag gct cgc ctg ctc gat 163
 Arg Ser Glu Ile Glu Ala Phe Leu Tyr Tyr Glu Ala Arg Leu Leu Asp
 10 15 20
 gac cgt aaa ttt gaa gaa tgg ctc gaa tgc tac cgc gag gac gcc gag 211
 Asp Arg Lys Phe Glu Glu Trp Leu Glu Cys Tyr Arg Glu Asp Ala Glu
 25 30 35
 ttt tgg atg cca gcc tgg gac gac aac ggt gaa ctg act gaa gat cca 259
 Phe Trp Met Pro Ala Trp Asp Asp Asn Gly Glu Leu Thr Glu Asp Pro
 40 45 50
 cag tct gaa att tcc ctc atc tac tac cca aac cgt ggt gga ctt gag 307
 Gln Ser Glu Ile Ser Leu Ile Tyr Tyr Pro Asn Arg Gly Gly Leu Glu

55	60	65	
gac cgc gtc ttc cgc atc cgc acc gaa cgc tcc tct gca act tcc cta			355
Asp Arg Val Phe Arg Ile Arg Thr Glu Arg Ser Ser Ala Thr Ser Leu			
70	75	80	85
cct gaa cca cgc acc ggc cac agc acc acc aac gtg gaa atc ctg gag			403
Pro Glu Pro Arg Thr Gly His Ser Thr Thr Asn Val Glu Ile Leu Glu			
	90	95	100
cgc cgc gac ggc gaa gta gat atc cgc ttc aac tgg atc acc ttc tac			451
Arg Arg Asp Gly Glu Val Asp Ile Arg Phe Asn Trp Ile Thr Phe Tyr			
	105	110	115
tac cgt tac aac acc acc gac acc tac ttc ggc acc acg ttt atc acc			499
Tyr Arg Tyr Asn Thr Thr Asp Thr Tyr Phe Gly Thr Thr Phe Ile Thr			
	120	125	130
ctt gat gtc agt ggt gaa acc ccg aag atc gtc aag aag aag gtc gtt			547
Leu Asp Val Ser Gly Glu Thr Pro Lys Ile Val Lys Lys Lys Val Val			
	135	140	145
ttg aag aac gac tac atc cac cac atc gtc gat att tac cac gtc			592
Leu Lys Asn Asp Tyr Ile His His Ile Val Asp Ile Tyr His Val			
	150	155	160
taggaggcac tcacatgact cac			615

<210> 430

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 430

Met Ser Glu Ile Thr Arg Ser Glu Ile Glu Ala Phe Leu Tyr Tyr Glu			
1	5	10	15
Ala Arg Leu Leu Asp Asp Arg Lys Phe Glu Glu Trp Leu Glu Cys Tyr			
	20	25	30
Arg Glu Asp Ala Glu Phe Trp Met Pro Ala Trp Asp Asp Asn Gly Glu			
	35	40	45
Leu Thr Glu Asp Pro Gln Ser Glu Ile Ser Leu Ile Tyr Tyr Pro Asn			
	50	55	60
Arg Gly Gly Leu Glu Asp Arg Val Phe Arg Ile Arg Thr Glu Arg Ser			
	65	70	75
Ser Ala Thr Ser Leu Pro Glu Pro Arg Thr Gly His Ser Thr Thr Asn			
	85	90	95
Val Glu Ile Leu Glu Arg Arg Asp Gly Glu Val Asp Ile Arg Phe Asn			
	100	105	110
Trp Ile Thr Phe Tyr Tyr Arg Tyr Asn Thr Thr Asp Thr Tyr Phe Gly			
	115	120	125
Thr Thr Phe Ile Thr Leu Asp Val Ser Gly Glu Thr Pro Lys Ile Val			
	130	135	140

Lys Lys Lys Val Val Leu Lys Asn Asp Tyr Ile His His Ile Val Asp
 145 150 155 160

Ile Tyr His Val

<210> 431

<211> 1659

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1636)

<223> RXA00643

<400> 431

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 accacatcgt cgatattttac cacgtctagg aggcaactcac atg act cac caa gtt 115
 Met Thr His Gln Val
 1 5
 gca ctt gcc ttt gaa gac ggc atc acc cga ttc atc gac tgc gaa gat 163
 Ala Leu Ala Phe Glu Asp Gly Ile Thr Arg Phe Ile Asp Cys Glu Asp
 10 15 20
 gac caa act gtt gca gat gcc gcc tac cag gca cgc atc aac att cct 211
 Asp Gln Thr Val Ala Asp Ala Ala Tyr Gln Ala Arg Ile Asn Ile Pro
 25 30 35
 ttc gac tgc cgc gac ggc gcc tgc gga acc tgc aaa gcg ttc tgc gaa 259
 Phe Asp Cys Arg Asp Gly Ala Cys Gly Thr Cys Lys Ala Phe Cys Glu
 40 45 50
 tcc ggc gac ttt gac gaa ggc gac tac atc gac gac gcc ctg tcc gaa 307
 Ser Gly Asp Phe Asp Glu Gly Asp Tyr Ile Asp Asp Ala Leu Ser Glu
 55 60 65
 gat gaa gca gcc gac ggc tac tgc ctg cct tgc cag atg acc cca aag 355
 Asp Glu Ala Ala Asp Gly Tyr Cys Leu Pro Cys Gln Met Thr Pro Lys
 70 75 80 85
 acc gac ctc atc ttg cag atc gcc acc acc tcc gtg ctg gca aag acc 403
 Thr Asp Leu Ile Leu Gln Ile Ala Thr Thr Ser Val Leu Ala Lys Thr
 90 95 100
 ggc gca tcc act ttc gat ggc gag ttg aag gag atc aat cac ttc tct 451
 Gly Ala Ser Thr Phe Asp Gly Glu Leu Lys Glu Ile Asn His Phe Ser
 105 110 115
 gat tcc acc atc ggc att gag atc gaa ctg gaa aac cgc caa gat ttg 499
 Asp Ser Thr Ile Gly Ile Glu Ile Glu Leu Glu Asn Arg Gln Asp Leu
 120 125 130
 gcg ttc ctc cct ggt caa tac atg aac atc cag gtt cca ggc agc gac 547
 Ala Phe Leu Pro Gly Gln Tyr Met Asn Ile Gln Val Pro Gly Ser Asp
 135 140 145

cag act cgt tcc tac tct ttc tcc tgc gct caa gat tcc ggc aac gtg	595
Gln Thr Arg Ser Tyr Ser Phe Ser Cys Ala Gln Asp Ser Gly Asn Val	
150 155 160 165	
cag ttc ctg atc aag gta acc cca ggt gga ctc atg acc acc tat ctc	643
Gln Phe Leu Ile Lys Val Thr Pro Gly Gly Leu Met Thr Thr Tyr Leu	
170 175 180	
acc gat cac gcg aag gtc ggc gac aag ctc acc ttg acc ggc ccg atg	691
Thr Asp His Ala Lys Val Gly Asp Lys Leu Thr Leu Thr Gly Pro Met	
185 190 195	
ggt tcc ttc ttc ctg cgt gaa cct gtc cgc ccg atc ctg ctg ctc gcc	739
Gly Ser Phe Phe Leu Arg Glu Pro Val Arg Pro Ile Leu Leu Leu Ala	
200 205 210	
ggc gga act gga ctt gca ccg atc ttg gct att ttg gaa aag ctt tcc	787
Gly Gly Thr Gly Leu Ala Pro Ile Leu Ala Ile Leu Glu Lys Leu Ser	
215 220 225	
cgc gat gag ctt ctc gac gtc cca atc cgc ctg gtt tac ggc gcg aac	835
Arg Asp Glu Leu Leu Asp Val Pro Ile Arg Leu Val Tyr Gly Ala Asn	
230 235 240 245	
ttc acc cac gat ctg gtg gaa ttg gat cga ctt gat gcc ttc aag gac	883
Phe Thr His Asp Leu Val Glu Leu Asp Arg Leu Asp Ala Phe Lys Asp	
250 255 260	
aag ttc gac ttc gat tac atc acc gtg ctt tcc gac aag gac acc gag	931
Lys Phe Asp Phe Asp Tyr Ile Thr Val Leu Ser Asp Lys Asp Thr Glu	
265 270 275	
cat cca cgc aag ggc tac gtc cca gca cac ctg acc ggc gaa tat gag	979
His Pro Arg Lys Gly Tyr Val Pro Ala His Leu Thr Gly Glu Tyr Glu	
280 285 290	
cca gat gag gac act gat gtg tac ctc tgc ggc cct cct cca atg gtc	1027
Pro Asp Glu Asp Thr Asp Val Tyr Leu Cys Gly Pro Pro Pro Met Val	
295 300 305	
gag gcc gtg cgc caa ttc ctg ggc acc ctg gag cat cct ccg ctg gac	1075
Glu Ala Val Arg Gln Phe Leu Gly Thr Leu Glu His Pro Pro Leu Asp	
310 315 320 325	
ttt tat tac gag aag ttc act tcc gcc gct gcc cct gct gct ggt aag	1123
Phe Tyr Tyr Glu Lys Phe Thr Ser Ala Ala Ala Pro Ala Ala Gly Lys	
330 335 340	
cca gag atc acc gtg gag acc agc gaa gtt gca gag gat ttc aac ctg	1171
Pro Glu Ile Thr Val Glu Thr Ser Glu Val Ala Glu Asp Phe Asn Leu	
345 350 355	
gtc gag gtg tcc act cca ggc atg tct tcc ggc gag gtg cac tct tct	1219
Val Glu Val Ser Thr Pro Gly Met Ser Ser Gly Glu Val His Ser Ser	
360 365 370	
gca acc cag ctg cag gcc cgc atg gct ctg gag ctc ggc gcg ctg gag	1267
Ala Thr Gln Leu Gln Ala Arg Met Ala Leu Glu Leu Gly Ala Leu Glu	
375 380 385	
ctt gcg atc aac aaa ctc ggc gag cgc gac atc gag cga ttc cgc aac	1315

Leu Ala Ile Asn Lys Leu Gly Glu Arg Asp Ile Glu Arg Phe Arg Asn
 390 395 400 405
 ttg gcc gac atc gcg aac tcc ttc atc gac ggc gat aag ttt atc gac 1363
 Leu Ala Asp Ile Ala Asn Ser Phe Ile Asp Gly Asp Lys Phe Ile Asp
 410 415 420
 gcg gtg aag ttc acc gag gcc aac gcc gat ttc cac gag ttc ctc ttc 1411
 Ala Val Lys Phe Thr Glu Ala Asn Ala Asp Phe His Glu Phe Leu Phe
 425 430 435
 cgc cgc gca aac aac gag gcg ctg ctt gcg gcg tac cag aac ctc cag 1459
 Arg Arg Ala Asn Asn Glu Ala Leu Leu Ala Ala Tyr Gln Asn Leu Gln
 440 445 450
 gtt gtt caa gaa atg aac gca acc ctt cca ggc gcc gag tgg att gat 1507
 Val Val Gln Glu Met Asn Ala Thr Leu Pro Gly Ala Glu Trp Ile Asp
 455 460 465
 ccg gca att gcc acc gag cac ttg gcg ctt gtc gac gcc gtc tcc cag 1555
 Pro Ala Ile Ala Thr Glu His Leu Ala Leu Val Asp Ala Val Ser Gln
 470 475 480 485
 aat gat ctc gag acc gcg aga aca atc att cgt gaa cac gcg gag cac 1603
 Asn Asp Leu Glu Thr Ala Arg Thr Ile Ile Arg Glu His Ala Glu His
 490 495 500
 ggc att gac act atg gtt aag gcc ctc gag aaa tgagcgcgcc agtaggacaa 1656
 Gly Ile Asp Thr Met Val Lys Ala Leu Glu Lys
 505 510
 ggc 1659

<210> 432

<211> 512

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Met Thr His Gln Val Ala Leu Ala Phe Glu Asp Gly Ile Thr Arg Phe
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 Ile Asp Cys Glu Asp Asp Gln Thr Val Ala Asp Ala Ala Tyr Gln Ala
 20 25 30
 Arg Ile Asn Ile Pro Phe Asp Cys Arg Asp Gly Ala Cys Gly Thr Cys
 35 40 45
 Lys Ala Phe Cys Glu Ser Gly Asp Phe Asp Glu Gly Asp Tyr Ile Asp
 50 55 60
 Asp Ala Leu Ser Glu Asp Glu Ala Ala Asp Gly Tyr Cys Leu Pro Cys
 65 70 75 80
 Gln Met Thr Pro Lys Thr Asp Leu Ile Leu Gln Ile Ala Thr Thr Ser
 85 90 95
 Val Leu Ala Lys Thr Gly Ala Ser Thr Phe Asp Gly Glu Leu Lys Glu
 100 105 110

Ile Asn His Phe Ser Asp Ser Thr Ile Gly Ile Glu Ile Glu Leu Glu
 115 120 125
 Asn Arg Gln Asp Leu Ala Phe Leu Pro Gly Gln Tyr Met Asn Ile Gln
 130 135 140
 Val Pro Gly Ser Asp Gln Thr Arg Ser Tyr Ser Phe Ser Cys Ala Gln
 145 150 155 160
 Asp Ser Gly Asn Val Gln Phe Leu Ile Lys Val Thr Pro Gly Gly Leu
 165 170 175
 Met Thr Thr Tyr Leu Thr Asp His Ala Lys Val Gly Asp Lys Leu Thr
 180 185 190
 Leu Thr Gly Pro Met Gly Ser Phe Phe Leu Arg Glu Pro Val Arg Pro
 195 200 205
 Ile Leu Leu Leu Ala Gly Gly Thr Gly Leu Ala Pro Ile Leu Ala Ile
 210 215 220
 Leu Glu Lys Leu Ser Arg Asp Glu Leu Leu Asp Val Pro Ile Arg Leu
 225 230 235 240
 Val Tyr Gly Ala Asn Phe Thr His Asp Leu Val Glu Leu Asp Arg Leu
 245 250 255
 Asp Ala Phe Lys Asp Lys Phe Asp Phe Asp Tyr Ile Thr Val Leu Ser
 260 265 270
 Asp Lys Asp Thr Glu His Pro Arg Lys Gly Tyr Val Pro Ala His Leu
 275 280 285
 Thr Gly Glu Tyr Glu Pro Asp Glu Asp Thr Asp Val Tyr Leu Cys Gly
 290 295 300
 Pro Pro Pro Met Val Glu Ala Val Arg Gln Phe Leu Gly Thr Leu Glu
 305 310 315 320
 His Pro Pro Leu Asp Phe Tyr Tyr Glu Lys Phe Thr Ser Ala Ala Ala
 325 330 335
 Pro Ala Ala Gly Lys Pro Glu Ile Thr Val Glu Thr Ser Glu Val Ala
 340 345 350
 Glu Asp Phe Asn Leu Val Glu Val Ser Thr Pro Gly Met Ser Ser Gly
 355 360 365
 Glu Val His Ser Ser Ala Thr Gln Leu Gln Ala Arg Met Ala Leu Glu
 370 375 380
 Leu Gly Ala Leu Glu Leu Ala Ile Asn Lys Leu Gly Glu Arg Asp Ile
 385 390 395 400
 Glu Arg Phe Arg Asn Leu Ala Asp Ile Ala Asn Ser Phe Ile Asp Gly
 405 410 415
 Asp Lys Phe Ile Asp Ala Val Lys Phe Thr Glu Ala Asn Ala Asp Phe
 420 425 430
 His Glu Phe Leu Phe Arg Arg Ala Asn Asn Glu Ala Leu Leu Ala Ala

435	440	445
Tyr Gln Asn Leu Gln Val Val Gln Glu Met Asn Ala Thr Leu Pro Gly		
450	455	460
Ala Glu Trp Ile Asp Pro Ala Ile Ala Thr Glu His Leu Ala Leu Val		
465	470	475
Asp Ala Val Ser Gln Asn Asp Leu Glu Thr Ala Arg Thr Ile Ile Arg		
	485	490
Glu His Ala Glu His Gly Ile Asp Thr Met Val Lys Ala Leu Glu Lys		
500	505	510

<210> 433
 <211> 1166
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (16)..(1143)
 <223> RXN01993

<400> 433
 ctttaggagt tcacc atg aca ctg tcc gaa cgc aag ctc acc acc acc gcc 51
 Met Thr Leu Ser Glu Arg Lys Leu Thr Thr Ala
 1 5 10

aag att ctt ccc cac cca ctc aac gcc tgg tac gtc gcc gct tgg gat 99
 Lys Ile Leu Pro His Pro Leu Asn Ala Trp Tyr Val Ala Ala Trp Asp
 15 20 25

tat gaa gtc aca tct aaa aag ccc atg gcc agg aca atc gcc aac aaa 147
 Tyr Glu Val Thr Ser Lys Lys Pro Met Ala Arg Thr Ile Ala Asn Lys
 30 35 40

cca ctc gct ttg tac cgc acc aaa gat ggc cga gcc gtt gcc ctt gca 195
 Pro Leu Ala Leu Tyr Arg Thr Lys Asp Gly Arg Ala Val Ala Leu Ala
 45 50 55 60

gac gcc tgc tgg cac cgc ctc gca ccg cta tcc aag gga aaa ctc gtg 243
 Asp Ala Cys Trp His Arg Leu Ala Pro Leu Ser Lys Gly Lys Leu Val
 65 70 75

ggc aca gac gga atc caa tgc cct tat cac ggc ttg gag tac aac tcc 291
 Gly Thr Asp Gly Ile Gln Cys Pro Tyr His Gly Leu Glu Tyr Asn Ser
 80 85 90

gcg ggc cgc tgc atg aaa atg ccc gcg cag gaa acc ctc aac ccg tca 339
 Ala Gly Arg Cys Met Lys Met Pro Ala Gln Glu Thr Leu Asn Pro Ser
 95 100 105

gca gcc gtc aac tcc tac ccc gtg gtg gaa gcc cac cgc ttt gtg tgg 387
 Ala Ala Val Asn Ser Tyr Pro Val Val Glu Ala His Arg Phe Val Trp
 110 115 120

gtg tgg ctg ggc gat ccc aca ttg gca gat ccc acc caa gta ccc gat 435
 Val Trp Leu Gly Asp Pro Thr Leu Ala Asp Pro Thr Gln Val Pro Asp
 125 130 135 140

atg cac cag atg agc cac ccc gaa tgg gca ggc gat gga cgc acc atc	483
Met His Gln Met Ser His Pro Glu Trp Ala Gly Asp Gly Arg Thr Ile	
145 150 155	
tcc gct gac tgc aac tac caa tta gtg ctg gac aac ttg atg gac ctc	531
Ser Ala Asp Cys Asn Tyr Gln Leu Val Leu Asp Asn Leu Met Asp Leu	
160 165 170	
acc cac gaa gag ttc gtg cac tcc tcc agc atc gga caa gac gaa ctt	579
Thr His Glu Glu Phe Val His Ser Ser Ser Ile Gly Gln Asp Glu Leu	
175 180 185	
agt gaa tca gag ttc gtg gtc acc cac act gaa gat tcc gtg acg gtc	627
Ser Glu Ser Glu Phe Val Val Thr His Thr Glu Asp Ser Val Thr Val	
190 195 200	
acc cgc tgg atg cat gac ata gat gca cca ccg ttt tgg caa aag aac	675
Thr Arg Trp Met His Asp Ile Asp Ala Pro Pro Phe Trp Gln Lys Asn	
205 210 215 220	
atg aat gat aag ttc cca gga ttt gaa ggc aag gtg gat cgt tgg cag	723
Met Asn Asp Lys Phe Pro Gly Phe Glu Gly Lys Val Asp Arg Trp Gln	
225 230 235	
atc atc cac tac tac tac cct tcc acc atc tgc att gat gtt ggt gta	771
Ile Ile His Tyr Tyr Tyr Pro Ser Thr Ile Cys Ile Asp Val Gly Val	
240 245 250	
gca aag gct gga act ggc gcg cag gaa ggc gac cgc agc cag ggc gtt	819
Ala Lys Ala Gly Thr Gly Ala Gln Glu Gly Asp Arg Ser Gln Gly Val	
255 260 265	
aat ggg tat gtc atg aac acc att acc cca gat tca gat cgt tcc tct	867
Asn Gly Tyr Val Met Asn Thr Ile Thr Pro Asp Ser Asp Arg Ser Ser	
270 275 280	
cat tac ttc tgg gca ttc atg cgc aac tac cgc ctg gaa agc caa acc	915
His Tyr Phe Trp Ala Phe Met Arg Asn Tyr Arg Leu Glu Ser Gln Thr	
285 290 295 300	
atc acc acc cag ctg cgc gac ggt gta tcc ggt gta ttc aaa gaa gac	963
Ile Thr Thr Gln Leu Arg Asp Gly Val Ser Gly Val Phe Lys Glu Asp	
305 310 315	
gaa gac atg ctg acc gct cag caa gat gcc atc gac gcc aac acc gac	1011
Glu Asp Met Leu Thr Ala Gln Gln Asp Ala Ile Asp Ala Asn Thr Asp	
320 325 330	
tac gag ttt tac agc ctc aac att gat gcc ggt ggc atg tgg gtg cgc	1059
Tyr Glu Phe Tyr Ser Leu Asn Ile Asp Ala Gly Gly Met Trp Val Arg	
335 340 345	
cga atc ctc gag gaa gca ctc tcc aag gaa ggc cga ctg gat atc ccc	1107
Arg Ile Leu Glu Glu Ala Leu Ser Lys Glu Gly Arg Leu Asp Ile Pro	
350 355 360	
acc aca ttc ccc cgc gca aca ccg aag ccg gag gca taaaccatga	1153
Thr Thr Phe Pro Arg Ala Thr Pro Lys Pro Glu Ala	
365 370 375	

actcgcaatg gca

1166

<210> 434

<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 434

Met	Thr	Leu	Ser	Glu	Arg	Lys	Leu	Thr	Thr	Thr	Ala	Lys	Ile	Leu	Pro
1				5				10						15	

His	Pro	Leu	Asn	Ala	Trp	Tyr	Val	Ala	Ala	Trp	Asp	Tyr	Glu	Val	Thr
			20					25					30		

Ser	Lys	Lys	Pro	Met	Ala	Arg	Thr	Ile	Ala	Asn	Lys	Pro	Leu	Ala	Leu
		35					40					45			

Tyr	Arg	Thr	Lys	Asp	Gly	Arg	Ala	Val	Ala	Leu	Ala	Asp	Ala	Cys	Trp
	50					55					60				

His	Arg	Leu	Ala	Pro	Leu	Ser	Lys	Gly	Lys	Leu	Val	Gly	Thr	Asp	Gly
65					70					75					80

Ile	Gln	Cys	Pro	Tyr	His	Gly	Leu	Glu	Tyr	Asn	Ser	Ala	Gly	Arg	Cys
				85					90					95	

Met	Lys	Met	Pro	Ala	Gln	Glu	Thr	Leu	Asn	Pro	Ser	Ala	Ala	Val	Asn
			100					105					110		

Ser	Tyr	Pro	Val	Val	Glu	Ala	His	Arg	Phe	Val	Trp	Val	Trp	Leu	Gly
		115					120					125			

Asp	Pro	Thr	Leu	Ala	Asp	Pro	Thr	Gln	Val	Pro	Asp	Met	His	Gln	Met
	130					135					140				

Ser	His	Pro	Glu	Trp	Ala	Gly	Asp	Gly	Arg	Thr	Ile	Ser	Ala	Asp	Cys
145					150				155						160

Asn	Tyr	Gln	Leu	Val	Leu	Asp	Asn	Leu	Met	Asp	Leu	Thr	His	Glu	Glu
			165					170						175	

Phe	Val	His	Ser	Ser	Ser	Ile	Gly	Gln	Asp	Glu	Leu	Ser	Glu	Ser	Glu
			180				185						190		

Phe	Val	Val	Thr	His	Thr	Glu	Asp	Ser	Val	Thr	Val	Thr	Arg	Trp	Met
		195				200						205			

His	Asp	Ile	Asp	Ala	Pro	Pro	Phe	Trp	Gln	Lys	Asn	Met	Asn	Asp	Lys
	210					215					220				

Phe	Pro	Gly	Phe	Glu	Gly	Lys	Val	Asp	Arg	Trp	Gln	Ile	Ile	His	Tyr
225					230					235					240

Tyr	Tyr	Pro	Ser	Thr	Ile	Cys	Ile	Asp	Val	Gly	Val	Ala	Lys	Ala	Gly
				245					250					255	

Thr	Gly	Ala	Gln	Glu	Gly	Asp	Arg	Ser	Gln	Gly	Val	Asn	Gly	Tyr	Val
			260					265					270		

Met	Asn	Thr	Ile	Thr	Pro	Asp	Ser	Asp	Arg	Ser	Ser	His	Tyr	Phe	Trp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

275	280	285
Ala Phe Met Arg Asn Tyr Arg Leu Glu Ser Gln Thr Ile Thr Thr Gln		
290	295	300
Leu Arg Asp Gly Val Ser Gly Val Phe Lys Glu Asp Glu Asp Met Leu		
305	310	315
Thr Ala Gln Gln Asp Ala Ile Asp Ala Asn Thr Asp Tyr Glu Phe Tyr		
	325	330
		335
Ser Leu Asn Ile Asp Ala Gly Gly Met Trp Val Arg Arg Ile Leu Glu		
	340	345
		350
Glu Ala Leu Ser Lys Glu Gly Arg Leu Asp Ile Pro Thr Thr Phe Pro		
	355	360
		365
Arg Ala Thr Pro Lys Pro Glu Ala		
370	375	

<210> 435
 <211> 389
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(366)
 <223> FRXA01993

<400> 435	
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Ala Gly Thr Gly Ala Gln Asp Gly Asp Arg Ser Gln Gly Val Asn Gly	
1 5 10 15	
tat gtc atg aac acc att acc cca gat tca gat cgt ttt tct cat tac	96
Tyr Val Met Asn Thr Ile Thr Pro Asp Ser Asp Arg Phe Ser His Tyr	
20 25 30	
ttc tgg gca ttc atg cgc aac tac cgc ctg gaa agc caa acc atc acc	144
Phe Trp Ala Phe Met Arg Asn Tyr Arg Leu Glu Ser Gln Thr Ile Thr	
35 40 45	
acc cag ctg cgc gac ggt gta tcc ggt gta ttc aaa gaa gac gaa gac	192
Thr Gln Leu Arg Asp Gly Val Ser Gly Val Phe Lys Glu Asp Glu Asp	
50 55 60	
atg ctg acc gct cag caa gat gcc atc gac gcc aac acc gac tac gag	240
Met Leu Thr Ala Gln Gln Asp Ala Ile Asp Ala Asn Thr Asp Tyr Glu	
65 70 75 80	
ttt tac agc ctc aac att gat gcc ggt ggc atg tgg gtg cgc cga atc	288
Phe Tyr Ser Leu Asn Ile Asp Ala Gly Gly Met Trp Val Arg Arg Ile	
85 90 95	
ctc gag gaa gca ctc tcc aag gaa ggc cga ctg gat atc ccc acc aca	336
Leu Glu Glu Ala Leu Ser Lys Glu Gly Arg Leu Asp Ile Pro Thr Thr	
100 105 110	
ttc ccc cgc gca aca ccg aag ccg gag gca taaaccatga actcgcaatg gca	389

Phe Pro Arg Ala Thr Pro Lys Pro Glu Ala
 115 120

<210> 436

<211> 122

<212> PRT

<213> Corynebacterium glutamicum

<400> 436

Ala Gly Thr Gly Ala Gln Asp Gly Asp Arg Ser Gln Gly Val Asn Gly
 1 5 10 15

Tyr Val Met Asn Thr Ile Thr Pro Asp Ser Asp Arg Phe Ser His Tyr
 20 25 30

Phe Trp Ala Phe Met Arg Asn Tyr Arg Leu Glu Ser Gln Thr Ile Thr
 35 40 45

Thr Gln Leu Arg Asp Gly Val Ser Gly Val Phe Lys Glu Asp Glu Asp
 50 55 60

Met Leu Thr Ala Gln Gln Asp Ala Ile Asp Ala Asn Thr Asp Tyr Glu
 65 70 75 80

Phe Tyr Ser Leu Asn Ile Asp Ala Gly Gly Met Trp Val Arg Arg Ile
 85 90 95

Leu Glu Glu Ala Leu Ser Lys Glu Gly Arg Leu Asp Ile Pro Thr Thr
 100 105 110

Phe Pro Arg Ala Thr Pro Lys Pro Glu Ala
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<210> 437

<211> 669

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(669)

<223> FRXA02012

<400> 437

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 Phe Thr Met Thr Leu Ser Glu Arg Lys Leu Thr Thr Thr Ala Lys Ile
 1 5 10 15

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 Leu Pro His Pro Leu Asn Ala Trp Tyr Val Ala Ala Trp Asp Tyr Glu
 20 25 30

gtc aca tct aaa aag ccc atg gcc agg aca atc gcc aac aaa cca ctc 144
 Val Thr Ser Lys Lys Pro Met Ala Arg Thr Ile Ala Asn Lys Pro Leu
 35 40 45

gct ttg tac cgc acc aaa gat ggc cga gcc gtt gcc ctt gca gac gcc 192
 Ala Leu Tyr Arg Thr Lys Asp Gly Arg Ala Val Ala Leu Ala Asp Ala
 50 55 60

tgc tgg cac cgc ctc gca ccg cta tcc aag gga aaa ctc gtg ggc aca 240
 Cys Trp His Arg Leu Ala Pro Leu Ser Lys Gly Lys Leu Val Gly Thr
 65 70 75 80
 gac gga atc caa tgc cct tat cac ggc ttg gag tac aac tcc gcg ggc 288
 Asp Gly Ile Gln Cys Pro Tyr His Gly Leu Glu Tyr Asn Ser Ala Gly
 85 90 95
 cgc tgc atg aaa atg ccc gcg cag gaa acc ctc aac ccg tca gca gcc 336
 Arg Cys Met Lys Met Pro Ala Gln Glu Thr Leu Asn Pro Ser Ala Ala
 100 105 110
 gtc aac tcc tac ccc gtg gtg gaa gcc cac cgc ttt gtg tgg gtg tgg 384
 Val Asn Ser Tyr Pro Val Val Glu Ala His Arg Phe Val Trp Val Trp
 115 120 125
 ctg ggc gat ccc aca ttg gca gat ccc acc caa gta ccc gat atg cac 432
 Leu Gly Asp Pro Thr Leu Ala Asp Pro Thr Gln Val Pro Asp Met His
 130 135 140
 cag atg agc cac ccc gaa tgg gca ggc gat gga cgc acc atc tcc gct 480
 Gln Met Ser His Pro Glu Trp Ala Gly Asp Gly Arg Thr Ile Ser Ala
 145 150 155 160
 gac tgc aac tac caa tta gtg ctg gac aac ttg atg gac ctc acc cac 528
 Asp Cys Asn Tyr Gln Leu Val Leu Asp Asn Leu Met Asp Leu Thr His
 165 170 175
 caa gag ttc gtg cac tcc tcc agc atc gga caa gac gaa ctt agt gaa 576
 Gln Glu Phe Val His Ser Ser Ser Ile Gly Gln Asp Glu Leu Ser Glu
 180 185 190
 tca gag ttc gtg gtc acc cac act gaa gat tcc gtg acg gtc acc cgc 624
 Ser Glu Phe Val Val Thr His Thr Glu Asp Ser Val Thr Val Thr Arg
 195 200 205
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<210> 438

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 438

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 20 25 30
 Val Thr Ser Lys Lys Pro Met Ala Arg Thr Ile Ala Asn Lys Pro Leu
 35 40 45
 Ala Leu Tyr Arg Thr Lys Asp Gly Arg Ala Val Ala Leu Ala Asp Ala
 50 55 60
 Cys Trp His Arg Leu Ala Pro Leu Ser Lys Gly Lys Leu Val Gly Thr

65		70		75		80
Asp Gly Ile Gln Cys Pro Tyr His Gly Leu Glu Tyr Asn Ser Ala Gly						
		85		90		95
Arg Cys Met Lys Met Pro Ala Gln Glu Thr Leu Asn Pro Ser Ala Ala						
		100		105		110
Val Asn Ser Tyr Pro Val Val Glu Ala His Arg Phe Val Trp Val Trp						
		115		120		125
Leu Gly Asp Pro Thr Leu Ala Asp Pro Thr Gln Val Pro Asp Met His						
		130		135		140
Gln Met Ser His Pro Glu Trp Ala Gly Asp Gly Arg Thr Ile Ser Ala						
		145		150		155
Asp Cys Asn Tyr Gln Leu Val Leu Asp Asn Leu Met Asp Leu Thr His						
		165		170		175
Gln Glu Phe Val His Ser Ser Ser Ile Gly Gln Asp Glu Leu Ser Glu						
		180		185		190
Ser Glu Phe Val Val Thr His Thr Glu Asp Ser Val Thr Val Thr Arg						
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Trp Met His Asp Ile Asp Ala Pro Pro Phe Trp Gln Lys Asn Met						
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<210> 439

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1075)

<223> RXA01994

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				Met Asn Ser Gln Trp	
				1 5	

caa gat gca cat gtt gtt tcc agc gaa atc atc gct gca gac att cgg	163
Gln Asp Ala His Val Val Ser Ser Glu Ile Ile Ala Ala Asp Ile Arg	
	10 15 20

cga ata gaa cta tcc ccg aaa ttt gcg att cca gta aaa ccc ggc gaa	211
Arg Ile Glu Leu Ser Pro Lys Phe Ala Ile Pro Val Lys Pro Gly Glu	
	25 30 35

cat ctc aag atc atg gtg ccc cta aaa act gga cag gaa aag aga tcg	259
His Leu Lys Ile Met Val Pro Leu Lys Thr Gly Gln Glu Lys Arg Ser	
	40 45 50

tac tcc atc gtt gac gct cgt cac gac ggt tcg act ctc gcc ctg agc	307
Tyr Ser Ile Val Asp Ala Arg His Asp Gly Ser Thr Leu Ala Leu Ser	

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cct ctc cgc gtg ggt gcg cct gag tat gta ctt gtt gcc ggc gga att Pro Leu Arg Val Gly Ala Pro Glu Tyr Val Leu Val Ala Gly Gly Ile 105 110 115			451
gga atc aca gcg atc cgt tca atg gca tct tta tta aag aaa ttg gga Gly Ile Thr Ala Ile Arg Ser Met Ala Ser Leu Leu Lys Lys Leu Gly 120 125 130			499
gcg aac tac cgc atc cat ttc gca gca cgc agc ctt gat gcc atg gct Ala Asn Tyr Arg Ile His Phe Ala Ala Arg Ser Leu Asp Ala Met Ala 135 140 145			547
tac aaa gat gag ctc gtg gca gaa cac ggc gac aag ctg cac ctg cat Tyr Lys Asp Glu Leu Val Ala Glu His Gly Asp Lys Leu His Leu His 150 155 160 165			595
cta gat tct gaa ggc acc acc atc gat gtc cca gca ttg atc gaa acc Leu Asp Ser Glu Gly Thr Thr Ile Asp Val Pro Ala Leu Ile Glu Thr 170 175 180			643
tta aac ccc cac act gag ctt tat atg tgc ggc ccc atc cgc ttg atg Leu Asn Pro His Thr Glu Leu Tyr Met Cys Gly Pro Ile Arg Leu Met 185 190 195			691
gat gcc atc cgg cgc gca tgg aac acc cgc gga ctt gac ccc acc aat Asp Ala Ile Arg Arg Ala Trp Asn Thr Arg Gly Leu Asp Pro Thr Asn 200 205 210			739
ctg cgt ttc gaa acg ttt gga aac agt gga tgg ttc tcc cca gag gtt Leu Arg Phe Glu Thr Phe Gly Asn Ser Gly Trp Phe Ser Pro Glu Val 215 220 225			787
ttc cac atc caa gta cca gag ctg ggg ctt cac gcc aca gtc aac aag Phe His Ile Gln Val Pro Glu Leu Gly Leu His Ala Thr Val Asn Lys 230 235 240 245			835
gat gaa agc atg ctg gag gct ttg caa aag gct ggg gcg aat atg atg Asp Glu Ser Met Leu Glu Ala Leu Gln Lys Ala Gly Ala Asn Met Met 250 255 260			883
ttt gat tgt cga aaa ggc gaa tgt ggt ttg tgc cag gtt cgc gtt cta Phe Asp Cys Arg Lys Gly Glu Cys Gly Leu Cys Gln Val Arg Val Leu 265 270 275			931
gaa gtc gat ggc cag gtt gat cac cgc gat gtg ttc ttc tct gat cgt Glu Val Asp Gly Gln Val Asp His Arg Asp Val Phe Phe Ser Asp Arg 280 285 290			979
caa aaa gaa tcc gac gca aag gca tgc gcc tgc gtg tct cga gta gtc Gln Lys Glu Ser Asp Ala Lys Ala Cys Ala Cys Val Ser Arg Val Val 295 300 305			1027

tcc tcc cct tcc tcg tcc cca acc tcg acc att acg gtc gcc ctc tcc 1075
 Ser Ser Pro Ser Ser Ser Pro Thr Ser Thr Ile Thr Val Ala Leu Ser
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taaaggagcc tggcatggat atc 1098

<210> 440

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 440

Met Asn Ser Gln Trp Gln Asp Ala His Val Val Ser Ser Glu Ile Ile
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Ala Ala Asp Ile Arg Arg Ile Glu Leu Ser Pro Lys Phe Ala Ile Pro
 20 25 30

Val Lys Pro Gly Glu His Leu Lys Ile Met Val Pro Leu Lys Thr Gly
 35 40 45

Gln Glu Lys Arg Ser Tyr Ser Ile Val Asp Ala Arg His Asp Gly Ser
 50 55 60

Thr Leu Ala Leu Ser Val Leu Lys Thr Arg Asn Ser Arg Gly Gly Ser
 65 70 75 80

Glu Phe Met His Thr Leu Arg Ala Gly Asp Thr Val Thr Val Ser Arg
 85 90 95

Pro Ser Gln Asp Phe Pro Leu Arg Val Gly Ala Pro Glu Tyr Val Leu
 100 105 110

Val Ala Gly Gly Ile Gly Ile Thr Ala Ile Arg Ser Met Ala Ser Leu
 115 120 125

Leu Lys Lys Leu Gly Ala Asn Tyr Arg Ile His Phe Ala Ala Arg Ser
 130 135 140

Leu Asp Ala Met Ala Tyr Lys Asp Glu Leu Val Ala Glu His Gly Asp
 145 150 155 160

Lys Leu His Leu His Leu Asp Ser Glu Gly Thr Thr Ile Asp Val Pro
 165 170 175

Ala Leu Ile Glu Thr Leu Asn Pro His Thr Glu Leu Tyr Met Cys Gly
 180 185 190

Pro Ile Arg Leu Met Asp Ala Ile Arg Arg Ala Trp Asn Thr Arg Gly
 195 200 205

Leu Asp Pro Thr Asn Leu Arg Phe Glu Thr Phe Gly Asn Ser Gly Trp
 210 215 220

Phe Ser Pro Glu Val Phe His Ile Gln Val Pro Glu Leu Gly Leu His
 225 230 235 240

Ala Thr Val Asn Lys Asp Glu Ser Met Leu Glu Ala Leu Gln Lys Ala
 245 250 255

Gly Ala Asn Met Met Phe Asp Cys Arg Lys Gly Glu Cys Gly Leu Cys
 260 265 270

Gln Val Arg Val Leu Glu Val Asp Gly Gln Val Asp His Arg Asp Val
 275 280 285

Phe Phe Ser Asp Arg Gln Lys Glu Ser Asp Ala Lys Ala Cys Ala Cys
 290 295 300

Val Ser Arg Val Val Ser Ser Pro Ser Ser Ser Pro Thr Ser Thr Ile
 305 310 315 320

Thr Val Ala Leu Ser
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<210> 441
 <211> 1278
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1255)
 <223> RXA02535

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ctgcgcacct tttaccttga ttaggtgcac aatagggagt gtg aca cct cgc cct 115
 Val Thr Pro Arg Pro
 1 5

gtt tct tct gtt gcg cga ctc gtt gag gat aac gcg caa gat ttt ctt 163
 Val Ser Ser Val Ala Arg Leu Val Glu Asp Asn Ala Gln Asp Phe Leu
 10 15 20

cgc gcc gtt cag gcg aaa ctt tta acg ctc gcg cca cag gct cgt ggg 211
 Arg Ala Val Gln Ala Lys Leu Leu Thr Leu Ala Pro Gln Ala Arg Gly
 25 30 35

cat ttt ccc act gcg gat gat gcg act cat atc agc atc gcc gaa atg 259
 His Phe Pro Thr Ala Asp Asp Ala Thr His Ile Ser Ile Ala Glu Met
 40 45 50

gtg agt gcg ctg ttg gaa ggc act ggt gag gaa ggg aaa gta gac gac 307
 Val Ser Ala Leu Leu Glu Gly Thr Gly Glu Glu Gly Lys Val Asp Asp
 55 60 65

aaa aca ctg gag ttc ttt aaa gaa gcg gcg tta gat gcg cgt cga ttt 355
 Lys Thr Leu Glu Phe Phe Lys Glu Ala Ala Leu Asp Ala Arg Arg Phe
 70 75 80 85

ggc ctg acc cca gaa atg cac agc gct ttg ggt gag gcc gtg cgc agc 403
 Gly Leu Thr Pro Glu Met His Ser Ala Leu Gly Glu Ala Val Arg Ser
 90 95 100

gaa cta ttg tca tta tgc gag gat ctt ccc ttt gaa aat gtg ctg ttt 451
 Glu Leu Leu Ser Leu Cys Glu Asp Leu Pro Phe Glu Asn Val Leu Phe
 105 110 115

gcc gag cgt gcg att gct gca acc acg gct gtt tcc gtc gag gcg gtt Ala Glu Arg Ala Ile Ala Ala Thr Thr Ala Val Ser Val Glu Ala Val 120 125 130	499
cgt gaa gct gat gag gca cac att cct gcc tca tat cag gca gaa att Arg Glu Ala Asp Glu Ala His Ile Pro Ala Ser Tyr Gln Ala Glu Ile 135 140 145	547
gta gaa gtt gaa aag cgc agc cgt agg ttc acc gtc gtg cgc atg caa Val Glu Val Glu Lys Arg Ser Arg Arg Phe Thr Val Val Arg Met Gln 150 155 160 165	595
gct gaa acg caa ctg ccc tac cta ccg gga caa tat ctt gca gca act Ala Glu Thr Gln Leu Pro Tyr Leu Pro Gly Gln Tyr Leu Ala Ala Thr 170 175 180	643
gcg gat ttt ctg ccc aac aca tgg cgc tac ctg tgc cct tcg atc ccc Ala Asp Phe Leu Pro Asn Thr Trp Arg Tyr Leu Cys Pro Ser Ile Pro 185 190 195	691
act aac gaa tgg ggg cag gtg gag ttt cac atc caa tca gac gca gat Thr Asn Glu Trp Gly Gln Val Glu Phe His Ile Gln Ser Asp Ala Asp 200 205 210	739
gat atc gct gga ctt tta gcc acc aca cgc ctt ggc gat aaa tgg cga Asp Ile Ala Gly Leu Leu Ala Thr Thr Arg Leu Gly Asp Lys Trp Arg 215 220 225	787
ctt ggc ccc ggt cgt gga gat ttc gga caa agc aaa att agt tcc ggc Leu Gly Pro Gly Arg Gly Asp Phe Gly Gln Ser Lys Ile Ser Ser Gly 230 235 240 245	835
aat gat ttg tta ttt att gca cat gga acg ggc cta gct cct ctt cgc Asn Asp Leu Leu Phe Ile Ala His Gly Thr Gly Leu Ala Pro Leu Arg 250 255 260	883
gct tac atg ttt gag ctg atg aac caa gca gca cct cca cgt ttg cac Ala Tyr Met Phe Glu Leu Met Asn Gln Ala Ala Pro Pro Arg Leu His 265 270 275	931
ttt ttc gtc ggt gcc gac tac ccc ggt gag ctg tat gaa ctc acc ggc Phe Phe Val Gly Ala Asp Tyr Pro Gly Glu Leu Tyr Glu Leu Thr Gly 280 285 290	979
atg tgg aat ttt gct gca gcc agc cca tgg ctt tct gtc gta ccg gtg Met Trp Asn Phe Ala Ala Ala Ser Pro Trp Leu Ser Val Val Pro Val 295 300 305	1027
tca acg cat gac aag gat gcg tgg tgg gtt caa gcc acc gaa gca tcg Ser Thr His Asp Lys Asp Ala Trp Trp Val Gln Ala Thr Glu Ala Ser 310 315 320 325	1075
cag cca ccg agg ggt ttg cat ttg cat caa acg ggt tcg atg gcg aag Gln Pro Pro Arg Gly Leu His Leu His Gln Thr Gly Ser Met Ala Lys 330 335 340	1123
atc gtc acc gaa gca ggt gct tgg gcc gac cgc gac gtg tta att gct Ile Val Thr Glu Ala Gly Ala Trp Ala Asp Arg Asp Val Leu Ile Ala 345 350 355	1171

caccgggctg acc 1278

<213> Corynebacterium glutamicum

Gly Asp Lys Trp Arg Leu Gly Pro Gly Arg Gly Asp Phe Gly Gln Ser
225 230 235 240

Lys Ile Ser Ser Gly Asn Asp Leu Leu Phe Ile Ala His Gly Thr Gly
 245 250 255
 Leu Ala Pro Leu Arg Ala Tyr Met Phe Glu Leu Met Asn Gln Ala Ala
 260 265 270
 Pro Pro Arg Leu His Phe Phe Val Gly Ala Asp Tyr Pro Gly Glu Leu
 275 280 285
 Tyr Glu Leu Thr Gly Met Trp Asn Phe Ala Ala Ala Ser Pro Trp Leu
 290 295 300
 Ser Val Val Pro Val Ser Thr His Asp Lys Asp Ala Trp Trp Val Gln
 305 310 315 320
 Ala Thr Glu Ala Ser Gln Pro Pro Arg Gly Leu His Leu His Gln Thr
 325 330 335
 Gly Ser Met Ala Lys Ile Val Thr Glu Ala Gly Ala Trp Ala Asp Arg
 340 345 350
 Asp Val Leu Ile Ala Gly Pro Glu Ser Trp Ala Arg Asp Val Arg Arg
 355 360 365
 Ala Met Ile Arg Arg Gly Thr Pro Ala Gln Gln Ile Glu Ile Leu Gly
 370 375 380
 Phe
 385

<210> 443
 <211> 1248
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1225)
 <223> RXA00964

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 Met Gly Ala Pro Gly
 1 5
 aaa aac gat tac gca act gaa cac gtc aag caa gaa gtc cca ccc gca 163
 Lys Asn Asp Tyr Ala Thr Glu His Val Lys Gln Glu Val Pro Pro Ala
 10 15 20
 act cca gaa gag cag gca gag ctg gac acc atg tat aaa cgc atg gat 211
 Thr Pro Glu Glu Gln Ala Glu Leu Asp Thr Met Tyr Lys Arg Met Asp
 25 30 35
 gac ctg cat cta aag ccc ctg tgg act caa atc ggt ggg ttg atg cca 259
 Asp Leu His Leu Lys Pro Leu Trp Thr Gln Ile Gly Gly Leu Met Pro
 40 45 50

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ctc	ctg	aag	ctc	gcg	cag	cgc	tcc	ggc	gaa	ctc	gtt	cca	gtt	ggg	cgc	355
Leu	Leu	Lys	Leu	Ala	Gln	Arg	Ser	Gly	Glu	Leu	Val	Pro	Val	Gly	Arg	
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Gly	Gly	Glu	Arg	Arg	Ala	Ile	Gly	Leu	Ala	Asn	Pro	Gly	Leu	Asp	Gly	
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aat	acc	tac	atc	tcc	cct	acc	ctg	tgg	gca	gca	att	cag	tac	ctc	gct	451
Asn	Thr	Tyr	Ile	Ser	Pro	Thr	Leu	Trp	Ala	Ala	Ile	Gln	Tyr	Leu	Ala	
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Pro	Gly	Glu	Asn	Ala	Pro	Glu	His	Arg	His	Ser	Gln	Asn	Ala	Phe	Arg	
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Phe	Val	Ile	Glu	Gly	Glu	Gly	Val	Trp	Thr	Val	Val	Asn	Gly	Asp	Pro	
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gta	cca	atg	cga	cgc	ggc	gac	ttc	ctg	ctc	acc	cca	ggc	tgg	aac	tac	595
Val	Pro	Met	Arg	Arg	Gly	Asp	Phe	Leu	Leu	Thr	Pro	Gly	Trp	Asn	Tyr	
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His	Gly	His	His	Asn	Ile	Ala	Thr	Glu	Pro	Met	Ala	Trp	Leu	Asp	Gly	
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ctc	gat	atc	cca	ttt	gcc	tac	caa	atg	gac	acc	gga	ttc	ttt	gag	tac	691
Leu	Asp	Ile	Pro	Phe	Ala	Tyr	Gln	Met	Asp	Thr	Gly	Phe	Phe	Glu	Tyr	
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		200					205					210				
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Glu	Arg	Leu	Trp	Ala	His	Pro	Gly	Leu	Arg	Pro	Val	Ser	Phe	Pro	Gly	
	215					220					225					
aaa	act	tcc	tac	tca	cca	att	ggg	cgc	tac	gcc	tgg	gag	cac	acc	gac	835
Lys	Thr	Ser	Tyr	Ser	Pro	Ile	Gly	Arg	Tyr	Ala	Trp	Glu	His	Thr	Asp	
230					235					240					245	
gca	gca	ctc	aac	gat	cag	ctg	gca	ttg	gaa	gaa	gca	gga	cac	cca	gga	883
Ala	Ala	Leu	Asn	Asp	Gln	Leu	Ala	Leu	Glu	Glu	Ala	Gly	His	Pro	Gly	
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aca	gtc	gcg	ccg	gga	cat	gct	gcg	att	cgc	ttc	tcc	aac	cca	act	acc	931
Thr	Val	Ala	Pro	Gly	His	Ala	Ala	Ile	Arg	Phe	Ser	Asn	Pro	Thr	Thr	
			265					270					275			
ggc	ggc	gat	gtc	atg	acc	acc	atc	cgc	gcg	gag	ttc	cac	cgc	ctg	cgc	979
Gly	Gly	Asp	Val	Met	Thr	Thr	Ile	Arg	Ala	Glu	Phe	His	Arg	Leu	Arg	
		280					285					290				
cca	ggc	gca	tcc	act	gcc	ccc	att	cat	gag	gta	gga	aac	cgt	tgc	ttc	1027

Pro Gly Ala Ser Thr Ala Pro Ile His Glu Val Gly Asn Arg Cys Phe
 295 300 305

cag gta ttt gag ggt tcc gca aca atc aat gtt gga gat aaa acc ttt 1075
 Gln Val Phe Glu Gly Ser Ala Thr Ile Asn Val Gly Asp Lys Thr Phe
 310 315 320 325

gaa gct aac cac ggc gat gtg atc aat gta ccg tgc tgg cag aag tgg 1123
 Glu Ala Asn His Gly Asp Val Ile Asn Val Pro Ser Trp Gln Lys Trp
 330 335 340

aat atc gtc gct ggc tct gac ggc gtc gac ttg ttc tgc ttc tct gat 1171
 Asn Ile Val Ala Gly Ser Asp Gly Val Asp Leu Phe Cys Phe Ser Asp
 345 350 355

aca cca att ttc gag gcc ctt aac ctc gca cgt act ttt act ccg gaa 1219
 Thr Pro Ile Phe Glu Ala Leu Asn Leu Ala Arg Thr Phe Thr Pro Glu
 360 365 370

gga atc tagaacttat gcgtcttgca aca 1248
 Gly Ile
 375

<210> 444

<211> 375

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 444

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Glu Val Pro Pro Ala Thr Pro Glu Glu Gln Ala Glu Leu Asp Thr Met
 20 25 30

Tyr Lys Arg Met Asp Asp Leu His Leu Lys Pro Leu Trp Thr Gln Ile
 35 40 45

Gly Gly Leu Met Pro Asn His Pro Glu Pro Arg Ala Val Ala His Lys
 50 55 60

Trp Asp Trp Ala Glu Leu Leu Lys Leu Ala Gln Arg Ser Gly Glu Leu
 65 70 75 80

Val Pro Val Gly Arg Gly Gly Glu Arg Arg Ala Ile Gly Leu Ala Asn
 85 90 95

Pro Gly Leu Asp Gly Asn Thr Tyr Ile Ser Pro Thr Leu Trp Ala Ala
 100 105 110

Ile Gln Tyr Leu Ala Pro Gly Glu Asn Ala Pro Glu His Arg His Ser
 115 120 125

Gln Asn Ala Phe Arg Phe Val Ile Glu Gly Glu Gly Val Trp Thr Val
 130 135 140

Val Asn Gly Asp Pro Val Pro Met Arg Arg Gly Asp Phe Leu Leu Thr
 145 150 155 160

Pro Gly Trp Asn Tyr His Gly His His Asn Ile Ala Thr Glu Pro Met

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                                         Met Thr Pro Asn Gly
                                         1                               5

cgc agg caa ctc ctc ctg gag cgt ggc gca gca ttt agc aaa aac cgt 163
Arg Arg Gln Leu Leu Leu Glu Arg Gly Ala Ala Phe Ser Lys Asn Arg

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Thr	Pro	Gly	Leu	Lys	His	Val	Asp	Arg	His	Thr	Ile	Val	Asp	Ser	Asp				
25				30				35											
ggc	ctc	agc	atc	cac	acg	tac	atg	gtt	ggc	cat	gcc	gaa	aat	gcc	acg	259			
Gly	Leu	Ser	Ile	His	Thr	Tyr	Met	Val	Gly	His	Ala	Glu	Asn	Ala	Thr				
40				45				50											
gca	acg	gtc	gtg	ttc	atc	cac	ggc	ttc	acc	ctc	gcc	gcc	gaa	gtg	tat	307			
Ala	Thr	Val	Val	Phe	Ile	His	Gly	Phe	Thr	Leu	Ala	Ala	Glu	Val	Tyr				
55				60				65											
tac	atg	cag	gtc	gac	tac	cta	caa	acc	ttt	tac	cca	aat	att	aaa	agc	355			
Tyr	Met	Gln	Val	Asp	Tyr	Leu	Gln	Thr	Phe	Tyr	Pro	Asn	Ile	Lys	Ser				
70				75				80				85							
gtg	ctt	atc	gac	gcc	cgc	ggc	cac	ggc	gcc	acc	ggc	cag	atc	cgc	cca	403			
Val	Leu	Ile	Asp	Ala	Arg	Gly	His	Gly	Ala	Thr	Gly	Gln	Ile	Arg	Pro				
90				95				100											
gag	ctc	tgc	acc	atc	gaa	gga	aca	gcg	aac	gat	gtt	ctc	gca	gcc	atc	451			
Glu	Leu	Cys	Thr	Ile	Glu	Gly	Thr	Ala	Asn	Asp	Val	Leu	Ala	Ala	Ile				
105				110				115											
cac	gaa	cac	gca	ccg	acc	ggc	ccg	ctc	att	ttg	gtt	ggg	cat	tcc	ctc	499			
His	Glu	His	Ala	Pro	Thr	Gly	Pro	Leu	Ile	Leu	Val	Gly	His	Ser	Leu				
120				125				130											
ggc	gga	ctc	acg	gca	ctt	aac	ctg	gtt	aaa	cgg	gca	gat	cac	tca	ctt	547			
Gly	Gly	Leu	Thr	Ala	Leu	Asn	Leu	Val	Lys	Arg	Ala	Asp	His	Ser	Leu				
135				140				145											
cgg	aag	agg	atc	gtc	ggc	atg	gtt	cta	gtc	gcc	aca	tcg	atc	gaa	tca	595			
Arg	Lys	Arg	Ile	Val	Gly	Met	Val	Leu	Val	Ala	Thr	Ser	Ile	Glu	Ser				
150				155				160				165							
tta	tcc	acc	caa	ggt	cta	cca	caa	gtc	ctg	gca	tca	ccc	ctt	gcc	gac	643			
Leu	Ser	Thr	Gln	Gly	Leu	Pro	Gln	Val	Leu	Ala	Ser	Pro	Leu	Ala	Asp				
170				175				180											
aac	atc	aaa	aac	gcc	gtc	gaa	gca	gcc	ccc	aac	gat	gcc	caa	aaa	ttc	691			
Asn	Ile	Lys	Asn	Ala	Val	Glu	Ala	Ala	Pro	Asn	Asp	Ala	Gln	Lys	Phe				
185				190				195											
cgc	caa	tac	gcc	acc	aca	ttt	cta	gcc	ccc	acc	ctg	gcc	acc	gca	gtc	739			
Arg	Gln	Tyr	Ala	Thr	Thr	Phe	Leu	Ala	Pro	Thr	Leu	Ala	Thr	Ala	Val				
200				205				210											
ttc	caa	cga	gac	aca	aac	gat	gaa	gtc	atc	gat	ttc	cac	gcc	gcc	atg	787			
Phe	Gln	Arg	Asp	Thr	Asn	Asp	Glu	Val	Ile	Asp	Phe	His	Ala	Ala	Met				
215				220				225											
atc	cac	gaa	acc	ccc	ttg	gat	acc	ttc	gtc	ggt	ttc	ttc	gac	gac	ctc	835			
Ile	His	Glu	Thr	Pro	Leu	Asp	Thr	Phe											


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ggc tac gtc ctt gcc ggc gaa tta gat gat gtc acc cca att agc caa 931
Gly Tyr Val Leu Ala Gly Glu Leu Asp Asp Val Thr Pro Ile Ser Gln
265 270 275

gcc gac cgc atc tgc gaa gtc tgg ccc ggc gca cgc ctt caa atc gca 979
Ala Asp Arg Ile Cys Glu Val Trp Pro Gly Ala Arg Leu Gln Ile Ala
280 285 290

gaa gga gca ggt cat atg ctt ccg ctt gaa gcg cca gga atc ctc aat 1027
Glu Gly Ala Gly His Met Leu Pro Leu Glu Ala Pro Gly Ile Leu Asn
295 300 305

aat gcg atc ggc aac att ttg gac ggg ctg ggc tgaggaacct gggtcgggcg 1080
Asn Ala Ile Gly Asn Ile Leu Asp Gly Leu Gly
310 315 320

tgg 1083

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<210> 446
<211> 320
<212> PRT
<213> Corynebacterium glutamicum

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<400> 446
Met Thr Pro Asn Gly Arg Arg Gln Leu Leu Leu Glu Arg Gly Ala Ala
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Phe Ser Lys Asn Arg Thr Pro Gly Leu Lys His Val Asp Arg His Thr
20 25 30

Ile Val Asp Ser Asp Gly Leu Ser Ile His Thr Tyr Met Val Gly His
35 40 45

Ala Glu Asn Ala Thr Ala Thr Val Val Phe Ile His Gly Phe Thr Leu
50 55 60

Ala Ala Glu Val Tyr Tyr Met Gln Val Asp Tyr Leu Gln Thr Phe Tyr
65 70 75 80

Pro Asn Ile Lys Ser Val Leu Ile Asp Ala Arg Gly His Gly Ala Thr
85 90 95

Gly Gln Ile Arg Pro Glu Leu Cys Thr Ile Glu Gly Thr Ala Asn Asp
100 105 110

Val Leu Ala Ala Ile His Glu His Ala Pro Thr Gly Pro Leu Ile Leu
115 120 125

Val Gly His Ser Leu Gly Gly Leu Thr Ala Leu Asn Leu Val Lys Arg
130 135 140

Ala Asp His Ser Leu Arg Lys Arg Ile Val Gly Met Val Leu Val Ala
145 150 155 160

Thr Ser Ile Glu Ser Leu Ser Thr Gln Gly Leu Pro Gln Val Leu Ala
165 170 175

Ser Pro Leu Ala Asp Asn Ile Lys Asn Ala Val Glu Ala Ala Pro Asn
180 185 190

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Asp Ala Gln Lys Phe Arg Gln Tyr Ala Thr Thr Phe Leu Ala Pro Thr
 195 200 205
 Leu Ala Thr Ala Val Phe Gln Arg Asp Thr Asn Asp Glu Val Ile Asp
 210 215 220
 Phe His Ala Ala Met Ile His Glu Thr Pro Leu Asp Thr Phe Val Gly
 225 230 235 240
 Phe Phe Asp Asp Leu Gln Glu His Asp Glu Leu Asp Ala Ala Pro Ala
 245 250 255
 Leu Glu Gly Leu Lys Gly Tyr Val Leu Ala Gly Glu Leu Asp Asp Val
 260 265 270
 Thr Pro Ile Ser Gln Ala Asp Arg Ile Cys Glu Val Trp Pro Gly Ala
 275 280 285
 Arg Leu Gln Ile Ala Glu Gly Ala Gly His Met Leu Pro Leu Glu Ala
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 Pro Gly Ile Leu Asn Asn Ala Ile Gly Asn Ile Leu Asp Gly Leu Gly
 305 310 315 320

<210> 447
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(922)
 <223> FRXA01466

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 cggtcattg cggggaaaag ctcataaagc aaggctaaag atg acg cca aat ggt 115
 Met Thr Pro Asn Gly
 1 5
 cgc agg caa ctc ctc ctg gag cgt ggc gca gca ttt agc aaa aac cgt 163
 Arg Arg Gln Leu Leu Leu Glu Arg Gly Ala Ala Phe Ser Lys Asn Arg
 10 15 20
 acc ccg ggt cta aaa cac gtc gac cgc cac acc atc gtg gac tcc gac 211
 Thr Pro Gly Leu Lys His Val Asp Arg His Thr Ile Val Asp Ser Asp
 25 30 35
 ggc ctc agc atc cac acg tac atg gtt ggc cat gcc gaa aat gcc acg 259
 Gly Leu Ser Ile His Thr Tyr Met Val Gly His Ala Glu Asn Ala Thr
 40 45 50
 gca acg gtc gtg ttc atc cac ggc ttc acc ctc gcc gcc gaa gtg tat 307
 Ala Thr Val Val Phe Ile His Gly Phe Thr Leu Ala Ala Glu Val Tyr
 55 60 65
 tac atg cag gtc gac tac cta caa acc ttt tac cca aat att aaa agc 355
 Tyr Met Gln Val Asp Tyr Leu Gln Thr Phe Tyr Pro Asn Ile Lys Ser

70	75	80	85	
gtg ctt atc gac gcc cgc ggc cac ggc gcc acc ggc cag atc cgc cca				403
Val Leu Ile Asp Ala Arg Gly His Gly Ala Thr Gly Gln Ile Arg Pro	90	95	100	
gag ctc tgc acc atc gaa gga aca gcg aac gat gtt ctc gca gcc atc				451
Glu Leu Cys Thr Ile Glu Gly Thr Ala Asn Asp Val Leu Ala Ala Ile	105	110	115	
cac gaa cac gca ccg acc ggc ccg ctc att ttg gtt ggg cat tcc ctc				499
His Glu His Ala Pro Thr Gly Pro Leu Ile Leu Val Gly His Ser Leu	120	125	130	
ggc gga ctc acg gca ctt aac ctg gtt aaa cgg gca gat cac tca ctt				547
Gly Gly Leu Thr Ala Leu Asn Leu Val Lys Arg Ala Asp His Ser Leu	135	140	145	
cgg aag agg atc gtc ggc atg gtt cta gtc gcc aca tcg atc gaa tca				595
Arg Lys Arg Ile Val Gly Met Val Leu Val Ala Thr Ser Ile Glu Ser	150	155	160	165
tta tcc acc caa ggt cta cca caa gtc ctg gca tca ccc ctt gcc gac				643
Leu Ser Thr Gln Gly Leu Pro Gln Val Leu Ala Ser Pro Leu Ala Asp	170	175	180	
aac atc aaa aac gcc gtc gaa gca gcc ccc aac gat gcc caa aaa ttc				691
Asn Ile Lys Asn Ala Val Glu Ala Ala Pro Asn Asp Ala Gln Lys Phe	185	190	195	
cgc caa tac gcc acc aca ttt cta gcc ccc acc ctg gcc acc gca gtc				739
Arg Gln Tyr Ala Thr Thr Phe Leu Ala Pro Thr Leu Ala Thr Ala Val	200	205	210	
ttc caa cga gac aca aac gat gaa gtc atc gat ttc cac gcc gcc atg				787
Phe Gln Arg Asp Thr Asn Asp Glu Val Ile Asp Phe His Ala Ala Met	215	220	225	
atc cac gaa acc ccc ttg gat acc ttc gtc ggt ttc ttc gac gac ctt				835
Ile His Glu Thr Pro Leu Asp Thr Phe Val Gly Phe Phe Asp Asp Leu	230	235	240	245
caa gaa cac gac gaa ctc gat gcc gca cca aca ttg gaa ggc ctc aaa				883
Gln Glu His Asp Glu Leu Asp Ala Ala Pro Thr Leu Glu Gly Leu Lys	250	255	260	
ggc tac gtc ctt gcc ggc gaa tta gat gat gtc acc cca				922
Gly Tyr Val Leu Ala Gly Glu Leu Asp Asp Val Thr Pro	265	270		

<210> 448

<211> 274

<212> PRT

<213> Corynebacterium glutamicum

<400> 448

Met	Thr	Pro	Asn	Gly	Arg	Arg	Gln	Leu	Leu	Leu	Glu	Arg	Gly	Ala	Ala
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Phe	Ser	Lys	Asn	Arg	Thr	Pro	Gly	Leu	Lys	His	Val	Asp	Arg	His	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20										25					30															
Ile	Val	Asp	Ser	Asp	Gly	Leu	Ser	Ile	His	Thr	Tyr	Met	Val	Gly	His															
		35					40					45																		
Ala	Glu	Asn	Ala	Thr	Ala	Thr	Val	Val	Phe	Ile	His	Gly	Phe	Thr	Leu															
	50					55					60																			
Ala	Ala	Glu	Val	Tyr	Tyr	Met	Gln	Val	Asp	Tyr	Leu	Gln	Thr	Phe	Tyr															
	65				70					75					80															
Pro	Asn	Ile	Lys	Ser	Val	Leu	Ile	Asp	Ala	Arg	Gly	His	Gly	Ala	Thr															
				85					90					95																
Gly	Gln	Ile	Arg	Pro	Glu	Leu	Cys	Thr	Ile	Glu	Gly	Thr	Ala	Asn	Asp															
			100					105					110																	
Val	Leu	Ala	Ala	Ile	His	Glu	His	Ala	Pro	Thr	Gly	Pro	Leu	Ile	Leu															
	115						120					125																		
Val	Gly	His	Ser	Leu	Gly	Gly	Leu	Thr	Ala	Leu	Asn	Leu	Val	Lys	Arg															
	130					135					140																			
Ala	Asp	His	Ser	Leu	Arg	Lys	Arg	Ile	Val	Gly	Met	Val	Leu	Val	Ala															
	145				150					155					160															
Thr	Ser	Ile	Glu	Ser	Leu	Ser	Thr	Gln	Gly	Leu	Pro	Gln	Val	Leu	Ala															
				165				170					175																	
Ser	Pro	Leu	Ala	Asp	Asn	Ile	Lys	Asn	Ala	Val	Glu	Ala	Ala	Pro	Asn															
			180				185						190																	
Asp	Ala	Gln	Lys	Phe	Arg	Gln	Tyr	Ala	Thr	Thr	Phe	Leu	Ala	Pro	Thr															
	195						200					205																		
Leu	Ala	Thr	Ala	Val	Phe	Gln	Arg	Asp	Thr	Asn	Asp	Glu	Val	Ile	Asp															
	210					215					220																			
Phe	His	Ala	Ala	Met	Ile	His	Glu	Thr	Pro	Leu	Asp	Thr	Phe	Val	Gly															
	225				230					235					240															
Phe	Phe	Asp	Asp	Leu	Gln	Glu	His	Asp	Glu	Leu	Asp	Ala	Ala	Pro	Thr															
			245						250				255																	
Leu	Glu	Gly	Leu	Lys	Gly	Tyr	Val	Leu	Ala	Gly	Glu	Leu	Asp	Asp	Val															
		260					265						270																	

Thr Pro

<210> 449
 <211> 766
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(766)
 <223> RXN03036

<400> 449

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                                         Met Ala Glu Gln Leu
                                         1                               5

cgt caa ttt gaa ggc agg gtc ctc cct aat caa tcc gag gac ttg gaa 163
Arg Gln Phe Glu Gly Arg Val Leu Pro Asn Gln Ser Glu Asp Leu Glu
                        10                        15                        20

gat cag ggt ttg gga ttt gac ctg gga acc gtt ttc tcc cgc agg aag 211
Asp Gln Gly Leu Gly Phe Asp Leu Gly Thr Val Phe Ser Arg Arg Lys
                        25                        30                        35

gtt ttg gga ttc atc ggt gtt ggt gga gca ggt gtg gca ctt gct gct 259
Val Leu Gly Phe Ile Gly Val Gly Gly Ala Gly Val Ala Leu Ala Ala
                        40                        45                        50

tgt tca cct tct ggt tct tcc gcg gca tcg agc acc tca agc gcg tcc 307
Cys Ser Pro Ser Gly Ser Ser Ala Ala Ser Ser Thr Ser Ser Ala Ser
                        55                        60                        65

agc agc gca gct gca acc acc agt gca gca gca gag act ttg act gag 355
Ser Ser Ala Ala Ala Thr Thr Ser Ala Ala Ala Glu Thr Leu Thr Glu
                        70                        75                        80                        85

atg aag tcg gag act gct ggt ccg tac ccg ggc gat ggt tcg aat ggt 403
Met Lys Ser Glu Thr Ala Gly Pro Tyr Pro Gly Asp Gly Ser Asn Gly
                        90                        95                        100

ccg gat gtg ttg gag gtc tcc ggt gtg gag cgc cag gac atc acc aag 451
Pro Asp Val Leu Glu Val Ser Gly Val Glu Arg Gln Asp Ile Thr Lys
                        105                        110                        115

tcg att gat tct gac acc gtg gca gag ggc gta cct ctg acg ttg act 499
Ser Ile Asp Ser Asp Thr Val Ala Glu Gly Val Pro Leu Thr Leu Thr
                        120                        125                        130

atg acc att ttg gac atg aac aac aac aat cag cca atg gag ggt gct 547
Met Thr Ile Leu Asp Met Asn Asn Asn Asn Gln Pro Met Glu Gly Ala
                        135                        140                        145

gcg gtg tac gtg tgg cac tgt gat gcg ccg ggt cga tat tcg atg tac 595
Ala Val Tyr Val Trp His Cys Asp Ala Pro Gly Arg Tyr Ser Met Tyr
                        150                        155                        160                        165

gac tct gag ctg gaa gat gag acc tat tta cgc ggt gtg cag att acc 643
Asp Ser Glu Leu Glu Asp Glu Thr Tyr Leu Arg Gly Val Gln Ile Thr
                        170                        175                        180

gat aag tat ggc cag gtc acg ttc gat acc att ttc cct ggt tgt tat 691
Asp Lys Tyr Gly Gln Val Thr Phe Asp Thr Ile Phe Pro Gly Cys Tyr
                        185                        190                        195

gcg ggc cgt tgg gtg cat att cat ttc gag gtg ttc ccg gat cga gac 739
Ala Gly Arg Trp Val His Ile His Phe Glu Val Phe Pro Asp Arg Asp
                        200                        205                        210

agc atc acg gat tcc acg aac aac att 766
Ser Ile Thr Asp Ser Thr Asn Asn Ile

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215

220

<210> 450

<211> 222

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 450

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Ser	Glu	Asp	Leu	Glu	Asp	Gln	Gly	Leu	Gly	Phe	Asp	Leu	Gly	Thr	Val
			20					25					30		

Phe	Ser	Arg	Arg	Lys	Val	Leu	Gly	Phe	Ile	Gly	Val	Gly	Gly	Ala	Gly
		35					40					45			

Val	Ala	Leu	Ala	Ala	Cys	Ser	Pro	Ser	Gly	Ser	Ser	Ala	Ala	Ser	Ser
	50					55					60				

Thr	Ser	Ser	Ala	Ser	Ser	Ser	Ala	Ala	Ala	Thr	Thr	Ser	Ala	Ala	Ala
65					70					75					80

Glu	Thr	Leu	Thr	Glu	Met	Lys	Ser	Glu	Thr	Ala	Gly	Pro	Tyr	Pro	Gly
				85					90					95	

Asp	Gly	Ser	Asn	Gly	Pro	Asp	Val	Leu	Glu	Val	Ser	Gly	Val	Glu	Arg
			100					105					110		

Gln	Asp	Ile	Thr	Lys	Ser	Ile	Asp	Ser	Asp	Thr	Val	Ala	Glu	Gly	Val
		115					120					125			

Pro	Leu	Thr	Leu	Thr	Met	Thr	Ile	Leu	Asp	Met	Asn	Asn	Asn	Asn	Gln
	130					135					140				

Pro	Met	Glu	Gly	Ala	Ala	Val	Tyr	Val	Trp	His	Cys	Asp	Ala	Pro	Gly
145					150					155					160

Arg	Tyr	Ser	Met	Tyr	Asp	Ser	Glu	Leu	Glu	Asp	Glu	Thr	Tyr	Leu	Arg
			165						170					175	

Gly	Val	Gln	Ile	Thr	Asp	Lys	Tyr	Gly	Gln	Val	Thr	Phe	Asp	Thr	Ile
			180					185					190		

Phe	Pro	Gly	Cys	Tyr	Ala	Gly	Arg	Trp	Val	His	Ile	His	Phe	Glu	Val
		195					200					205			

Phe	Pro	Asp	Arg	Asp	Ser	Ile	Thr	Asp	Ser	Thr	Asn	Asn	Ile		
	210					215					220				

<210> 451

<211> 766

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(766)

<223> FRXA02895

<400> 451

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tatcagcgta aacgtccgaa catgaaaggc tagaaaagcc atg gct gag cag ttg 115
                                         Met Ala Glu Gln Leu
                                         1                               5

cgt caa ttt gaa ggc agg gtc ctc cct aat caa tcc gag gac ttg gaa 163
Arg Gln Phe Glu Gly Arg Val Leu Pro Asn Gln Ser Glu Asp Leu Glu
                        10                               15                               20

gat cag ggt ttg gga ttt gac ctg gga acc gtt ttc tcc cgc agg aag 211
Asp Gln Gly Leu Gly Phe Asp Leu Gly Thr Val Phe Ser Arg Arg Lys
                        25                               30                               35

gtt ttg gga ttc atc ggt gtt ggt gga gca ggt gtg gca ctt gct gct 259
Val Leu Gly Phe Ile Gly Val Gly Gly Ala Gly Val Ala Leu Ala Ala
                        40                               45                               50

tgt tca cct tct ggt tct tcc gcg gca tcg agc acc tca agc gcg tcc 307
Cys Ser Pro Ser Gly Ser Ser Ala Ala Ser Ser Thr Ser Ser Ala Ser
                        55                               60                               65

agc agc gca gct gca acc acc agt gca gca gca gag act ttg act gag 355
Ser Ser Ala Ala Ala Thr Thr Ser Ala Ala Ala Glu Thr Leu Thr Glu
                        70                               75                               80                               85

atg aag tcg gag act gct ggt ccg tac ccg ggc gat ggt tcg aat ggt 403
Met Lys Ser Glu Thr Ala Gly Pro Tyr Pro Gly Asp Gly Ser Asn Gly
                        90                               95                               100

ccg gat gtg ttg gag gtc tcc ggt gtg gag cgc cag gac atc acc aag 451
Pro Asp Val Leu Glu Val Ser Gly Val Glu Arg Gln Asp Ile Thr Lys
                        105                               110                               115

tcg att gat tct gac acc gtg gca gag ggc gta cct ctg acg ttg act 499
Ser Ile Asp Ser Asp Thr Val Ala Glu Gly Val Pro Leu Thr Leu Thr
                        120                               125                               130

atg acc att ttg gac atg aac aac aac aat cag cca atg gag ggt gct 547
Met Thr Ile Leu Asp Met Asn Asn Asn Asn Gln Pro Met Glu Gly Ala
                        135                               140                               145

gcg gtg tac gtg tgg cac tgt gat gcg ccg ggt cga tat tcg atg tac 595
Ala Val Tyr Val Trp His Cys Asp Ala Pro Gly Arg Tyr Ser Met Tyr
                        150                               155                               160                               165

gac tct gag ctg gaa gat gag acc tat tta cgc ggt gtg cag att acc 643
Asp Ser Glu Leu Glu Asp Glu Thr Tyr Leu Arg Gly Val Gln Ile Thr
                        170                               175                               180

gat aag tat ggc cag gtc acg ttc gat acc att ttc cct ggt tgt tat 691
Asp Lys Tyr Gly Gln Val Thr Phe Asp Thr Ile Phe Pro Gly Cys Tyr
                        185                               190                               195

gcg ggc cgt tgg gtg cat att cat ttc gag gtg ttc ccg gat cga gac 739
Ala Gly Arg Trp Val His Ile His Phe Glu Val Phe Pro Asp Arg Asp
                        200                               205                               210

agc atc acg gat tcc acg aac aac att 766

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Ser Ile Thr Asp Ser Thr Asn Asn Ile
 215 220

<210> 452
 <211> 222
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 452
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 Ser Glu Asp Leu Glu Asp Gln Gly Leu Gly Phe Asp Leu Gly Thr Val
 20 25 30
 Phe Ser Arg Arg Lys Val Leu Gly Phe Ile Gly Val Gly Gly Ala Gly
 35 40 45
 Val Ala Leu Ala Ala Cys Ser Pro Ser Gly Ser Ser Ala Ala Ser Ser
 50 55 60
 Thr Ser Ser Ala Ser Ser Ser Ala Ala Ala Thr Thr Ser Ala Ala Ala
 65 70 75 80
 Glu Thr Leu Thr Glu Met Lys Ser Glu Thr Ala Gly Pro Tyr Pro Gly
 85 90 95
 Asp Gly Ser Asn Gly Pro Asp Val Leu Glu Val Ser Gly Val Glu Arg
 100 105 110
 Gln Asp Ile Thr Lys Ser Ile Asp Ser Asp Thr Val Ala Glu Gly Val
 115 120 125
 Pro Leu Thr Leu Thr Met Thr Ile Leu Asp Met Asn Asn Asn Asn Gln
 130 135 140
 Pro Met Glu Gly Ala Ala Val Tyr Val Trp His Cys Asp Ala Pro Gly
 145 150 155 160
 Arg Tyr Ser Met Tyr Asp Ser Glu Leu Glu Asp Glu Thr Tyr Leu Arg
 165 170 175
 Gly Val Gln Ile Thr Asp Lys Tyr Gly Gln Val Thr Phe Asp Thr Ile
 180 185 190
 Phe Pro Gly Cys Tyr Ala Gly Arg Trp Val His Ile His Phe Glu Val
 195 200 205
 Phe Pro Asp Arg Asp Ser Ile Thr Asp Ser Thr Asn Asn Ile
 210 215 220

<210> 453
 <211> 1026
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1003)

<223> RXA02449

<400> 453

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tactcagtaa ctaacccggc gattttttcaa ggagaaaatc atg aca acc acc acc 115
                Met Thr Thr Thr Thr
                1                    5

gca gac cac aac atc agc gcg cag caa aag gct gtt gaa gaa aat ctg 163
Ala Asp His Asn Ile Ser Ala Gln Gln Lys Ala Val Glu Glu Asn Leu
                10                15                20

gtg aac cgt gtc ctc caa tct ttt gat gcg tgt gaa aac ccg cgc ctc 211
Val Asn Arg Val Leu Gln Ser Phe Asp Ala Cys Glu Asn Pro Arg Leu
                25                30                35

aag cag ctg atg gaa tcg ctg gtt gtg cat ctg cac gat ttc atc cgg 259
Lys Gln Leu Met Glu Ser Leu Val Val His Leu His Asp Phe Ile Arg
                40                45                50

gat gtg cgc ctc acc gag gat gag tgg aat tac gcc att gat ttc ctc 307
Asp Val Arg Leu Thr Glu Asp Glu Trp Asn Tyr Ala Ile Asp Phe Leu
                55                60                65

aca gcg gtt ggc cac att act gat gac aag cgc caa gag ttt gtg ttg 355
Thr Ala Val Gly His Ile Thr Asp Asp Lys Arg Gln Glu Phe Val Leu
                70                75                80                85

ctt tcc gat acc ttg ggc gcc tcg atg cag acc atc gcg gtg aac aac 403
Leu Ser Asp Thr Leu Gly Ala Ser Met Gln Thr Ile Ala Val Asn Asn
                90                95                100

gaa gcg tat gaa aac tca acg gaa gct aca gtc ttt ggt cca ttc ttc 451
Glu Ala Tyr Glu Asn Ser Thr Glu Ala Thr Val Phe Gly Pro Phe Phe
                105                110                115

ctc gat gac gct cct gag gtt gag ctg ggt gga gat atc gcc ggc ggc 499
Leu Asp Asp Ala Pro Glu Val Glu Leu Gly Gly Asp Ile Ala Gly Gly
                120                125                130

gcc cag ggg cag gca gcg tgg att gaa gga acc gtc acc gac act gaa 547
Ala Gln Gly Gln Ala Ala Trp Ile Glu Gly Thr Val Thr Asp Thr Glu
                135                140                145

ggc aat ccc gtt ccg aat gct cgt atc gag gtg tgg gag tgc gat gaa 595
Gly Asn Pro Val Pro Asn Ala Arg Ile Glu Val Trp Glu Cys Asp Glu
                150                155                160                165

gat gga ctc tac gat gtc caa tat gcc gat gag cgc atg gcg ggt cgc 643
Asp Gly Leu Tyr Asp Val Gln Tyr Ala Asp Glu Arg Met Ala Gly Arg
                170                175                180

gcg tat atg cac acc gac gcc aat ggc gat tac cgc ttc tgg ggt ctg 691
Ala Tyr Met His Thr Asp Ala Asn Gly Asp Tyr Arg Phe Trp Gly Leu
                185                190                195

act ccg gtt cct tat cca atc ccc cac gat ggc ccc gtg ggc aac atg 739
Thr Pro Val Pro Tyr Pro Ile Pro His Asp Gly Pro Val Gly Asn Met
                200                205                210

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ctc aag gcg gtt ggt cgt tcg ccg gtg cgc tgc gcc cac ctt cac ttc 787
 Leu Lys Ala Val Gly Arg Ser Pro Val Arg Cys Ala His Leu His Phe
 215 220 225

 atg gtg acc gct cct gaa ttg cgc acc ttg gtc act cac att ttc gtt 835
 Met Val Thr Ala Pro Glu Leu Arg Thr Leu Val Thr His Ile Phe Val
 230 235 240 245

 gag ggt gat ccg cag cta gaa atc ggc gat tcc gtc ttc ggg gtc aag 883
 Glu Gly Asp Pro Gln Leu Glu Ile Gly Asp Ser Val Phe Gly Val Lys
 250 255 260

 gac tcg ttg atc aag aag ttt gag gag cag gcg cca ggc act cct acc 931
 Asp Ser Leu Ile Lys Lys Phe Glu Glu Gln Ala Pro Gly Thr Pro Thr
 265 270 275

 cca gat ggt cgg gat ctc ggc gat cag acg tgg gcg cgc acg cgc ttc 979
 Pro Asp Gly Arg Asp Leu Gly Asp Gln Thr Trp Ala Arg Thr Arg Phe
 280 285 290

 gac atc gtg ctc gcg ccg ggc gcg taggatttcg cttttcgacg caa 1026
 Asp Ile Val Leu Ala Pro Gly Ala
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<210> 454

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 454

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 Glu Asn Pro Arg Leu Lys Gln Leu Met Glu Ser Leu Val Val His Leu
 35 40 45

 His Asp Phe Ile Arg Asp Val Arg Leu Thr Glu Asp Glu Trp Asn Tyr
 50 55 60

 Ala Ile Asp Phe Leu Thr Ala Val Gly His Ile Thr Asp Asp Lys Arg
 65 70 75 80

 Gln Glu Phe Val Leu Leu Ser Asp Thr Leu Gly Ala Ser Met Gln Thr
 85 90 95

 Ile Ala Val Asn Asn Glu Ala Tyr Glu Asn Ser Thr Glu Ala Thr Val
 100 105 110

 Phe Gly Pro Phe Phe Leu Asp Asp Ala Pro Glu Val Glu Leu Gly Gly
 115 120 125

 Asp Ile Ala Gly Gly Ala Gln Gly Gln Ala Ala Trp Ile Glu Gly Thr
 130 135 140

 Val Thr Asp Thr Glu Gly Asn Pro Val Pro Asn Ala Arg Ile Glu Val
 145 150 155 160

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aacggcgacg atccagcaac tttgaattaa ggagaccaac atg act att tca gca 115
Met Thr Ile Ser Ala
1 5

caa cag caa gca gtg gaa gaa gac ctt gta gag cgc gta ctc gca tct 163
Gln Gln Gln Ala Val Glu Glu Asp Leu Val Glu Arg Val Leu Ala Ser
10 15 20

ttt gat tcg tgt gaa aac cct cgc ctc aaa cta gtg atg aaa tcc ctg 211
Phe Asp Ser Cys Glu Asn Pro Arg Leu Lys Leu Val Met Lys Ser Leu
25 30 35

act gtg cat ctc cat gat ttc atc cgc gat gtt cga ctc act gaa gaa 259
Thr Val His Leu His Asp Phe Ile Arg Asp Val Arg Leu Thr Glu Glu
40 45 50

gag tgg aac tac gcc att gat ttc ctc acc aag gtt ggg cat atc acc 307
Glu Trp Asn Tyr Ala Ile Asp Phe Leu Thr Lys Val Gly His Ile Thr
55 60 65

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gac gat aag cgc caa gaa ttc gtg ttg ctc tct gac acc ttg ggt gca	355
Asp Asp Lys Arg Gln Glu Phe Val Leu Leu Ser Asp Thr Leu Gly Ala	
70 75 80 85	
tcc atg cag acc atc gct gtt aat aac gaa gca tat gaa gac gct acc	403
Ser Met Gln Thr Ile Ala Val Asn Asn Glu Ala Tyr Glu Asp Ala Thr	
90 95 100	
gaa gca aca gtc ttt ggc ccc ttc ttt gtc gat gat gcg cca ctg gtc	451
Glu Ala Thr Val Phe Gly Pro Phe Phe Val Asp Asp Ala Pro Leu Val	
105 110 115	
caa aac gga gat gac att gcc ttt ggc gca gtc ggc cag ccg gca tgg	499
Gln Asn Gly Asp Asp Ile Ala Phe Gly Ala Val Gly Gln Pro Ala Trp	
120 125 130	
gtg gag gga acg gtc aaa gac act gaa gga aac ccc att ccc aat gca	547
Val Glu Gly Thr Val Lys Asp Thr Glu Gly Asn Pro Ile Pro Asn Ala	
135 140 145	
cgc att gaa gta tgg gaa tgc gat gaa gat gga ctt tat gat gtg caa	595
Arg Ile Glu Val Trp Glu Cys Asp Glu Asp Gly Leu Tyr Asp Val Gln	
150 155 160 165	
tac gcc gat gag cgc agt gct gga cgc gca cac ctg tat tca gat gaa	643
Tyr Ala Asp Glu Arg Ser Ala Gly Arg Ala His Leu Tyr Ser Asp Glu	
170 175 180	
aac ggc gaa tac cac ttc tgg gga cta act ccc gtg cca tat ccc atc	691
Asn Gly Glu Tyr His Phe Trp Gly Leu Thr Pro Val Pro Tyr Pro Ile	
185 190 195	
cca cac gat ggt cca gta gga caa atg ctc caa gca gtt ggt cgt tcc	739
Pro His Asp Gly Pro Val Gly Gln Met Leu Gln Ala Val Gly Arg Ser	
200 205 210	
ccc gtt cgt tgc gcg cac cta cac ttc atg gtg act gcg cca gag aag	787
Pro Val Arg Cys Ala His Leu His Phe Met Val Thr Ala Pro Glu Lys	
215 220 225	
cga acc ttg gta acc cat atc ttc gtt gag ggc gat ccg cag cta gag	835
Arg Thr Leu Val Thr His Ile Phe Val Glu Gly Asp Pro Gln Leu Glu	
230 235 240 245	
atc ggc gat tcc gtg ttt ggc gtg aag gac tca ctg att aag aaa ttc	883
Ile Gly Asp Ser Val Phe Gly Val Lys Asp Ser Leu Ile Lys Lys Phe	
250 255 260	
gtt gag caa cct gca gga acc gca act cca gat ggt cgc gat gtg ggt	931
Val Glu Gln Pro Ala Gly Thr Ala Thr Pro Asp Gly Arg Asp Val Gly	
265 270 275	
gat caa acc tgg gca cgc aca cgt ttt gat att gtg ctc gcc ccc ggc	979
Asp Gln Thr Trp Ala Arg Thr Arg Phe Asp Ile Val Leu Ala Pro Gly	
280 285 290	
aat gtc taagtagaag cagcaaaaaa cca	1008
Asn Val	
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<210> 456

<211> 295

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 456

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Arg Val Leu Ala Ser Phe Asp Ser Cys Glu Asn Pro Arg Leu Lys Leu
 20 25 30

Val Met Lys Ser Leu Thr Val His Leu His Asp Phe Ile Arg Asp Val
 35 40 45

Arg Leu Thr Glu Glu Glu Trp Asn Tyr Ala Ile Asp Phe Leu Thr Lys
 50 55 60

Val Gly His Ile Thr Asp Asp Lys Arg Gln Glu Phe Val Leu Leu Ser
 65 70 75 80

Asp Thr Leu Gly Ala Ser Met Gln Thr Ile Ala Val Asn Asn Glu Ala
 85 90 95

Tyr Glu Asp Ala Thr Glu Ala Thr Val Phe Gly Pro Phe Phe Val Asp
 100 105 110

Asp Ala Pro Leu Val Gln Asn Gly Asp Asp Ile Ala Phe Gly Ala Val
 115 120 125

Gly Gln Pro Ala Trp Val Glu Gly Thr Val Lys Asp Thr Glu Gly Asn
 130 135 140

Pro Ile Pro Asn Ala Arg Ile Glu Val Trp Glu Cys Asp Glu Asp Gly
 145 150 155 160

Leu Tyr Asp Val Gln Tyr Ala Asp Glu Arg Ser Ala Gly Arg Ala His
 165 170 175

Leu Tyr Ser Asp Glu Asn Gly Glu Tyr His Phe Trp Gly Leu Thr Pro
 180 185 190

Val Pro Tyr Pro Ile Pro His Asp Gly Pro Val Gly Gln Met Leu Gln
 195 200 205

Ala Val Gly Arg Ser Pro Val Arg Cys Ala His Leu His Phe Met Val
 210 215 220

Thr Ala Pro Glu Lys Arg Thr Leu Val Thr His Ile Phe Val Glu Gly
 225 230 235 240

Asp Pro Gln Leu Glu Ile Gly Asp Ser Val Phe Gly Val Lys Asp Ser
 245 250 255

Leu Ile Lys Lys Phe Val Glu Gln Pro Ala Gly Thr Ala Thr Pro Asp
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Gly Arg Asp Val Gly Asp Gln Thr Trp Ala Arg Thr Arg Phe Asp Ile
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Val Leu Ala Pro Gly Asn Val

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<222> (101) .. (985)
<223> FRXA00178
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aacggcgacg	atccagcaac	tttgaattaa	ggagaccaac	atg	act	att	tca	gca							115	
				Met	Thr	Ile	Ser	Ala								
					1			5								
caa	cag	caa	gca	gtg	gaa	gaa	gac	ctt	gta	gag	cgc	gta	ctc	gca	tct	163
Gln	Gln	Gln	Ala	Val	Glu	Glu	Asp	Leu	Val	Glu	Arg	Val	Leu	Ala	Ser	
				10					15					20		
ttt	gat	tcg	tgt	gaa	aac	cct	cgc	ctc	aaa	cta	gtg	atg	aaa	tcc	ctg	211
Phe	Asp	Ser	Cys	Glu	Asn	Pro	Arg	Leu	Lys	Leu	Val	Met	Lys	Ser	Leu	
			25					30					35			
act	gtg	cat	ctc	cat	gat	ttc	atc	cgc	gat	ggt	cga	ctc	act	gaa	gaa	259
Thr	Val	His	Leu	His	Asp	Phe	Ile	Arg	Asp	Val	Arg	Leu	Thr	Glu	Glu	
		40					45					50				
gag	tgg	aac	tac	gcc	att	gat	ttc	ctc	acc	aag	ggt	ggg	cat	atc	acc	307
Glu	Trp	Asn	Tyr	Ala	Ile	Asp	Phe	Leu	Thr	Lys	Val	Gly	His	Ile	Thr	
	55					60					65					
gac	gat	aag	cgc	caa	gaa	ttc	gtg	ttg	ctc	tct	gac	acc	ttg	ggg	gca	355
Asp	Asp	Lys	Arg	Gln	Glu	Phe	Val	Leu	Leu	Ser	Asp	Thr	Leu	Gly	Ala	
70					75					80					85	
tcc	atg	cag	acc	atc	gct	gtt	aat	aac	gaa	gca	tat	gaa	gac	gct	acc	403
Ser	Met	Gln	Thr	Ile	Ala	Val	Asn	Asn	Glu	Ala	Tyr	Glu	Asp	Ala	Thr	
				90					95					100		
gaa	gca	aca	gtc	ttt	ggc	ccc	ttc	ttt	gtc	gat	gat	gcg	cca	ctg	gtc	451
Glu	Ala	Thr	Val	Phe	Gly	Pro	Phe	Phe	Val	Asp	Asp	Ala	Pro	Leu	Val	
			105					110					115			
caa	aac	gga	gat	gac	att	gcc	ttt	ggc	gca	gtc	ggc	cag	ccg	gca	tgg	499
Gln	Asn	Gly	Asp	Asp	Ile	Ala	Phe	Gly	Ala	Val	Gly	Gln	Pro	Ala	Trp	
		120					125					130				
gtg	gag	gga	acg	gtc	aaa	gac	act	gaa	gga	aac	ccc	att	ccc	aat	gca	547
Val	Glu	Gly	Thr	Val	Lys	Asp	Thr	Glu	Gly	Asn	Pro	Ile	Pro	Asn	Ala	
	135					140					145					
cgc	att	gaa	gta	tgg	gaa	tgc	gat	gaa	gat	gga	ctt	tat	gat	gtg	caa	595
Arg	Ile	Glu	Val	Trp	Glu	Cys	Asp	Glu	Asp	Gly	Leu	Tyr	Asp	Val	Gln	
150					155					160					165	
tac	gcc	gat	gag	cgc	agt	gct	gga	cgc	gca	cac	ctg	tat	tca	gat	gaa	643

Tyr Ala Asp Glu Arg Ser Ala Gly Arg Ala His Leu Tyr Ser Asp Glu
 170 175 180
 aac ggc gaa tac cac ttc tgg gga cta act ccc gtg cca tat ccc atc 691
 Asn Gly Glu Tyr His Phe Trp Gly Leu Thr Pro Val Pro Tyr Pro Ile
 185 190 195
 cca cac gat ggt cca gta gga caa atg ctc caa gca gtt ggt cgt tcc 739
 Pro His Asp Gly Pro Val Gly Gln Met Leu Gln Ala Val Gly Arg Ser
 200 205 210
 ccc gtt cgt tgc gcg cac cta cac ttc atg gtg act gcg cca gag aag 787
 Pro Val Arg Cys Ala His Leu His Phe Met Val Thr Ala Pro Glu Lys
 215 220 225
 cga acc ttg gta acc cat atc ttc gtt gag ggc gat ccg cag cta gag 835
 Arg Thr Leu Val Thr His Ile Phe Val Glu Gly Asp Pro Gln Leu Glu
 230 235 240 245
 atc ggc gat tcc gtg ttt ggc gtg aag gac tca ctg att aag aaa ttc 883
 Ile Gly Asp Ser Val Phe Gly Val Lys Asp Ser Leu Ile Lys Lys Phe
 250 255 260
 gtt gag caa cct gca gga acc gca act cca gat ggt cgc gat gtg ggt 931
 Val Glu Gln Pro Ala Gly Thr Ala Thr Pro Asp Gly Arg Asp Val Gly
 265 270 275
 gat caa acc tgg gca cgc aca cgt ttt gat att gtg ctc gcc ccc ggc 979
 Asp Gln Thr Trp Ala Arg Thr Arg Phe Asp Ile Val Leu Ala Pro Gly
 280 285 290
 aat gtc taagtagaag cagcaaaaaa cca 1008
 Asn Val
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 458
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 Arg Val Leu Ala Ser Phe Asp Ser Cys Glu Asn Pro Arg Leu Lys Leu
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 Val Met Lys Ser Leu Thr Val His Leu His Asp Phe Ile Arg Asp Val
 35 40 45
 Arg Leu Thr Glu Glu Glu Trp Asn Tyr Ala Ile Asp Phe Leu Thr Lys
 50 55 60
 Val Gly His Ile Thr Asp Asp Lys Arg Gln Glu Phe Val Leu Leu Ser
 65 70 75 80
 Asp Thr Leu Gly Ala Ser Met Gln Thr Ile Ala Val Asn Asn Glu Ala
 85 90 95
 Tyr Glu Asp Ala Thr Glu Ala Thr Val Phe Gly Pro Phe Phe Val Asp

100	105	110
Asp Ala Pro Leu Val Gln Asn Gly Asp Asp Ile Ala Phe Gly Ala Val 115 120 125		
Gly Gln Pro Ala Trp Val Glu Gly Thr Val Lys Asp Thr Glu Gly Asn 130 135 140		
Pro Ile Pro Asn Ala Arg Ile Glu Val Trp Glu Cys Asp Glu Asp Gly 145 150 155 160		
Leu Tyr Asp Val Gln Tyr Ala Asp Glu Arg Ser Ala Gly Arg Ala His 165 170 175		
Leu Tyr Ser Asp Glu Asn Gly Glu Tyr His Phe Trp Gly Leu Thr Pro 180 185 190		
Val Pro Tyr Pro Ile Pro His Asp Gly Pro Val Gly Gln Met Leu Gln 195 200 205		
Ala Val Gly Arg Ser Pro Val Arg Cys Ala His Leu His Phe Met Val 210 215 220		
Thr Ala Pro Glu Lys Arg Thr Leu Val Thr His Ile Phe Val Glu Gly 225 230 235 240		
Asp Pro Gln Leu Glu Ile Gly Asp Ser Val Phe Gly Val Lys Asp Ser 245 250 255		
Leu Ile Lys Lys Phe Val Glu Gln Pro Ala Gly Thr Ala Thr Pro Asp 260 265 270		
Gly Arg Asp Val Gly Asp Gln Thr Trp Ala Arg Thr Arg Phe Asp Ile 275 280 285		
Val Leu Ala Pro Gly Asn Val 290 295		

<210> 459
 <211> 1407
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1384)
 <223> RXA02111

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 Met Thr Thr Ser Ile
 1 5
 acc cca tct gtc aac ctt gca ttg aaa aat gcc aat agc tgc aac agt 163
 Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala Asn Ser Cys Asn Ser
 10 15 20
 gaa ctc aaa gac gga ccc tgg ttc ctc gac cag ccc gga atg ccg gat 211

Glu	Leu	Lys	Asp	Gly	Pro	Trp	Phe	Leu	Asp	Gln	Pro	Gly	Met	Pro	Asp		
			25					30					35				
gtc	tac	ggc	ccc	ggc	gcg	tca	caa	aac	gat	ccg	atc	cct	gcg	cat	gct	259	
Val	Tyr	Gly	Pro	Gly	Ala	Ser	Gln	Asn	Asp	Pro	Ile	Pro	Ala	His	Ala		
		40					45					50					
ccg	cgc	cag	cag	gtt	ctc	ccc	gag	gag	tac	cag	cgc	gca	agt	gat	gac	307	
Pro	Arg	Gln	Gln	Val	Leu	Pro	Glu	Glu	Tyr	Gln	Arg	Ala	Ser	Asp	Asp		
	55					60					65						
gaa	ctg	cat	cgt	agg	atc	cgg	gaa	gcg	aaa	gac	acc	ctg	ggt	gac	aaa	355	
Glu	Leu	His	Arg	Arg	Ile	Arg	Glu	Ala	Lys	Asp	Thr	Leu	Gly	Asp	Lys		
70					75					80					85		
gtg	gtt	atc	cta	gga	cac	ttc	tac	cag	cgc	gat	gaa	gtt	atc	caa	cac	403	
Val	Val	Ile	Leu	Gly	His	Phe	Tyr	Gln	Arg	Asp	Glu	Val	Ile	Gln	His		
			90						95					100			
gca	gat	ttt	gtt	ggt	gac	tct	ttc	caa	ctt	gcc	cgc	gct	gcc	aaa	acc	451	
Ala	Asp	Phe	Val	Gly	Asp	Ser	Phe	Gln	Leu	Ala	Arg	Ala	Ala	Lys	Thr		
		105						110					115				
cga	ccc	gag	gcg	gaa	gcg	att	gtg	ttc	tgc	ggt	gtg	cac	ttc	atg	gct	499	
Arg	Pro	Glu	Ala	Glu	Ala	Ile	Val	Phe	Cys	Gly	Val	His	Phe	Met	Ala		
		120					125					130					
gaa	acc	gct	gat	ctg	tta	tcc	acg	gat	gaa	caa	tca	gtg	atc	ctc	ccc	547	
Glu	Thr	Ala	Asp	Leu	Leu	Ser	Thr	Asp	Glu	Gln	Ser	Val	Ile	Leu	Pro		
	135					140					145						
aac	ctt	gcc	gca	ggt	tgc	tcc	atg	gca	gac	atg	gct	gac	ctt	gat	tcc	595	
Asn	Leu	Ala	Ala	Gly	Cys	Ser	Met	Ala	Asp	Met	Ala	Asp	Leu	Asp	Ser		
150					155					160					165		
gtc	gaa	gac	tgc	tgg	gag	caa	ctc	acc	tca	att	tat	ggc	gat	gac	acc	643	
Val	Glu	Asp	Cys	Trp	Glu	Gln	Leu	Thr	Ser	Ile	Tyr	Gly	Asp	Asp	Thr		
			170						175					180			
ctg	atc	cct	gtg	acc	tac	atg	aat	tcc	tct	gca	gcg	ctc	aaa	ggt	ttc	691	
Leu	Ile	Pro	Val	Thr	Tyr	Met	Asn	Ser	Ser	Ala	Ala	Leu	Lys	Gly	Phe		
			185					190					195				
gtg	ggt	gag	cac	ggc	gga	att	gta	tgc	acc	tcc	tca	aat	gca	cgt	tcc	739	
Val	Gly	Glu	His	Gly	Gly	Ile	Val	Cys	Thr	Ser	Ser	Asn	Ala	Arg	Ser		
		200					205					210					
gta	ttg	gag	tgg	gcg	ttt	gaa	cgc	ggc	caa	cga	gtc	ctg	ttc	ttc	ccc	787	
Val	Leu	Glu	Trp	Ala	Phe	Glu	Arg	Gly	Gln	Arg	Val	Leu	Phe	Phe	Pro		
	215					220					225						
gat	cag	cac	ttg	ggt	cga	aac	acc	gcg	aaa	gcc	atg	ggc	att	ggg	atc	835	
Asp	Gln	His	Leu	Gly	Arg	Asn	Thr	Ala	Lys	Ala	Met	Gly	Ile	Gly	Ile		
230					235					240					245		
gat	caa	atg	ccc	ctg	tgg	aat	ccc	aac	aaa	cca	ctg	ggt	ggc	aac	acc	883	
Asp	Gln	Met	Pro	Leu	Trp	Asn	Pro	Asn	Lys	Pro	Leu	Gly	Gly	Asn	Thr		
			250						255					260			
gtt	tcc	gag	cta	gaa	aac	gca	aag	gta	ctg	ctc	tgg	cat	ggt	ttc	tgc	931	
Val	Ser	Glu	Leu	Glu	Asn	Ala	Lys	Val	Leu	Leu	Trp	His	Gly	Phe	Cys		

265	270	275	
tct gta cac aag cgc ttt act gtc	gag cag atc aac aaa gcc cgc gcc	979	
Ser Val His Lys Arg Phe Thr	Val Glu Gln Ile Asn Lys Ala Arg Ala		
280	285 290		
gag tac ccc gac gtt cac gtc	atc gtg cac cct gaa tcc ccc atg cca	1027	
Glu Tyr Pro Asp Val His Val	Ile Val His Pro Glu Ser Pro Met Pro		
295	300 305		
gtt gtt gac gcc gcc gac tca tcc gga tcc act gac ttc att gtg aaa	1075		
Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr Asp Phe Ile Val Lys			
310	315 320 325		
gcc att caa gca gca ccg gca gga tct acc ttt gcg atc ggc acc gaa	1123		
Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe Ala Ile Gly Thr Glu			
330	335 340		
atc aac ttg gtt cag cgc ctg gca gcc cag tac ccg cag cac acc atc	1171		
Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr Pro Gln His Thr Ile			
345	350 355		
ttc tgc ctc gac cct gtc atc tgc cca tgc tcc acc atg tat cgc att	1219		
Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser Thr Met Tyr Arg Ile			
360	365 370		
cac cct ggt tac ctg gcc tgg gca ctt gag gag ttg gtg gct gga aac	1267		
His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu Leu Val Ala Gly Asn			
375 380 385			
gtg att aac cag att tct gtc tct gaa tcc gtg gcg gca ccg gcg cga	1315		
Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val Ala Ala Pro Ala Arg			
390	395 400 405		
gtc gct ttg gaa agg atg cta tct gtt gtt cca gca gct cct gtt act	1363		
Val Ala Leu Glu Arg Met Leu Ser Val Val Pro Ala Ala Pro Val Thr			
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Pro Ser Ser Ser Lys Asp Ala			
425			

<210> 460

<211> 428

<212> PRT

<213> Corynebacterium glutamicum

<400> 460

Met Thr Thr Ser Ile Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala
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Asn Ser Cys Asn Ser Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln
20 25 30

Pro Gly Met Pro Asp Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro
35 40 45

Ile Pro Ala His Ala Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln
50 55 60

Arg Ala Ser Asp Asp Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp
 65 70 75 80
 Thr Leu Gly Asp Lys Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp
 85 90 95
 Glu Val Ile Gln His Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala
 100 105 110
 Arg Ala Ala Lys Thr Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly
 115 120 125
 Val His Phe Met Ala Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln
 130 135 140
 Ser Val Ile Leu Pro Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met
 145 150 155 160
 Ala Asp Leu Asp Ser Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile
 165 170 175
 Tyr Gly Asp Asp Thr Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala
 180 185 190
 Ala Leu Lys Gly Phe Val Gly Glu His Gly Gly Ile Val Cys Thr Ser
 195 200 205
 Ser Asn Ala Arg Ser Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg
 210 215 220
 Val Leu Phe Phe Pro Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala
 225 230 235 240
 Met Gly Ile Gly Ile Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro
 245 250 255
 Leu Gly Gly Asn Thr Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu
 260 265 270
 Trp His Gly Phe Cys Ser Val His Lys Arg Phe Thr Val Glu Gln Ile
 275 280 285
 Asn Lys Ala Arg Ala Glu Tyr Pro Asp Val His Val Ile Val His Pro
 290 295 300
 Glu Ser Pro Met Pro Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr
 305 310 315 320
 Asp Phe Ile Val Lys Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe
 325 330 335
 Ala Ile Gly Thr Glu Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr
 340 345 350
 Pro Gln His Thr Ile Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser
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 Thr Met Tyr Arg Ile His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu
 370 375 380
 Leu Val Ala Gly Asn Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val

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Met Ser Ala Pro Val 1 5																
gga caa ggc atc gaa ggt cgc ccc act cac gtc acc ccg gaa cgc ttc 163																
Gly Gln Gly Ile Glu Gly Arg Pro Thr His Val Thr Pro Glu Arg Phe 10 15 20																
ttt ggc cag ggt gtt gtg gtt acc gga gcg gct caa ggc atc ggc atg 211																
Phe Gly Gln Gly Val Val Val Thr Gly Ala Ala Gln Gly Ile Gly Met 25 30 35																
gca gtg gca cac cgc atc gca tat gag gat ggc aac cta gtg ttg gtg 259																
Ala Val Ala His Arg Ile Ala Tyr Glu Asp Gly Asn Leu Val Leu Val 40 45 50																
gac cgt tcc ccg ctg gtg cat gaa gtt gcc gaa gag ctg cgt aaa gca 307																
Asp Arg Ser Pro Leu Val His Glu Val Ala Glu Glu Leu Arg Lys Ala 55 60 65																
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Gly Ala Thr Asp Ala Leu Glu Phe Ala Gly Gln Lys Leu Lys Asn Leu 90 95 100																
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Asp Val Val Ile Asn Asn Val Gly Gly Thr Ile Trp Ala Lys Pro Tyr 105 110 115																
cag gaa tac tct gag gaa gag atc cgc aag gaa atc aac cga agc ctc 499																
Gln Glu Tyr Ser Glu Glu Glu Ile Arg Lys Glu Ile Asn Arg Ser Leu 120 125 130																
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Phe Pro Thr Leu Trp Met Cys Arg Ala Ala Leu Pro Ile Leu Ile Gly 135 140 145																

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 Asn Gly Gly Gly Thr Ile Val Asn Val Ser Ser Ile Ala Thr Gly Gly
 150 155 160 165

 atc aac cgt gtt cct tat gct gca gca aag ggt ggc gtc aac ggc att 643
 Ile Asn Arg Val Pro Tyr Ala Ala Ala Lys Gly Gly Val Asn Gly Ile
 170 175 180

 gtt tct gcc atg gcc cgc gaa gct gca ccg cat aat gtg cgc gtg gtg 691
 Val Ser Ala Met Ala Arg Glu Ala Ala Pro His Asn Val Arg Val Val
 185 190 195

 gca acg gct ccc ggt ggc acg ctc gct ccg gaa cgt gcc gtc aaa cga 739
 Ala Thr Ala Pro Gly Gly Thr Leu Ala Pro Glu Arg Ala Val Lys Arg
 200 205 210

 ggc cct ggg cca gag ggc gaa ttg gaa gaa aag tgg tat cag caa atc 787
 Gly Pro Gly Pro Glu Gly Glu Leu Glu Glu Lys Trp Tyr Gln Gln Ile
 215 220 225

 gtt gat caa acc att gat tcc agt ttg atg aag cgc tac ggc acc cta 835
 Val Asp Gln Thr Ile Asp Ser Ser Leu Met Lys Arg Tyr Gly Thr Leu
 230 235 240 245

 gag gag cag gtc gcg ccg atc tgt ttc ctc gct tct gag gaa gct tcc 883
 Glu Glu Gln Val Ala Pro Ile Cys Phe Leu Ala Ser Glu Glu Ala Ser
 250 255 260

 tac atc act gga tca gtc atg cca gtc ggt gga ggc gac cag gga 928
 Tyr Ile Thr Gly Ser Val Met Pro Val Gly Gly Gly Asp Gln Gly
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<211> 276

<212> PRT

<213> *Corynebacterium glutamicum*

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 20 25 30

 Gln Gly Ile Gly Met Ala Val Ala His Arg Ile Ala Tyr Glu Asp Gly
 35 40 45

 Asn Leu Val Leu Val Asp Arg Ser Pro Leu Val His Glu Val Ala Glu
 50 55 60

 Glu Leu Arg Lys Ala Gly Ala Gly Thr Val Asp Ser Phe Ile Ala Asp
 65 70 75 80

 Leu Glu Thr Phe Glu Gly Ala Thr Asp Ala Leu Glu Phe Ala Gly Gln
 85 90 95

 Lys Leu Lys Asn Leu Asp Val Val Ile Asn Asn Val Gly Gly Thr Ile

100	105	110
Trp Ala Lys Pro Tyr Gln Glu Tyr Ser Glu Glu Glu Ile Arg Lys Glu 115 120 125		
Ile Asn Arg Ser Leu Phe Pro Thr Leu Trp Met Cys Arg Ala Ala Leu 130 135 140		
Pro Ile Leu Ile Gly Asn Gly Gly Gly Thr Ile Val Asn Val Ser Ser 145 150 155 160		
Ile Ala Thr Gly Gly Ile Asn Arg Val Pro Tyr Ala Ala Ala Lys Gly 165 170 175		
Gly Val Asn Gly Ile Val Ser Ala Met Ala Arg Glu Ala Ala Pro His 180 185 190		
Asn Val Arg Val Val Ala Thr Ala Pro Gly Gly Thr Leu Ala Pro Glu 195 200 205		
Arg Ala Val Lys Arg Gly Pro Gly Pro Glu Gly Glu Leu Glu Glu Lys 210 215 220		
Trp Tyr Gln Gln Ile Val Asp Gln Thr Ile Asp Ser Ser Leu Met Lys 225 230 235 240		
Arg Tyr Gly Thr Leu Glu Glu Gln Val Ala Pro Ile Cys Phe Leu Ala 245 250 255		
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 <212> DNA
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 <222> (101)..(1168)
 <223> RXN00177

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 Met Ser Leu Gln Phe
 1 5
 gat cat gaa acc ctc ggt caa cga gtt ctg ttc ggt tca ggt gag gcg 163
 Asp His Glu Thr Leu Gly Gln Arg Val Leu Phe Gly Ser Gly Glu Ala
 10 15 20
 gcg caa aat ctc gcc gct gaa att agc cga ctc gat gcc aaa aac gtc 211
 Ala Gln Asn Leu Ala Ala Glu Ile Ser Arg Leu Asp Ala Lys Asn Val
 25 30 35

atg gtg gtt gcc ggt gat ttc gag ctt ccc atg gca cgg caa gta gca	259
Met Val Val Ala Gly Asp Phe Glu Leu Pro Met Ala Arg Gln Val Ala	
40 45 50	
gca gat att gat gtc aag gtg tgg cat tca aat gtc gtc atg cat gtc	307
Ala Asp Ile Asp Val Lys Val Trp His Ser Asn Val Val Met His Val	
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ccc atc gaa aca gca gaa gaa gca cgc agt gtt gcg aaa gaa aac gac	355
Pro Ile Glu Thr Ala Glu Glu Ala Arg Ser Val Ala Lys Glu Asn Asp	
70 75 80 85	
att gat gtt gtc gtc tgt gtc ggc ggt gga tcc aca aca ggt cta gct	403
Ile Asp Val Val Val Cys Val Gly Gly Gly Ser Thr Thr Gly Leu Ala	
90 95 100	
aaa gcg att gcc atg acc acc gca ttg ccg atc att gcg gta ccc act	451
Lys Ala Ile Ala Met Thr Thr Ala Leu Pro Ile Ile Ala Val Pro Thr	
105 110 115	
act tat gca ggt tct gaa gca aca aat gtc tgg gga ttg acc gaa gcc	499
Thr Tyr Ala Gly Ser Glu Ala Thr Asn Val Trp Gly Leu Thr Glu Ala	
120 125 130	
gcg cgc aaa aca act ggt gtt gat aac aaa gtc ctg cca gtc aca gtt	547
Ala Arg Lys Thr Thr Gly Val Asp Asn Lys Val Leu Pro Val Thr Val	
135 140 145	
atc tac gat tca gcg tta acc atg tct ttg ccg gta gaa atg tcg gtt	595
Ile Tyr Asp Ser Ala Leu Thr Met Ser Leu Pro Val Glu Met Ser Val	
150 155 160 165	
gct tct ggt ctc aat ggt ttg gct cac tgc att gat tct ttg tgg gga	643
Ala Ser Gly Leu Asn Gly Leu Ala His Cys Ile Asp Ser Leu Trp Gly	
170 175 180	
ccg aag gcg gat ccc atc aat gcg gct atg gct gct gag gga att cga	691
Pro Lys Ala Asp Pro Ile Asn Ala Ala Met Ala Ala Glu Gly Ile Arg	
185 190 195	
gca ctt tct gct ggc ctt ccc aag att gtc gca gat gct cag gac gta	739
Ala Leu Ser Ala Gly Leu Pro Lys Ile Val Ala Asp Ala Gln Asp Val	
200 205 210	
gat ggt cgc gat gaa gcg ctc tac ggt gcc tac ctg gct gcg gtc tct	787
Asp Gly Arg Asp Glu Ala Leu Tyr Gly Ala Tyr Leu Ala Ala Val Ser	
215 220 225	
ttt gcc tct gct ggc tct ggt ctc cac cac aag atc tgc cac gtc ttg	835
Phe Ala Ser Ala Gly Ser Gly Leu His His Lys Ile Cys His Val Leu	
230 235 240 245	
ggt gga act ttt aac ctt cca cac gcg caa acc cat gca aca gta ctg	883
Gly Gly Thr Phe Asn Leu Pro His Ala Gln Thr His Ala Thr Val Leu	
250 255 260	
cct tat gtt ctt gcc ttc aac gcg cca tat gcg cca cag gca gaa caa	931
Pro Tyr Val Leu Ala Phe Asn Ala Pro Tyr Ala Pro Gln Ala Glu Gln	
265 270 275	
cgc gca gcg gca gct ttc ggt tct gcg aca gca ctt gaa gga ttg caa	979

Arg Ala Ala Ala Ala Phe Gly Ser Ala Thr Ala Leu Glu Gly Leu Gln
 280 285 290
 cag ctg cgt gcc caa gtg gga gca cca cag cga cta tcc gat tac gga 1027
 Gln Leu Arg Ala Gln Val Gly Ala Pro Gln Arg Leu Ser Asp Tyr Gly
 295 300 305
 ttc acc gca gca gga atc cca gag gca gtg gaa atc atc ttg gag aaa 1075
 Phe Thr Ala Ala Gly Ile Pro Glu Ala Val Glu Ile Ile Leu Glu Lys
 310 315 320 325
 gta ccg gcg aat aat cca cgg acg gtc aca gaa gaa aac ctc act gcg 1123
 Val Pro Ala Asn Asn Pro Arg Thr Val Thr Glu Glu Asn Leu Thr Ala
 330 335 340
 ctg ctt acc aca gcg ctc aac ggc gac gat cca gca act ttg aat 1168
 Leu Leu Thr Thr Ala Leu Asn Gly Asp Asp Pro Ala Thr Leu Asn
 345 350 355
 taaggagacc aacatgacta ttt 1191

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 <211> 356
 <212> PRT
 <213> Corynebacterium glutamicum

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 Asp Ala Lys Asn Val Met Val Val Ala Gly Asp Phe Glu Leu Pro Met
 35 40 45
 Ala Arg Gln Val Ala Ala Asp Ile Asp Val Lys Val Trp His Ser Asn
 50 55 60
 Val Val Met His Val Pro Ile Glu Thr Ala Glu Glu Ala Arg Ser Val
 65 70 75 80
 Ala Lys Glu Asn Asp Ile Asp Val Val Val Cys Val Gly Gly Gly Ser
 85 90 95
 Thr Thr Gly Leu Ala Lys Ala Ile Ala Met Thr Thr Ala Leu Pro Ile
 100 105 110
 Ile Ala Val Pro Thr Thr Tyr Ala Gly Ser Glu Ala Thr Asn Val Trp
 115 120 125
 Gly Leu Thr Glu Ala Ala Arg Lys Thr Thr Gly Val Asp Asn Lys Val
 130 135 140
 Leu Pro Val Thr Val Ile Tyr Asp Ser Ala Leu Thr Met Ser Leu Pro
 145 150 155 160
 Val Glu Met Ser Val Ala Ser Gly Leu Asn Gly Leu Ala His Cys Ile
 165 170 175

Asp Ser Leu Trp Gly Pro Lys Ala Asp Pro Ile Asn Ala Ala Met Ala
 180 185 190
 Ala Glu Gly Ile Arg Ala Leu Ser Ala Gly Leu Pro Lys Ile Val Ala
 195 200 205
 Asp Ala Gln Asp Val Asp Gly Arg Asp Glu Ala Leu Tyr Gly Ala Tyr
 210 215 220
 Leu Ala Ala Val Ser Phe Ala Ser Ala Gly Ser Gly Leu His His Lys
 225 230 235 240
 Ile Cys His Val Leu Gly Gly Thr Phe Asn Leu Pro His Ala Gln Thr
 245 250 255
 His Ala Thr Val Leu Pro Tyr Val Leu Ala Phe Asn Ala Pro Tyr Ala
 260 265 270
 Pro Gln Ala Glu Gln Arg Ala Ala Ala Phe Gly Ser Ala Thr Ala
 275 280 285
 Leu Glu Gly Leu Gln Gln Leu Arg Ala Gln Val Gly Ala Pro Gln Arg
 290 295 300
 Leu Ser Asp Tyr Gly Phe Thr Ala Ala Gly Ile Pro Glu Ala Val Glu
 305 310 315 320
 Ile Ile Leu Glu Lys Val Pro Ala Asn Asn Pro Arg Thr Val Thr Glu
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 Glu Asn Leu Thr Ala Leu Leu Thr Thr Ala Leu Asn Gly Asp Asp Pro
 340 345 350
 Ala Thr Leu Asn
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<210> 465

<211> 311

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(288)

<223> FRXA00177

<400> 465

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 Gln Arg Ala Ala Ala Ala Phe Gly Ser Ala Thr Ala Leu Glu Gly Leu
 20 25 30
 caa cag ctg cgt gcc caa gtg gga gca cca cag cga cta tcc gat tac 144
 Gln Gln Leu Arg Ala Gln Val Gly Ala Pro Gln Arg Leu Ser Asp Tyr
 35 40 45
 gga ttc acc gca gca gga atc cca gag gca gtg gaa atc atc ttg gag 192

Gly Phe Thr Ala Ala Gly Ile Pro Glu Ala Val Glu Ile Ile Leu Glu
 50 55 60
 aaa gta ccg gcg aat aat cca cgg acg gtc aca gaa gaa aac ctc act 240
 Lys Val Pro Ala Asn Asn Pro Arg Thr Val Thr Glu Glu Asn Leu Thr
 65 70 75 80
 gcg ctg ctt acc aca gcg ctc aac ggc gac gat cca gca act ttg aat 288
 Ala Leu Leu Thr Thr Ala Leu Asn Gly Asp Asp Pro Ala Thr Leu Asn
 85 90 95
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<210> 466
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 <213> Corynebacterium glutamicum

<400> 466
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 20 25 30
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 35 40 45
 Gly Phe Thr Ala Ala Gly Ile Pro Glu Ala Val Glu Ile Ile Leu Glu
 50 55 60
 Lys Val Pro Ala Asn Asn Pro Arg Thr Val Thr Glu Glu Asn Leu Thr
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 Ala Leu Leu Thr Thr Ala Leu Asn Gly Asp Asp Pro Ala Thr Leu Asn
 85 90 95

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 <223> RXA02448

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 Val Asn Asn Ser Leu
 1 5
 gca ttc aac cac gac acc ctc cca cag aaa gtc atg ttt gga tat ggc 163
 Ala Phe Asn His Asp Thr Leu Pro Gln Lys Val Met Phe Gly Tyr Gly
 10 15 20
 aag tcc agt gca ttc tta aag cag gaa gtt gaa cgc cgc ggc tca gcc 211

Lys	Ser	Ser	Ala	Phe	Leu	Lys	Gln	Glu	Val	Glu	Arg	Arg	Gly	Ser	Ala		
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Lys	Val	Met	Val	Ile	Ala	Gly	Glu	Arg	Glu	Met	Ser	Ile	Ala	His	Lys		
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gtg	gcc	tca	gaa	att	gag	gtg	gcg	atc	tgg	cac	gac	gaa	gtt	gtc	atg	307	
Val	Ala	Ser	Glu	Ile	Glu	Val	Ala	Ile	Trp	His	Asp	Glu	Val	Val	Met		
	55					60					65						
cac	gtg	ccc	atc	gaa	gta	gcc	gaa	cgt	gcg	cgt	gca	gtg	gca	acc	gac	355	
His	Val	Pro	Ile	Glu	Val	Ala	Glu	Arg	Ala	Arg	Ala	Val	Ala	Thr	Asp		
	70				75					80					85		
aat	gag	att	gat	ctg	ctg	gtg	tgt	gtt	ggc	ggc	gga	tcc	acc	ata	ggg	403	
Asn	Glu	Ile	Asp	Leu	Leu	Val	Cys	Val	Gly	Gly	Gly	Ser	Thr	Ile	Gly		
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ttg	gcc	aaa	gca	att	gcc	atg	acc	act	gcc	ctg	ccc	atc	gtc	gcg	atc	451	
Leu	Ala	Lys	Ala	Ile	Ala	Met	Thr	Thr	Ala	Leu	Pro	Ile	Val	Ala	Ile		
			105					110					115				
ccc	acc	acc	tac	gca	gga	tcg	gaa	gca	acc	aac	gtg	tgg	ggg	ctg	acg	499	
Pro	Thr	Thr	Tyr	Ala	Gly	Ser	Glu	Ala	Thr	Asn	Val	Trp	Gly	Leu	Thr		
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gaa	gca	gcg	cgc	aaa	aca	acc	ggg	gtt	gat	ctg	aag	gtg	ctc	ccc	gaa	547	
Glu	Ala	Ala	Arg	Lys	Thr	Thr	Gly	Val	Asp	Leu	Lys	Val	Leu	Pro	Glu		
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aca	gtc	att	tac	gat	tcc	gaa	ctc	acc	atg	tcg	ctt	cca	gtg	gag	atg	595	
Thr	Val	Ile	Tyr	Asp	Ser	Glu	Leu	Thr	Met	Ser	Leu	Pro	Val	Glu	Met		
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Ser	Val	Ala	Ser	Gly	Leu	Asn	Gly	Leu	Ala	His	Cys	Ile	Asp	Ser	Leu		
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tgg	gga	ccc	aac	gcc	gat	ccc	atc	aac	gca	gtg	ctt	gca	gcc	gaa	gga	691	
Trp	Gly	Pro	Asn	Ala	Asp	Pro	Ile	Asn	Ala	Val	Leu	Ala	Ala	Glu	Gly		
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atc	cgc	gca	ctc	aac	cag	gga	ctg	ccg	aaa	att	gtt	gcg	aac	ccg	cac	739	
Ile	Arg	Ala	Leu	Asn	Gln	Gly	Leu	Pro	Lys	Ile	Val	Ala	Asn	Pro	His		
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Ser	Ile	Glu	Gly	Arg	Asp	Glu	Ala	Leu	Tyr	Gly	Ala	Tyr	Leu	Ala	Ala		
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Val	Ser	Phe	Ala	Ser	Ala	Gly	Ser	Gly	Leu	His	His	Lys	Ile	Cys	His		
	230				235					240					245		
acc	ttg	gga	ggc	acc	ttc	aac	ctc	ccc	cac	gcc	caa	acc	cac	gca	acc	883	
Thr	Leu	Gly	Gly	Thr	Phe	Asn	Leu	Pro	His	Ala	Gln	Thr	His	Ala	Thr		
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gtg	ctg	ccg	tat	gtt	ttg	gca	ttc	aac	gca	ggc	gac	gca	cca	gaa	gct	931	
Val	Leu	Pro	Tyr	Val	Leu	Ala	Phe	Asn	Ala	Gly	Asp	Ala	Pro	Glu	Ala		

265										270					275					
gaa	cgc	cgc	gca	gcc	gca	gcc	ttt	gga	act	gac	acc	gca	cta	gaa	ggc	979				
Glu	Arg	Arg	Ala	Ala	Ala	Ala	Phe	Gly	Thr	Asp	Thr	Ala	Leu	Glu	Gly					
280						285						290								
ctg	caa	cgc	ctc	cgc	ttg	tca	gtc	aac	gca	ccg	aaa	cga	ctt	tcc	gac	1027				
Leu	Gln	Arg	Leu	Arg	Leu	Ser	Val	Asn	Ala	Pro	Lys	Arg	Leu	Ser	Asp					
295						300						305								
tac	ggc	ttc	gag	gct	tca	gga	att	gct	gag	gca	gtg	gac	gtc	acg	ttg	1075				
Tyr	Gly	Phe	Glu	Ala	Ser	Gly	Ile	Ala	Glu	Ala	Val	Asp	Val	Thr	Leu					
310				315						320			325							
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Glu	Lys	Val	Pro	Ala	Asn	Asn	Pro	Arg	Pro	Val	Thr	Arg	Glu	Asn	Leu					
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Ser	Arg	Leu	Leu	Glu	Ala	Ala	Leu	Asn	Gly	Glu	Asp	Pro	Ala	Val	Leu					
			345						350			355								
agc	gca	gta	ctc	agt	aac	taaccgcggcg atttttcaag gag										1212				
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<211> 363

<212> PRT

<213> Corynebacterium glutamicum

<400> 468

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			35				40				45				
Ser	Ile	Ala	His	Lys	Val	Ala	Ser	Glu	Ile	Glu	Val	Ala	Ile	Trp	His
			50				55				60				
Asp	Glu	Val	Val	Met	His	Val	Pro	Ile	Glu	Val	Ala	Glu	Arg	Ala	Arg
65				70				75				80			
Ala	Val	Ala	Thr	Asp	Asn	Glu	Ile	Asp	Leu	Leu	Val	Cys	Val	Gly	Gly
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Gly	Ser	Thr	Ile	Gly	Leu	Ala	Lys	Ala	Ile	Ala	Met	Thr	Thr	Ala	Leu
			100				105				110				
Pro	Ile	Val	Ala	Ile	Pro	Thr	Thr	Tyr	Ala	Gly	Ser	Glu	Ala	Thr	Asn
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Val	Trp	Gly	Leu	Thr	Glu	Ala	Ala	Arg	Lys	Thr	Thr	Gly	Val	Asp	Leu
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Lys	Val	Leu	Pro	Glu	Thr	Val	Ile	Tyr	Asp	Ser	Glu	Leu	Thr	Met	Ser

145						150						155						160
Leu	Pro	Val	Glu	Met	Ser	Val	Ala	Ser	Gly	Leu	Asn	Gly	Leu	Ala	His			
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Cys	Ile	Asp	Ser	Leu	Trp	Gly	Pro	Asn	Ala	Asp	Pro	Ile	Asn	Ala	Val			
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Leu	Ala	Ala	Glu	Gly	Ile	Arg	Ala	Leu	Asn	Gln	Gly	Leu	Pro	Lys	Ile			
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Val	Ala	Asn	Pro	His	Ser	Ile	Glu	Gly	Arg	Asp	Glu	Ala	Leu	Tyr	Gly			
				210					215					220				
Ala	Tyr	Leu	Ala	Ala	Val	Ser	Phe	Ala	Ser	Ala	Gly	Ser	Gly	Leu	His			
225					230					235					240			
His	Lys	Ile	Cys	His	Thr	Leu	Gly	Gly	Thr	Phe	Asn	Leu	Pro	His	Ala			
				245					250					255				
Gln	Thr	His	Ala	Thr	Val	Leu	Pro	Tyr	Val	Leu	Ala	Phe	Asn	Ala	Gly			
				260					265					270				
Asp	Ala	Pro	Glu	Ala	Glu	Arg	Arg	Ala	Ala	Ala	Ala	Phe	Gly	Thr	Asp			
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Thr	Ala	Leu	Glu	Gly	Leu	Gln	Arg	Leu	Arg	Leu	Ser	Val	Asn	Ala	Pro			
				290					295					300				
Lys	Arg	Leu	Ser	Asp	Tyr	Gly	Phe	Glu	Ala	Ser	Gly	Ile	Ala	Glu	Ala			
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Val	Asp	Val	Thr	Leu	Glu	Lys	Val	Pro	Ala	Asn	Asn	Pro	Arg	Pro	Val			
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Thr	Arg	Glu	Asn	Leu	Ser	Arg	Leu	Leu	Glu	Ala	Ala	Leu	Asn	Gly	Glu			
				340					345					350				
Asp	Pro	Ala	Val	Leu	Ser	Ala	Val	Leu	Ser	Asn								
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<210> 469
<211> 1782
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1759)  
<223> RXA00048
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gcgaaggcgt gggcataggg aaaaccttag ctgatctgcg gtgacttaaa tataaggggg 60

tggaatgggg gtattgtaaa atctgaaccc ttgttcattt atg aat cat gat tca 115
                                         Met Asn His Asp Ser
                                         1                               5

gaa tgt gat cta gat aat gtt gtt cag ttc act att caa gaa ggg tta 163
Glu Cys Asp Leu Asp Asn Val Val Gln Phe Thr Ile Gln Glu Gly Leu

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10								15				20				
gat	ccc	atg	tca	ccc	aat	aac	ttc	gat	acc	gat	gtc	tgc	atc	gtc	ggc	211
Asp	Pro	Met	Ser	Pro	Asn	Asn	Phe	Asp	Thr	Asp	Val	Cys	Ile	Val	Gly	
			25								30			35		
gga	ggc	cct	acc	gga	acg	ctc	ctt	gca	gta	ctg	ctc	ggc	caa	aaa	ggc	259
Gly	Gly	Pro	Thr	Gly	Thr	Leu	Leu	Ala	Val	Leu	Leu	Gly	Gln	Lys	Gly	
		40					45					50				
cac	cgc	gtc	acc	atc	ctg	gaa	aag	tgg	cca	aca	ttc	tac	gaa	cga	cct	307
His	Arg	Val	Thr	Ile	Leu	Glu	Lys	Trp	Pro	Thr	Phe	Tyr	Glu	Arg	Pro	
	55					60					65					
cgt	gca	gtc	acc	ttt	gac	cac	gaa	atc	gca	cgg	atc	ctt	gga	tac	att	355
Arg	Ala	Val	Thr	Phe	Asp	His	Glu	Ile	Ala	Arg	Ile	Leu	Gly	Tyr	Ile	
	70				75					80					85	
ggc	att	gat	tct	gaa	aac	gac	gaa	gcc	atc	gat	tac	cac	tcc	gac	agc	403
Gly	Ile	Asp	Ser	Glu	Asn	Asp	Glu	Ala	Ile	Asp	Tyr	His	Ser	Asp	Ser	
				90					95					100		
tac	gac	tgg	aag	aac	gca	gcg	ggg	gag	acg	ctt	ttg	gaa	gtc	gat	tgg	451
Tyr	Asp	Trp	Lys	Asn	Ala	Ala	Gly	Glu	Thr	Leu	Leu	Glu	Val	Asp	Trp	
			105						110				115			
acc	tcc	atg	aca	gat	tcc	gga	tgg	cgc	acc	cga	tac	tgg	ttc	tac	cag	499
Thr	Ser	Met	Thr	Asp	Ser	Gly	Trp	Arg	Thr	Arg	Tyr	Trp	Phe	Tyr	Gln	
		120					125					130				
cca	gaa	ctt	gaa	aag	cgt	ctg	cgc	gat	ctg	gcc	ctg	acc	atg	gat	ttt	547
Pro	Glu	Leu	Glu	Lys	Arg	Leu	Arg	Asp	Leu	Ala	Leu	Thr	Met	Asp	Phe	
	135					140					145					
gta	gat	att	cgc	tgt	ggc	ttc	acc	gct	gtc	gga	ttg	tcc	caa	gat	gaa	595
Val	Asp	Ile	Arg	Cys	Gly	Phe	Thr	Ala	Val	Gly	Leu	Ser	Gln	Asp	Glu	
	150				155					160					165	
aac	tcc	gcc	atc	att	cac	ggc	att	gtc	act	gat	acc	cca	gag	aac	att	643
Asn	Ser	Ala	Ile	Ile	His	Gly	Ile	Val	Thr	Asp	Thr	Pro	Glu	Asn	Ile	
				170					175					180		
cca	gca	gat	gct	cag	cgc	gaa	gat	atc	cga	gcg	aag	tat	gtc	atc	ggc	691
Pro	Ala	Asp	Ala	Gln	Arg	Glu	Asp	Ile	Arg	Ala	Lys	Tyr	Val	Ile	Gly	
			185						190				195			
gca	gac	gga	gct	aac	agt	ttc	gtg	cgt	aac	tcc	ctt	ggc	tta	gag	atg	739
Ala	Asp	Gly	Ala	Asn	Ser	Phe	Val	Arg	Asn	Ser	Leu	Gly	Leu	Glu	Met	
		200					205					210				
aat	gat	ctt	gga	tac	ttc	ttc	gac	tgg	ctg	atc	ctg	gac	ctc	aag	cca	787

gaa ttc atg gcg ctg cct ggt gaa gat ctc aag gaa ctc gct tct gaa	931
Glu Phe Met Ala Leu Pro Gly Glu Asp Leu Lys Glu Leu Ala Ser Glu	
265 270 275	
gaa agc gcg tgg aat cta ctt gag cca tgg gat gtc aca cct ggc aag	979
Glu Ser Ala Trp Asn Leu Leu Glu Pro Trp Asp Val Thr Pro Gly Lys	
280 285 290	
gcc att ctc gag cgc tcc gca gtg tat cga ttc caa gct cgc tgg gcc	1027
Ala Ile Leu Glu Arg Ser Ala Val Tyr Arg Phe Gln Ala Arg Trp Ala	
295 300 305	
cag gaa tgg cgc tcc gga aga gct ctc atc gca ggc gat gcc gct cac	1075
Gln Glu Trp Arg Ser Gly Arg Ala Leu Ile Ala Gly Asp Ala Ala His	
310 315 320 325	
ctc atg cca cct ttc gca ggt gaa ggc atg tgc gct ggc ctg aga gac	1123
Leu Met Pro Pro Phe Ala Gly Glu Gly Met Cys Ala Gly Leu Arg Asp	
330 335 340	
tca ctg gcg ttg gca tgg cgt ctt gat ttg gtg ctg agc gga aaa tca	1171
Ser Leu Ala Leu Ala Trp Arg Leu Asp Leu Val Leu Ser Gly Lys Ser	
345 350 355	
gat gat gca ttg cta gac acc tac gga gaa gaa cgc cgc gaa cac gtc	1219
Asp Asp Ala Leu Leu Asp Thr Tyr Gly Glu Glu Arg Arg Glu His Val	
360 365 370	
cac tac tac att gat ttc tcc atg gac ctg ggc aat gtc atc tgc att	1267
His Tyr Tyr Ile Asp Phe Ser Met Asp Leu Gly Asn Val Ile Cys Ile	
375 380 385	
act gat gaa gat gaa gca cgt ttg cgc gat gag cgc atg att aaa gag	1315
Thr Asp Glu Asp Glu Ala Arg Leu Arg Asp Glu Arg Met Ile Lys Glu	
390 395 400 405	
ctt gaa gca caa gac ggg gtc cct gtt aat acc gat gtc gca cac ttg	1363
Leu Glu Ala Gln Asp Gly Val Pro Val Asn Thr Asp Val Ala His Leu	
410 415 420	
gga ccg gga att tgg gat aaa gat tct tcc cat ggt ggc gag cta gcg	1411
Gly Pro Gly Ile Trp Asp Lys Asp Ser Ser His Gly Gly Glu Leu Ala	
425 430 435	
aag cag ggc ata gtg gaa tac caa ggt cga aag gcg cgt ttc gac gac	1459
Lys Gln Gly Ile Val Glu Tyr Gln Gly Arg Lys Ala Arg Phe Asp Asp	
440 445 450	
gca gtc ggc cgt ggc tgg gca gtt tta ggc ctc aac act gat cca cga	1507
Ala Val Gly Arg Gly Trp Ala Val Leu Gly Leu Asn Thr Asp Pro Arg	
455 460 465	
gaa gtg ctt gat gag gat tcg ctt gtg gca ctt gac gcc atc ggt gca	1555
Glu Val Leu Asp Glu Asp Ser Leu Val Ala Leu Asp Ala Ile Gly Ala	
470 475 480 485	
atc gtc gaa tca gta ggt gat gca act tcc gca gtt tta gat gtt gaa	1603
Ile Val Glu Ser Val Gly Asp Ala Thr Ser Ala Val Leu Asp Val Glu	
490 495 500	

ggt ctt tac act cgc tgg ctc aag gaa gcc ggg gca aca ttt att att 1651
 Gly Leu Tyr Thr Arg Trp Leu Lys Glu Ala Gly Ala Thr Phe Ile Ile
 505 510 515

acc cgc ccc gat ttc tac gtc tat tcc aca gca gtg gac gct gaa caa 1699
 Thr Arg Pro Asp Phe Tyr Val Tyr Ser Thr Ala Val Asp Ala Glu Gln
 520 525 530

ctt caa aca cag att aag cag cta tcg gat cta ctt cac ctc aac tca 1747
 Leu Gln Thr Gln Ile Lys Gln Leu Ser Asp Leu Leu His Leu Asn Ser
 535 540 545

gtt gtc gga gca taggagctaa aaatgtcttt aca 1782
 Val Val Gly Ala
 550

<210> 470

<211> 553

<212> PRT

<213> Corynebacterium glutamicum

<400> 470

Met Asn His Asp Ser Glu Cys Asp Leu Asp Asn Val Val Gln Phe Thr
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Ile Gln Glu Gly Leu Asp Pro Met Ser Pro Asn Asn Phe Asp Thr Asp
 20 25 30

Val Cys Ile Val Gly Gly Gly Pro Thr Gly Thr Leu Leu Ala Val Leu
 35 40 45

Leu Gly Gln Lys Gly His Arg Val Thr Ile Leu Glu Lys Trp Pro Thr
 50 55 60

Phe Tyr Glu Arg Pro Arg Ala Val Thr Phe Asp His Glu Ile Ala Arg
 65 70 75 80

Ile Leu Gly Tyr Ile Gly Ile Asp Ser Glu Asn Asp Glu Ala Ile Asp
 85 90 95

Tyr His Ser Asp Ser Tyr Asp Trp Lys Asn Ala Ala Gly Glu Thr Leu
 100 105 110

Leu Glu Val Asp Trp Thr Ser Met Thr Asp Ser Gly Trp Arg Thr Arg
 115 120 125

Tyr Trp Phe Tyr Gln Pro Glu Leu Glu Lys Arg Leu Arg Asp Leu Ala
 130 135 140

Leu Thr Met Asp Phe Val Asp Ile Arg Cys Gly Phe Thr Ala Val Gly
 145 150 155 160

Leu Ser Gln Asp Glu Asn Ser Ala Ile Ile His Gly Ile Val Thr Asp
 165 170 175

Thr Pro Glu Asn Ile Pro Ala Asp Ala Gln Arg Glu Asp Ile Arg Ala
 180 185 190

Lys Tyr Val Ile Gly Ala Asp Gly Ala Asn Ser Phe Val Arg Asn Ser
 195 200 205

Leu Gly Leu Glu Met Asn Asp Leu Gly Tyr Phe Phe Asp Trp Leu Ile
 210 215 220
 Leu Asp Leu Lys Pro Thr Gln Asp Ile Asp Tyr Gly Thr Asp His Trp
 225 230 235 240
 Gln Leu Cys Asp Pro Lys Arg Pro Thr Thr Ile Val Pro Gly Gly Pro
 245 250 255
 Gly Arg Arg Arg Trp Glu Phe Met Ala Leu Pro Gly Glu Asp Leu Lys
 260 265 270
 Glu Leu Ala Ser Glu Glu Ser Ala Trp Asn Leu Leu Glu Pro Trp Asp
 275 280 285
 Val Thr Pro Gly Lys Ala Ile Leu Glu Arg Ser Ala Val Tyr Arg Phe
 290 295 300
 Gln Ala Arg Trp Ala Gln Glu Trp Arg Ser Gly Arg Ala Leu Ile Ala
 305 310 315 320
 Gly Asp Ala Ala His Leu Met Pro Pro Phe Ala Gly Glu Gly Met Cys
 325 330 335
 Ala Gly Leu Arg Asp Ser Leu Ala Leu Ala Trp Arg Leu Asp Leu Val
 340 345 350
 Leu Ser Gly Lys Ser Asp Asp Ala Leu Leu Asp Thr Tyr Gly Glu Glu
 355 360 365
 Arg Arg Glu His Val His Tyr Tyr Ile Asp Phe Ser Met Asp Leu Gly
 370 375 380
 Asn Val Ile Cys Ile Thr Asp Glu Asp Glu Ala Arg Leu Arg Asp Glu
 385 390 395 400
 Arg Met Ile Lys Glu Leu Glu Ala Gln Asp Gly Val Pro Val Asn Thr
 405 410 415
 Asp Val Ala His Leu Gly Pro Gly Ile Trp Asp Lys Asp Ser Ser His
 420 425 430
 Gly Gly Glu Leu Ala Lys Gln Gly Ile Val Glu Tyr Gln Gly Arg Lys
 435 440 445
 Ala Arg Phe Asp Asp Ala Val Gly Arg Gly Trp Ala Val Leu Gly Leu
 450 455 460
 Asn Thr Asp Pro Arg Glu Val Leu Asp Glu Asp Ser Leu Val Ala Leu
 465 470 475 480
 Asp Ala Ile Gly Ala Ile Val Glu Ser Val Gly Asp Ala Thr Ser Ala
 485 490 495
 Val Leu Asp Val Glu Gly Leu Tyr Thr Arg Trp Leu Lys Glu Ala Gly
 500 505 510
 Ala Thr Phe Ile Ile Thr Arg Pro Asp Phe Tyr Val Tyr Ser Thr Ala
 515 520 525

Val Asp Ala Glu Gln Leu Gln Thr Gln Ile Lys Gln Leu Ser Asp Leu
 530 535 540

Leu His Leu Asn Ser Val Val Gly Ala
 545 550

<210> 471
 <211> 583
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(564)
 <223> RXA01126

<400> 471
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 Ser Ala Glu Ser Leu Pro Pro Thr Leu Phe Leu Lys Pro Pro Thr Ala
 1 5 10 15
 gtc acc gga cca gag tcc cca atc cga atc cct tcc ttt gcc acc aag 96
 Val Thr Gly Pro Glu Ser Pro Ile Arg Ile Pro Ser Phe Ala Thr Lys
 20 25 30
 gtg gaa ttc gaa ggt gag ctg gca gta gtt atc ggc aag ccc tgc aag 144
 Val Glu Phe Glu Gly Glu Leu Ala Val Val Ile Gly Lys Pro Cys Lys
 35 40 45
 aac gtc aag gct gat gac tgg aag tct gtc gtt ttg ggc ttc acc atc 192
 Asn Val Lys Ala Asp Asp Trp Lys Ser Val Val Leu Gly Phe Thr Ile
 50 55 60
 atc aac gac gtc tcc tcc cgt gac ctg cag ttc gct gac ggc cag tgg 240
 Ile Asn Asp Val Ser Ser Arg Asp Leu Gln Phe Ala Asp Gly Gln Trp
 65 70 75 80
 gca cgc gct aag ggc att gac acc ttc ggc ccc atc gga cca tgg att 288
 Ala Arg Ala Lys Gly Ile Asp Thr Phe Gly Pro Ile Gly Pro Trp Ile
 85 90 95
 gaa act gac atc aac tcc atc gac ttg gac aac ctg ccc atc aag gca 336
 Glu Thr Asp Ile Asn Ser Ile Asp Leu Asp Asn Leu Pro Ile Lys Ala
 100 105 110
 cgc ctg acc cac gac ggc gaa acc caa ttg aag cag gac tcc aac tcc 384
 Arg Leu Thr His Asp Gly Glu Thr Gln Leu Lys Gln Asp Ser Asn Ser
 115 120 125
 aac cag atg atc atg aag atg ggc gaa att atc gag ttc atc acc gcc 432
 Asn Gln Met Ile Met Lys Met Gly Glu Ile Ile Glu Phe Ile Thr Ala
 130 135 140
 tcc atg acc ctg ctg cca ggc gac gtt att gca acc ggt tct cca gca 480
 Ser Met Thr Leu Leu Pro Gly Asp Val Ile Ala Thr Gly Ser Pro Ala
 145 150 155 160
 ggc acc gaa gca atg gtt gac ggc gac tac atc gaa atc gaa att cca 528
 Gly Thr Glu Ala Met Val Asp Gly Asp Tyr Ile Glu Ile Glu Ile Pro
 165 170 175

ggc atc ggc aag ctg ggc aac cca gtt gtg gac gcc taaaatggat 574
 Gly Ile Gly Lys Leu Gly Asn Pro Val Val Asp Ala
 180 185

caccaccat 583

<210> 472
 <211> 188
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 472
 Ser Ala Glu Ser Leu Pro Pro Thr Leu Phe Leu Lys Pro Pro Thr Ala
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 Val Thr Gly Pro Glu Ser Pro Ile Arg Ile Pro Ser Phe Ala Thr Lys
 20 25 30
 Val Glu Phe Glu Gly Glu Leu Ala Val Val Ile Gly Lys Pro Cys Lys
 35 40 45
 Asn Val Lys Ala Asp Asp Trp Lys Ser Val Val Leu Gly Phe Thr Ile
 50 55 60
 Ile Asn Asp Val Ser Ser Arg Asp Leu Gln Phe Ala Asp Gly Gln Trp
 65 70 75 80
 Ala Arg Ala Lys Gly Ile Asp Thr Phe Gly Pro Ile Gly Pro Trp Ile
 85 90 95
 Glu Thr Asp Ile Asn Ser Ile Asp Leu Asp Asn Leu Pro Ile Lys Ala
 100 105 110
 Arg Leu Thr His Asp Gly Glu Thr Gln Leu Lys Gln Asp Ser Asn Ser
 115 120 125
 Asn Gln Met Ile Met Lys Met Gly Glu Ile Ile Glu Phe Ile Thr Ala
 130 135 140
 Ser Met Thr Leu Leu Pro Gly Asp Val Ile Ala Thr Gly Ser Pro Ala
 145 150 155 160
 Gly Thr Glu Ala Met Val Asp Gly Asp Tyr Ile Glu Ile Glu Ile Pro
 165 170 175
 Gly Ile Gly Lys Leu Gly Asn Pro Val Val Asp Ala
 180 185

<210> 473
 <211> 864
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(841)
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<400> 473

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cccttgtgca tatgatgaac attacgttag catgtctcac atg att aac aag agc 115
Met Ile Asn Lys Ser
1 5

att tct tcc act gct gaa gcg gtg gcc gat atc cca gac ggt gcg tcc 163
Ile Ser Ser Thr Ala Glu Ala Val Ala Asp Ile Pro Asp Gly Ala Ser
10 15 20

atc gcc gtc ggt ggt ttc ggc ctc gtg ggc atc ccc act gca ttg atc 211
Ile Ala Val Gly Gly Phe Gly Leu Val Gly Ile Pro Thr Ala Leu Ile
25 30 35

ctc gcc ctc cgc gaa caa ggc gca ggc gat ctg acc atc att tcc aac 259
Leu Ala Leu Arg Glu Gln Gly Ala Gly Asp Leu Thr Ile Ile Ser Asn
40 45 50

aac cta ggc acc gac ggt ttc ggc ctc gga ctg ttg ctt ttg gat aag 307
Asn Leu Gly Thr Asp Gly Phe Gly Leu Gly Leu Leu Leu Asp Lys
55 60 65

aag atc tcc aag tcc atc ggc tcc tac ctt ggc tcc aac aag gaa tat 355
Lys Ile Ser Lys Ser Ile Gly Ser Tyr Leu Gly Ser Asn Lys Glu Tyr
70 75 80 85

gca cgc cag tac ctg gaa gga gaa ctc acc gtc gag ttc acc ccg cag 403
Ala Arg Gln Tyr Leu Glu Gly Glu Leu Thr Val Glu Phe Thr Pro Gln
90 95 100

ggc acc ttg gct gaa cgc ctc cgc gca ggt ggc gcc ggc atc cct gcg 451
Gly Thr Leu Ala Glu Arg Leu Arg Ala Gly Gly Ala Gly Ile Pro Ala
105 110 115

ttt tac acc acc gca ggc gtg ggc acc cag gtc gca gaa ggc gga ctc 499
Phe Tyr Thr Thr Ala Gly Val Gly Thr Gln Val Ala Glu Gly Gly Leu
120 125 130

cca cag cgc tac aac acc gac ggc acc gtc gcc gtg gtg tcc cag cca 547
Pro Gln Arg Tyr Asn Thr Asp Gly Thr Val Ala Val Val Ser Gln Pro
135 140 145

aag gaa acc cgc gaa ttc aac ggc cag ctc tac gtc atg gaa gag ggc 595
Lys Glu Thr Arg Glu Phe Asn Gly Gln Leu Tyr Val Met Glu Glu Gly
150 155 160 165

atc cgc gcc gat tac gca ctc gtg cac gca cac aaa gca gat cgc ttt 643
Ile Arg Ala Asp Tyr Ala Leu Val His Ala His Lys Ala Asp Arg Phe
170 175 180

ggc aac ctg gtg ttc cgc aag acc gcg cag aac ttc aac cca gat gca 691
Gly Asn Leu Val Phe Arg Lys Thr Ala Gln Asn Phe Asn Pro Asp Ala
185 190 195

gca atg agc ggc aag atc acc att gct cag gtc gag cac ttt gta gac 739
Ala Met Ser Gly Lys Ile Thr Ile Ala Gln Val Glu His Phe Val Asp
200 205 210

gaa ctc cac cca gat gag atc gat ctg cca gga att tac gtc aac cgc 787
Glu Leu His Pro Asp Glu Ile Asp Leu Pro Gly Ile Tyr Val Asn Arg

215 220 225

gtc gtc cac gtt gga ccg cag gaa acc gga atc gaa aac agg acg gtg 835
 Val Val His Val Gly Pro Gln Glu Thr Gly Ile Glu Asn Arg Thr Val
 230 235 240 245

tct aac taatgacttg ggatcataac caa 864
 Ser Asn

<210> 474
 <211> 247
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 474
 Met Ile Asn Lys Ser Ile Ser Ser Thr Ala Glu Ala Val Ala Asp Ile
 1 5 10 15

Pro Asp Gly Ala Ser Ile Ala Val Gly Gly Phe Gly Leu Val Gly Ile
 20 25 30

Pro Thr Ala Leu Ile Leu Ala Leu Arg Glu Gln Gly Ala Gly Asp Leu
 35 40 45

Thr Ile Ile Ser Asn Asn Leu Gly Thr Asp Gly Phe Gly Leu Gly Leu
 50 55 60

Leu Leu Leu Asp Lys Lys Ile Ser Lys Ser Ile Gly Ser Tyr Leu Gly
 65 70 75 80

Ser Asn Lys Glu Tyr Ala Arg Gln Tyr Leu Glu Gly Glu Leu Thr Val
 85 90 95

Glu Phe Thr Pro Gln Gly Thr Leu Ala Glu Arg Leu Arg Ala Gly Gly
 100 105 110

Ala Gly Ile Pro Ala Phe Tyr Thr Thr Ala Gly Val Gly Thr Gln Val
 115 120 125

Ala Glu Gly Gly Leu Pro Gln Arg Tyr Asn Thr Asp Gly Thr Val Ala
 130 135 140

Val Val Ser Gln Pro Lys Glu Thr Arg Glu Phe Asn Gly Gln Leu Tyr
 145 150 155 160

Val Met Glu Glu Gly Ile Arg Ala Asp Tyr Ala Leu Val His Ala His
 165 170 175

Lys Ala Asp Arg Phe Gly Asn Leu Val Phe Arg Lys Thr Ala Gln Asn
 180 185 190

Phe Asn Pro Asp Ala Ala Met Ser Gly Lys Ile Thr Ile Ala Gln Val
 195 200 205

Glu His Phe Val Asp Glu Leu His Pro Asp Glu Ile Asp Leu Pro Gly
 210 215 220

Ile Tyr Val Asn Arg Val Val His Val Gly Pro Gln Glu Thr Gly Ile
 225 230 235 240

Glu Asn Arg Thr Val Ser Asn
245

<210> 475
<211> 1629
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1606)
<223> RXA00772

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gaaaaatttg aaaaagtccg attacctgag gaggtattca atg tct gat cgc att 115
Met Ser Asp Arg Ile
1 5
gct tca gaa aag ctg cgc tcc aag ctc atg tcc gcc gac gag gcg gca 163
Ala Ser Glu Lys Leu Arg Ser Lys Leu Met Ser Ala Asp Glu Ala Ala
10 15 20
cag ttt gtt aac cac ggt gac aag gtt ggt ttc tcc ggc ttc acc ggc 211
Gln Phe Val Asn His Gly Asp Lys Val Gly Phe Ser Gly Phe Thr Gly
25 30 35
gct ggc tac cca aag gca ctg cct acg gca atc gct aac cgg gct aaa 259
Ala Gly Tyr Pro Lys Ala Leu Pro Thr Ala Ile Ala Asn Arg Ala Lys
40 45 50
gaa gca cac ggt gca ggc aac gac tac gca atc gac ctg ttc act ggc 307
Glu Ala His Gly Ala Gly Asn Asp Tyr Ala Ile Asp Leu Phe Thr Gly
55 60 65
gca tcg acc gcc cct gac tgc gat ggc gta ctt gca gaa gct gac gct 355
Ala Ser Thr Ala Pro Asp Cys Asp Gly Val Leu Ala Glu Ala Asp Ala
70 75 80 85
atc cgc tgg cgc atg cca tac gca tct gat cca atc atg cgt aac aag 403
Ile Arg Trp Arg Met Pro Tyr Ala Ser Asp Pro Ile Met Arg Asn Lys
90 95 100
atc aac tcc ggc tcc atg gga tac tcc gat atc cac ctg tcc cac tcc 451
Ile Asn Ser Gly Ser Met Gly Tyr Ser Asp Ile His Leu Ser His Ser
105 110 115
ggc cag cag gtt gaa gag ggc ttc ttc ggc cag ctc aac gta gct gtc 499
Gly Gln Gln Val Glu Glu Gly Phe Phe Gly Gln Leu Asn Val Ala Val
120 125 130
att gaa atc acc cgc atc act gaa gag ggc tac atc atc cct tct tcc 547
Ile Glu Ile Thr Arg Ile Thr Glu Glu Gly Tyr Ile Ile Pro Ser Ser
135 140 145
tcc gtg ggt aac aac gtt gag tgg ctc aac gct gca gag aag gtc atc 595
Ser Val Gly Asn Asn Val Glu Trp Leu Asn Ala Ala Glu Lys Val Ile
150 155 160 165

ctc gag gtt aac tct tgg cag tct gaa gac ctc gaa ggt atg cac gac Leu Glu Val Asn Ser Trp Gln Ser Glu Asp Leu Glu Gly Met His Asp 170 175 180	643
atc tgg tct gtt cct gcc ctg cca aac cgc att gcc gtg cca atc aac Ile Trp Ser Val Pro Ala Leu Pro Asn Arg Ile Ala Val Pro Ile Asn 185 190 195	691
aag cca ggc gac cgc atc ggt aag acc tac atc gag ttc gac acc gac Lys Pro Gly Asp Arg Ile Gly Lys Thr Tyr Ile Glu Phe Asp Thr Asp 200 205 210	739
aag gtt gtt gct gtt gtt gag acc aac acc gca gac cgc aac gca cca Lys Val Val Ala Val Val Glu Thr Asn Thr Ala Asp Arg Asn Ala Pro 215 220 225	787
ttc aag cct gtc gac gac atc tct aag aag atc gct ggc aac ttc ctc Phe Lys Pro Val Asp Asp Ile Ser Lys Lys Ile Ala Gly Asn Phe Leu 230 235 240 245	835
gac ttc ctg gaa agc gaa gtt gct gca ggt cgc ctg tcc tac gcg ggc Asp Phe Leu Glu Ser Glu Val Ala Ala Gly Arg Leu Ser Tyr Ala Gly 250 255 260	883
tac atc atg cag tcc ggc gtg ggc aac gtg cct aac gcg gtg atg gca Tyr Ile Met Gln Ser Gly Val Gly Asn Val Pro Asn Ala Val Met Ala 265 270 275	931
ggc ctg ctg gaa tcc aag ttt gag aac atc cag gcc tac acc gaa gtt Gly Leu Leu Glu Ser Lys Phe Glu Asn Ile Gln Ala Tyr Thr Glu Val 280 285 290	979
atc cag gac ggc atg gtg gac ctc atc gac gcc ggc aag atg acc gtt Ile Gln Asp Gly Met Val Asp Leu Ile Asp Ala Gly Lys Met Thr Val 295 300 305	1027
gca tcc gca act tcc ttc tcc ctg tct cct gag tac gca gag aag atg Ala Ser Ala Thr Ser Phe Ser Leu Ser Pro Glu Tyr Ala Glu Lys Met 310 315 320 325	1075
aac aac gag gct aag cgt tac cgc gag tcc att atc ctg cgc cca cag Asn Asn Glu Ala Lys Arg Tyr Arg Glu Ser Ile Ile Leu Arg Pro Gln 330 335 340	1123
cag atc tct aac cac cca gag gtc atc cgc cgc gtt ggc ctg atc gcc Gln Ile Ser Asn His Pro Glu Val Ile Arg Arg Val Gly Leu Ile Ala 345 350 355	1171
acc aac ggt ctc atc gag gct gac att tac ggc aac gtc aac tcc acc Thr Asn Gly Leu Ile Glu Ala Asp Ile Tyr Gly Asn Val Asn Ser Thr 360 365 370	1219
aac gtt tct ggc tcc cgc gtc atg aac ggc atc ggc ggc tcc ggc gac Asn Val Ser Gly Ser Arg Val Met Asn Gly Ile Gly Gly Ser Gly Asp 375 380 385	1267
ttc acc cgt aac ggc tac atc tcc agc ttc atc acc cct tca gag gca Phe Thr Arg Asn Gly Tyr Ile Ser Ser Phe Ile Thr Pro Ser Glu Ala 390 395 400 405	1315

aag ggc ggc gca atc tct gcg atc gtt cct ttc gca tcc cac atc gac 1363
 Lys Gly Gly Ala Ile Ser Ala Ile Val Pro Phe Ala Ser His Ile Asp
 410 415 420

cac acc gag cac gat gtc atg gtt gtt atc tct gag tac ggt tac gca 1411
 His Thr Glu His Asp Val Met Val Val Ile Ser Glu Tyr Gly Tyr Ala
 425 430 435

gac ctt cgt ggt ctg gct cca cgt gag cgc gtt gcc aag atg atc ggc 1459
 Asp Leu Arg Gly Leu Ala Pro Arg Glu Arg Val Ala Lys Met Ile Gly
 440 445 450

ctg gct cac cct gat tac cgc cca ctg ctc gag gag tac tac gct cgc 1507
 Leu Ala His Pro Asp Tyr Arg Pro Leu Leu Glu Glu Tyr Tyr Ala Arg
 455 460 465

gca acc tcc ggt gac aac aag tac atg cag acc cct cat gat ctt gca 1555
 Ala Thr Ser Gly Asp Asn Lys Tyr Met Gln Thr Pro His Asp Leu Ala
 470 475 480 485

acc gcg ttt gat ttc cac atc aac ctg gct aag aac ggc tcc atg aag 1603
 Thr Ala Phe Asp Phe His Ile Asn Leu Ala Lys Asn Gly Ser Met Lys
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gca taagtttttt cttggttttag aaa 1629
 Ala

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Ser Gly Phe Thr Gly Ala Gly Tyr Pro Lys Ala Leu Pro Thr Ala Ile
 35 40 45

Ala Asn Arg Ala Lys Glu Ala His Gly Ala Gly Asn Asp Tyr Ala Ile
 50 55 60

Asp Leu Phe Thr Gly Ala Ser Thr Ala Pro Asp Cys Asp Gly Val Leu
 65 70 75 80

Ala Glu Ala Asp Ala Ile Arg Trp Arg Met Pro Tyr Ala Ser Asp Pro
 85 90 95

Ile Met Arg Asn Lys Ile Asn Ser Gly Ser Met Gly Tyr Ser Asp Ile
 100 105 110

His Leu Ser His Ser Gly Gln Gln Val Glu Glu Gly Phe Phe Gly Gln
 115 120 125

Leu Asn Val Ala Val Ile Glu Ile Thr Arg Ile Thr Glu Glu Gly Tyr
 130 135 140

Ile Ile Pro Ser Ser Ser Val Gly Asn Asn Val Glu Trp Leu Asn Ala
 145 150 155 160
 Ala Glu Lys Val Ile Leu Glu Val Asn Ser Trp Gln Ser Glu Asp Leu
 165 170 175
 Glu Gly Met His Asp Ile Trp Ser Val Pro Ala Leu Pro Asn Arg Ile
 180 185 190
 Ala Val Pro Ile Asn Lys Pro Gly Asp Arg Ile Gly Lys Thr Tyr Ile
 195 200 205
 Glu Phe Asp Thr Asp Lys Val Val Ala Val Val Glu Thr Asn Thr Ala
 210 215 220
 Asp Arg Asn Ala Pro Phe Lys Pro Val Asp Asp Ile Ser Lys Lys Ile
 225 230 235 240
 Ala Gly Asn Phe Leu Asp Phe Leu Glu Ser Glu Val Ala Ala Gly Arg
 245 250 255
 Leu Ser Tyr Ala Gly Tyr Ile Met Gln Ser Gly Val Gly Asn Val Pro
 260 265 270
 Asn Ala Val Met Ala Gly Leu Leu Glu Ser Lys Phe Glu Asn Ile Gln
 275 280 285
 Ala Tyr Thr Glu Val Ile Gln Asp Gly Met Val Asp Leu Ile Asp Ala
 290 295 300
 Gly Lys Met Thr Val Ala Ser Ala Thr Ser Phe Ser Leu Ser Pro Glu
 305 310 315 320
 Tyr Ala Glu Lys Met Asn Asn Glu Ala Lys Arg Tyr Arg Glu Ser Ile
 325 330 335
 Ile Leu Arg Pro Gln Gln Ile Ser Asn His Pro Glu Val Ile Arg Arg
 340 345 350
 Val Gly Leu Ile Ala Thr Asn Gly Leu Ile Glu Ala Asp Ile Tyr Gly
 355 360 365
 Asn Val Asn Ser Thr Asn Val Ser Gly Ser Arg Val Met Asn Gly Ile
 370 375 380
 Gly Gly Ser Gly Asp Phe Thr Arg Asn Gly Tyr Ile Ser Ser Phe Ile
 385 390 395 400
 Thr Pro Ser Glu Ala Lys Gly Gly Ala Ile Ser Ala Ile Val Pro Phe
 405 410 415
 Ala Ser His Ile Asp His Thr Glu His Asp Val Met Val Val Ile Ser
 420 425 430
 Glu Tyr Gly Tyr Ala Asp Leu Arg Gly Leu Ala Pro Arg Glu Arg Val
 435 440 445
 Ala Lys Met Ile Gly Leu Ala His Pro Asp Tyr Arg Pro Leu Leu Glu
 450 455 460

Glu Tyr Tyr Ala Arg Ala Thr Ser Gly Asp Asn Lys Tyr Met Gln Thr
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Pro His Asp Leu Ala Thr Ala Phe Asp Phe His Ile Asn Leu Ala Lys
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Asn Gly Ser Met Lys Ala
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 Met Asn Gly Ile Gly
 1 5
 ggc tcg ggc gat ttc acg cgt aac gcc ttt gct tcc aca ttt atc tct 163
 Gly Ser Gly Asp Phe Thr Arg Asn Ala Phe Ala Ser Thr Phe Ile Ser
 10 15 20
 ccc tcg gca gcc aaa gtt gat gcg att tcc gcg att gtg cct ttc gcg 211
 Pro Ser Ala Ala Lys Val Asp Ala Ile Ser Ala Ile Val Pro Phe Ala
 25 30 35
 tcc cat atc gat cac acg gaa cat gat gcg atg gtt gtc att act gaa 259
 Ser His Ile Asp His Thr Glu His Asp Ala Met Val Val Ile Thr Glu
 40 45 50
 tat ggc tac gca gac ctg cgc ggg cta tcg cca aaa caa cga gtc ccc 307
 Tyr Gly Tyr Ala Asp Leu Arg Gly Leu Ser Pro Lys Gln Arg Val Pro
 55 60 65
 aaa atg att gcc atc gcc cac ccg gac tat cga cca ctg ctg gaa gca 355
 Lys Met Ile Ala Ile Ala His Pro Asp Tyr Arg Pro Leu Leu Glu Ala
 70 75 80 85
 tac ttt gac cgg gcg ctg aac agt gct gat tcc tat cag cac acc ctg 403
 Tyr Phe Asp Arg Ala Leu Asn Ser Ala Asp Ser Tyr Gln His Thr Leu
 90 95 100
 cat gat ctg cgc acc gcc ttc gat ttc cat aat cgc ttg aac tca caa 451
 His Asp Leu Arg Thr Ala Phe Asp Phe His Asn Arg Leu Asn Ser Gln
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 gga acc atg aaa atc gaa aaa gca tagtgctttt cgacgagccc tcc 498
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Met Asn Gly Ile Gly Gly Ser Gly Asp Phe Thr Arg Asn Ala Phe Ala
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Ser Thr Phe Ile Ser Pro Ser Ala Ala Lys Val Asp Ala Ile Ser Ala
 20 25 30

Ile Val Pro Phe Ala Ser His Ile Asp His Thr Glu His Asp Ala Met
 35 40 45

Val Val Ile Thr Glu Tyr Gly Tyr Ala Asp Leu Arg Gly Leu Ser Pro
 50 55 60

Lys Gln Arg Val Pro Lys Met Ile Ala Ile Ala His Pro Asp Tyr Arg
 65 70 75 80

Pro Leu Leu Glu Ala Tyr Phe Asp Arg Ala Leu Asn Ser Ala Asp Ser
 85 90 95

Tyr Gln His Thr Leu His Asp Leu Arg Thr Ala Phe Asp Phe His Asn
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Arg Leu Asn Ser Gln Gly Thr Met Lys Ile Glu Lys Ala
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17

B
(cont.)